TRANSMISSION DYNAMICS OF MYCOBACTERIUM TUBERCULOSIS IN SOUTHERN REGION OF ETHIOPIA

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List of abbreviations

AFB	Acid Fast Bacilli
AIDS	Acquired Immunodeficiency Syndrome
AAU	Addis Ababa University
AHRI	Armauer Hansen Research Institute
DOTS	Directly Observed Treatment Short course
DST	Drug-Susceptibility Testing
FMOH	Federal Ministry of Health
HDA	Health Development Army
HIV	Human Immunodeficiency Virus
INH	Isoniazid
IS	Insertion Sequences
LMICs	Low- and Middle-Income Countries
LSHTM	London School of Hygiene and Tropical Medicine
MDR-TB	Multi Drug Resistant Tuberculosis
MIRU- VTNR	Mycobacterial Interspersed Repetitive Units-Variable-number Tandem Repeats
MTA	Material Transfer Agreement
PTB	Pulmonary Tuberculosis
RD	Region of Difference
RFLP	Restriction Fragment Length Polymorphism
RPM	Rifampicin
SNPs	Single Nucleotide Polymorphisms
SSA	Sub Saharan Africa
TB	Tuberculosis
TDR	Totally Drug Resistant
WHO	World Health Organization
WGS	Whole genome sequencing
XDR- TB	Extensively Drug Resistant
XXDR-TB	Extremely drug resistant

Abstract

Background: Tuberculosis (TB) is a major global public health problem with countries in sub-Saharan Africa (SSA) including Ethiopia being most affected by the disease. Understanding the epidemiology of TB and the development and spread of drug-resistant TB is limited by scarce molecular epidemiologic data in SSA including Ethiopia. In terms of epidemiology of TB, control of TB in prisons is an important public health priority. In some settings, prisons have been recognized as a reservoir and sites of transmission for TB. Additionally, the spread of TB in rural settings deserves further attention. In rural settings, several factors may contribute to enhanced transmission of TB including either missed diagnosis or delays in diagnosis.

Objective: To describe the molecular epidemiology and drug resistance pattern of TB to better understand the transmission of TB and the development and spread of drug resistance in different settings of Southern Ethiopia.

Methods: Three studies were conducted, all using a cross-sectional design: a prison study in Hawassa Prison, a health facility-based study at nine health facilities in and around Shashemene areas of Western Arisi Zone (Oromia region) and a community-based study in the rural areas of Hawassa Zuria Woreda (Sidama Zone, Southern Region). In the prison study, incarcerated individuals were screened for TB using a symptom screen; those with a cough of ≥2 weeks had spot and morning sputum samples collected for AFB smear microscopy and molecular diagnostic testing (Xpert MTB/RIF). The study was conducted from June 15 through July 13, 2015. The health facility study was conducted among sputum smear positive patients with TB visiting nine diagnostic facilities in Southern Ethiopia. Three consecutive sputum samples (spot-morning-spot) per patient were examined using AFB smear microscopy with all smear positive specimens also having AFB cultures performed. Mtb isolates had drug susceptibility testing (DST) performed using the indirect proportion method and were genotyped with RD9 deletion typing and spoligotyping. Spoligotyping International Types (SIT) and sub-lineages (clades) were assigned according to the SITVITWEB data base. Geographic information system (GIS) was used to map

source sites of strains. Whole genome sequencing (WGS) was done on selected Mtb isolates. The study was conducted from June 2015 to May 2016. The population-based survey was conducted in six *Kebeles* (the lowest administrative units) of Hawassa Zuria Woreda using a community-based active case finding (ACF) strategy. Volunteer women community workers led a symptom screening program to identify community members with TB. Individuals with cough ≥ 2 weeks were asked to provide two sputum samples (spot and morning) for diagnostic testing for TB. AFB smear microscopy and culture and Xpert MTB/RIF were performed. The study was conducted from May 08, 2016 through June 09, 2016.

Results: Among 2068 prisoners, 372 (18%) had a positive cough screen. The median age of these 372 persons was 23 years, 97% were male and 63% were from urban areas. Among them, 8/372 (2%) had a positive AFB sputum smear microscopy result and 31/372 (8%) had a positive Xpert TB/RIF. The point prevalence of pulmonary TB at the prison was 1748 per 100,000 population as defined by Xpert TB/RIF. In the health facility study, among 250 newly diagnosed patients with TB, 154 (52%) were male and 143 (57%) came from rural areas. The prevalence of HIV co-infection was 4%. A total of 230 isolates were obtained from 250 sputum cultures. All 230 isolates were *M. tuberculosis* strains belonging to three lineages: Euro-American, 187 (81%); East-African-Indian, 31 (14%); and Lineage 7 (Ethiopian lineage), 8 (4%). The 230 isolates could be categorized into 65 different spoligotype patterns, of which 36 (55.0%) were already known in the international data base and 29 (45.0%) were new patterns (orphans). The dominant spoligotypes were SIT149 (21%), SIT53 (19%) and new strains (16%). One hundred ninety-three (84%) isolates were clustered into 29 spoligotype patterns and the remaining (37, 16%) strains fell into single spoligotypes, and clustering of strains by geographic locations was observed. DST revealed that 14% of Mtb isolates tested were resistant to ≥ 1 first line anti-TB drugs and 11% to isoniazid. SIT 149 was the most prevalent spoligotype among drug resistant isolates. WGS analysis identified different drug resistance mutations in Mtb isolates including on pyrazinamide which was not detected by phenotypic DST. MDR-TB was not identified both by phynotipic DST and WGS analysis. For the community study, all 24,517 adults in the study area had a symptom screen performed using 350 health development armies (HDAs); 544 (2.2%) had cough ≥ 2 weeks. Among persons with a positive symptom screen, 13/544

(2.4%) had a positive sputum AFB smear microscopy, 13/544 (2.4%) a positive culture and 32/544 (5.8%) a positive Xpert MTB/RIF test (including two with rifampin resistance identified). Overall, 34/544 TB cases (6%) were identified by culture and/or Xpert, which corresponds to a prevalence of 139 per 100,000 population (95% CI: 96-194).

Conclusion: Epidemiological data on TB including drug resistance in different settings is vital to look at the problem from different perspectives. A high prevalence of TB was detected among inmates at a large Ethiopian prison. Active case finding using cough symptom screening in combination with the Xpert test has high utility as a potential tool to interrupt transmission of *M. tuberculosis* in correctional facilities in high burden, low- and middle-income countries. The health facility study identified a heterogeneous pool of *M. tuberculosis* strains with several clusters including lineage 7 strains circulating in Southern Ethiopia. The presence of several clusters and of new strains of *M. tuberculosis* suggests recent transmission of TB, including of drug-resistant strains in southern Ethiopia. This calls for regular surveillance of drug susceptibility and wider monitoring and geospatial analysis of transmission trends to control TB in the southern Ethiopia. The community study demonstrated the capability of community health workers (volunteer and paid) to rapidly conduct a large-scale population TB screening evaluation and highlighted the high yield of such a program to detect previously undiagnosed cases when combined with Xpert MTB/RIF testing. This could be a model to implement in other similar settings. In general, the results of the three study findings could significantly impact the TB control program of the country in improving the prevention and control of the disease and add knowledge to the science.

CHAPTER I

INTRODUCTION

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1.1. Overview of Tuberculosis

Tuberculosis (TB) is an infectious disease caused by *Mycobacterium tuberculosis*, rod-shaped bacteria (bacillus). It is a type of "acid-fast" bacteria due to its staining characteristics in laboratory testing. Occasionally, the disease can also be caused by *Mycobacterium bovis* and *Mycobacterium africanum*. It is most commonly transmitted by inhalation of aerosolized droplet nuclei, which are discharged into the air when somebody with untreated sputum-positive pulmonary TB coughs or sneezes. It can also be transmitted by consumption of raw milk containing *Mycobacterium bovis* (Bates, 1980, Harries and Dye, 2006).

The risk of infection depends on the extent of an individual's exposure to droplet nuclei and on host susceptibility to infection. Infection risk is highest when a susceptible individual has close, prolonged, indoor exposure to a person with sputum smear-positive pulmonary TB (Loudon and Spohn, 1969, Grzybowski et al., 1975, Harries and Dye, 2006). TB affects individuals of all ages and sexes, and occurs in all countries. However, the age group between 15 and 54 years (which is a person's productive age period) is the main group affected by TB. Poverty, malnutrition and over-crowded living conditions are well known factors which increase the risk of developing active TB. Additionally, poor education, pollution and poor sanitation are some of the social issues that enhance TB risk (FMOH, 2016, Pezzella, 2019).

Human immunodeficiency virus **(**HIV) infection has been identified as a major risk factor for developing TB. HIV increases susceptibility to infection with *M. tuberculosis*, the risk of progression to TB disease, and the incidence and prevalence of TB. The life time risk of developing TB in people living with HIV is 20 times higher compared to HIV negative people (Melkamu et al., 2013), and HIV/TB co-infected patients have a high case fatality rate of 16–35%, which is ~4 times higher than individuals without HIV (Mukadi et al., 2001). HIV/TB co-infection also increases the likelihood of re-infections and TB relapses. In a population where TB/HIV is common, health services struggle to cope with the large

and rising number of TB. HIV/AIDS has a number of negative impacts on TB patients and national TB control programs (Bartlett, 2007, Friedland et al., 2007)**.** The emergence and growing incidences of drug-resistant TB including (DR-TB), MDR-TB (multidrug resistant), XDR-TB (extensively drug resistant), XXDR-TB (extremely drug resistant), and TDR-TB (totally drug resistant), represents a growing threat to public health and economic growth and poses another burden to TB control programmes (Gandhi et al., 2010, Pezzella, 2019).

In general, it is well recognized that the social characteristics of human populations (Lonnroth et al., 2009), host genetics (Abel et al., 2014), co-morbidities and environmental conditions such as the quality of TB control programs are crucial determinants of TB (Dye et al., 2009). However in addition to host and environmental conditions, during recent years it has become increasingly evident that the genetic diversity of the pathogen may also play a role in the outcome of TB infection and disease (Comas and Gagneux, 2009).

1.2. Genus Mycobacterium

Mycobacteria are curved rods that are acid fast and resistant to acids, alkalis and dehydration. The cell wall is complex and contains glycolipids. Growth on enriched media is very slow, with doubling times of ~18 to 24 hours which is why clinical isolates may require 4 to 6 weeks to grow. Mycobacteria are speculated to have existed as early as 150 million years ago, in the Jurassic period (Hayman, 1984). They are ubiquitous, occurring in every habitat and ecosystem of the world, except for the Polar Regions. *Mycobacterium leprae* was discovered as the first representative of the group under the name of *Bacillus leprae*, by Hansen in 1875 (Hansen, 1875) and in 1882 *Mycobacterium tuberculosis* was discovered by Robert Koch (Stead, 2001).

The genus *Mycobacterium* currently includes a total of 169 distinct species which are divided up into three major groups including: *Mycobacterium tuberculosis* complex (MTBC), *Mycobacterium leprae* and non-tuberculous mycobacteria (NTM) (Jagielski et al., 2016). Members of the MTBC are the causative agents of TB. They are strict, intracellular pathogens of humans and animals without any defined environmental reservoirs (Jagielski et al., 2016). *M. leprae*, which is also another obligate intracellular pathogen of human from the genus mycobacteria, causes leprosy in humans (Jagielski et al., 2016). While MTBC and

M. leprae are obligate pathogens, most NTM species are environmental organisms. Despite being free living saprophytes, NTM act as opportunistic pathogen causing a wide variety of clinical conditions in immune-compromised patients (Falkinham, 2002). The most prominent pathogenic NTM species include *M. avium* complex (MAC) and *M. kansasii*, both of which are most commonly associated with pulmonary disease (Daley and Griffith, 2010).

MTBC are closely related at the DNA level sharing 99.9% DNA sequence identity (Brites and Gagneux, 2015) and identical 16S rRNA gene sequences, but they differ in phenotypes and host preference (Brosch et al., 2000, Sreevatsan et al., 1997a). The MTBC includes the human-adapted strains *M. tuberculosis*, *M. africanum* and *M. cannetii* (Gutierrez et al., 2005). The MTBC also includes strains specifically adapted to infect domestic and wild animals. *M. bovis* is a pathogen of cattle*, M. microti* is a pathogen of rodents, *M. pinnipedii* causes disease in sea lions and seals, *M. caprae* is a pathogen of sheep and goats, *M. mungi* was isolated from mongoose (Alexander et al., 2010, Mostowy and Behr, 2005). Some of those animal-adapted lineages have zoonotic potential for humans (Jagielski et al., 2016). All members of the MTBC are thought to have arisen from clonal expansion of a single common ancestor (Brosch et al., 2002).

1.2.1. MTBC genome

The genome of MTBC is composed of the resistant lipid-rich cell wall and a high proportion of guanine and cytosine in their DNA (G-C content of 65%), which increases the stability of the genome (Sreevatsan et al., 1997a). While the members of the MTBC display diverse phenotypic characteristics and host ranges, their genome is highly conserved (genetically highly compact) and allelic polymorphisms are extremely rare among the members. They represent an extreme example of interspecies genetic homogeneity, with about synonymous nucleotide polymorphisms of 0.01- 0.03% (Mathema et al., 2006) and no significant evidence for horizontal genetic transfer between genomes, unlike most bacterial pathogens (Mathema et al., 2006).The absence of horizontal genetic exchange among MTBC members suggests their propagation seems to be clonal. However, some studies showed the existence of frequent horizontal genetic transfer in *M. canettii* which makes the bacterium to show a

bigger genetic diversity than other MTBC members. This horizontal exchange could occur also between *M. canetti* and *M. tuberculosis* (Koeck et al., 2011, Supply et al., 2013). Although horizontal gene transfer between MTBC and *M. canettii* has been detected (Rosas-Magallanes et al., 2006), the population structure within MTBC is largely clonal (Nicol and Wilkinson, 2008, Sreevatsan et al., 1997a). Even though, the MTBC genome is highly restricted (conserved) in relation to other bacterial pathogens, this monomorphic species does have polymorphic genomic regions which attributes for strains diversity among MTBC (Sreevatsan et al., 1997a).

1.2.2. Genomic diversity in MTBC

Genetic diversity within bacterial species is usually generated by mutations and/or by the exchange of genetic material such as plasmids. The process of horizontal gene transfer (HGT) is thought to be an important driver of bacterial evolution in both pathogenic and non-pathogenic bacteria (Becq et al., 2007). Horizontally transferred genes can be acquired in clusters known as genomic islands or pathogenecity islands. In the case of *M. tuberculosis*, there is evidence of ancient gene transfer events that may have taken place in a progenitor tubercle bacilli pool before the clonal expansion that gave rise to the MTBC (Gutierrez et al., 2005). One of these events involved the Rv0986-8 virulence operon (Rosas-Magallanes et al., 2006) that could have originated from genetic exchange between an environmental bacillus ancestor and other bacterial species (Nicol and Wilkinson, 2008). In the absence of recent events of HGT, modern *M. tuberculosis* lineages evolve essentially by mutations that alter its genome, resulting in single nucleotide polymorphism (SNPs) and large sequence polymorphism (LSPs), such as deletions and insertions, the latter mainly mediated by transposition of the IS*6110* insertion element (that cause genetic diversity in MTBC). Although allelic variation in MTBC organisms is quite restricted when compared with other pathogenic bacteria (Sreevatsan et al., 1997a), there is a growing recognition that there is substantial genetic diversity among isolates (due to genetic diversity in the MTBC genome).

1.2.2.1. Single nucleotide polymorphism (SNPs) in MTBC

Single nucleotide polymorphism (SNPs) represent single nucleotide differences between at least two DNA sequences. SNPs are the most common form of genetic variation in MTBC, after insertions and deletions (InDels). Depending on their position in the genome, SNPs can be either coding or non-coding and most of the SNPs in MTBC are in coding regions of the genome. Coding SNPs can be either synonymous (sSNP) or non-synonymous (nsSNP). In average nsSNPs are likely to have a stronger effect on the organism's fitness and will therefore be under a stronger selective pressure than sSNPs (Namouchi et al., 2012, Hershberg and Petrov, 2010). Up to two thirds of SNPs in MTBC are nsSNP, which is unlike most other organisms in which sSNPs predominate (Wheeler et al., 2008). Together with other bacterial pathogens such as *Yersinia pestis*, *Bacillus anthracis*, *Mycobacterium leprae* or *Salmonella enterica serovar Typhi*, MTBC has been referred to as "genetically monomorphic", even though MTBC harbors significantly more variation than other monomorphic bacteria (Achtman, 2008).

The large majority of SNPs in MTBC occur as singletons (variants that only occur in a single strain) (Hershberg et al., 2008, Pepperell et al., 2010). The comparably low frequency of SNPs and limited ongoing horizontal gene transfer in MTBC result in low levels of homoplasy i.e. the independent occurrence of the same SNP in phylogenetically unrelated strains (Comas et al., 2010, Hershberg et al., 2008). Hence, SNPs represent robust markers for inferring phylogenies and for strain classification (Gagneux and Small, 2007). SNPs can also be used to measure evolutionary distances between strains, i.e. to estimate the time of divergence of strains from their genetic distance, if a mutation rate is known (Ford et al., 2011). In addition to being useful phylogenetic markers, SNPs carry functional information. The best characterized SNPs in MTBC are drug resistance conferring mutations. Drug resistance in MTBC is largely caused by single nucleotide mutations (Musser, 1995, Telenti, 1997, Ramaswamy and Musser, 1998, Riska et al., 2000).

1.2.2.2. Large Sequence Polymorphisms (LPS)

LSPs, which is also known as regions of difference (RDs) includes both genomic insertions and deletions (Faksri et al., 2016) and have been identified as one of the main sources of genomic variability in MTBC. Large deletions have been shown to group closely related

strains and have been associated with phylogeographical lineages, suggesting that a deletion event is specific to a particular lineage (Tsolaki et al., 2004). Some LSPs occur rarely in the population and could have arisen from random genomic events and then become associated with a particular phylogenetic lineage (Alland et al., 2007). In contrast, some LSPs are present in multiple strains from different lineages, as a result of selective pressure, and are not necessarily associated with particular groups (Alland et al., 2007). Because on-going horizontal gene exchange is rare in MTBC, LSPs are essentially irreversible, making them ideal phylogenetic markers for strain classification (Coscolla and Gagneux, 2014). The two LSPs forms; deletion and insertions will be discussed below.

1.2.2.2.1. Genomic deletions

Large genomic deletions are a substantial source of genomic diversity within MTBC. Genomic deletions can result from transposition of mobile genetic elements. In addition, many genomic deletions occur through unknown mechanisms (Tsolaki et al., 2004). Region of differences (RDs) have been described in numerous surveys as important markers for molecular epidemiology of TB (Tsolaki et al., 2005). **Table 1.1** below depicts the different types of deletions of RDs and other segments of genome in different members of MTBC.

Deletion	*M. tuberculosis* H37Rv	*M. africanum*	*M. microti*	*M. bovis*	*M. bovis* BCG
RD2					
RD14					
RD1					
RD4					
RD12					
RD13					
RD7					
RD8					
RD10					
RD9					
RvD1					
TbD1					

Table 1.1: Distribution of deleted regions in *M.tuberculosis* complex members. Dark gray filled cells indicate the presence in all strains tested, light gray indicate the presence in some strains, white is

absence from all strains tested. Data taken from (Gordon et al., 1999, Brosch et al., 2002, Marmiesse et al., 2004, Brosch et al., 2000).

1.2.2.2.2. Insertions elements (IS)

The presence of insertion elements in various bacteria has been well appreciated as a means to bring change to the genome (Siguier et al., 2006). Insertion elements can reshape the genome of the bacteria and cause mutations and alter gene expression. In the case of *M. tuberculosis,* the presence of insertion elements can generate genotypic variation and mediate changes that can affect gene function. This variability can therefore alter bacterial properties such as strain variability, fitness and transmissibility and even play a role in the evolution of *M. tuberculosis*.

M. tuberculosis harbors four main insertion elements, IS*6110*, IS*1081*, IS*1547* and the IS-like element, all of them present in multiple copies. The best studied of these is the 1.36Kb IS*6110*, which belongs to the group of IS*3* elements (McEvoy et al., 2007). The IS*6110* element present exclusively in strains of the MTBC that can harbor from zero to 25 copies per genome (Brosch et al., 2002). For this reason and due to its high degree of copy number and insertion site variation, IS6110- RFLP has been widely used for epidemiological purposes.

The copy number of IS6110 elements in the genomes of *M. tuberculosis* strains can be highly variable (McEvoy et al., 2007). The insertion element IS*6110* is frequently found in a unique locus of the *M. tuberculosis* complex genome called the direct repeat (DR) region and DNA polymorphisms in this locus allow for strain typing (Hermans et al., 1990).

1.2.3. Genetic polymorphism in *M. tuberculosis*

M.tuberculosis is the most common cause of TB among member of the MTBC and its genome is composed of a GC-rich genome (G+C content; 65.5 %) of 4.4 Mb that contains ~4,000 genes (Cole et al., 1998). *M. tuberculosis* is considered genetically monomorphic because it has low levels of genetic diversity and homoplasies and very rare homologous recombination events. However, relative to other monomorphic bacteria, *M. tuberculosis* has substantial genetic variation (polymorphism) (Achtman, 2008) including large sequence polymorphisms (LSPs) (Tsolaki et al., 2004) and SNPs. Additionally variation can also be

caused by variability in number and location of the insertion element (IS) 6110 (McEvoy et al., 2007) and the polymorphic GC-rich repetitive sequences (PGRSs) as well as polymorphisms in the clustered regularly interspaced short palindromic repeats (CRISPRs) (van Embden et al., 2000) and variable number tandem repeats (VNTR) (Supply et al., 2000), and these are used as genetic markers in molecular epidemiologic studies.

In general, considering the limited role of HGT in mycobacteria, typing methods for MTBCs rely largely on minor changes of DNA sequences resulting from internal mutagenesis. Studies showed that genomic variation in the MTBC is due to deletions (Kato-Maeda et al., 2001, Tsolaki et al., 2004), duplications (Brosch et al., 2000), insertions (Brosch et al., 2002), mobile genetic element movements (Isaza et al., 2012), and SNPs (Walker et al., 2013). These polymorphism-borne genetic events have been extensively explored over the last years and have been employed to develop a number of typing methods (Jagielski et al., 2016).

A better insight on the diversity present in *M. tuberculosis* and other members of MTBC strains can lead us to a deeper understanding of the biological consequences associated with strain variability. It can provide great insight regarding the circulating strain which is critical for designing efforts relevant to public health and to the control, treatment and eradication of tuberculosis as strain variability has great impact on disease outcome, vaccine efficacy and drug resistance (Chen et al., 2017). Additionally, understanding the genetic diversity within the MTBC helps for the development of novel antibiotics and diagnostic tests for drug resistance (Koser et al., 2012).

1.2.4. Mycobacterium tuberculosis complex lineages

MTBC and the human host have a long-term co evolutionary relationship. It is presumed that *M. tuberculosis* originated in Africa and co-evolved into modern lineages with the out-migration of humans from Africa 70–80 thousand years ago (Galagan, 2014). Current evidence indicates that the Horn of Africa is the most likely origin of MTBC from which it has spread to other parts of the world (Comas et al., 2013).

The MTBC comprises seven phylogenetic lineages (based on the SNPs and RDs characterized from WGS analysis) and humans are the only known host for them to maintain

their complete cycle of infection, disease and airborne infection (Ernst, 2012), thus these lineages are referred as "human adapted" MTBC. The geographic spread of these lineages differs globally where some exhibit a global distribution and others a strong geographical restriction (Gagneux and Small, 2007) leading to the hypothesis that the strain-types are specifically adapted to people of different genetic background.

The seven MTCB lineages are: lineage 1 (Indo-Oceanic), lineage 2 (East Asian including "Beijing"), lineage 3 (East-Africa-India including CAS/Delhi), lineage 4 (Euro-American including Latin American Mediterranean (LAM), Haarlem, X type and T families), lineage 5 and lineage 6 (*M. africanum* West African 1 and 2, respectively), and lineage 7 (Ethiopian lineage) (Yimer et al., 2016, Comas et al., 2013, Firdessa et al., 2013). Lineages 1 and 3 are prevalent in East Africa, Central, South-and South-East Asia, lineages 2 and 4 are the most widely distributed worldwide, while lineages 5 and 6 are localized to West Africa (de Jong et al., 2010, Gehre et al., 2013). Lineage 7 is a *M. tuberculosis* lineage recently discovered in northwestern Ethiopia and among Ethiopian immigrants in Djibouti (Blouin et al., 2012, Firdessa et al., 2013, Yimer et al., 2013, Comas et al., 2015). Lineages 2, 3 and 4 belong to the evolutionary modern group and are considered more recently diversified compared to the ancient lineages of 1, 5 and 6 (Coscolla and Gagneux, 2014) while lineage 7 is phylogenetically located between the ancient and modern lineages (Firdessa et al., 2013, Takiff and Feo, 2015). (Figures 1.1.and 1.2).

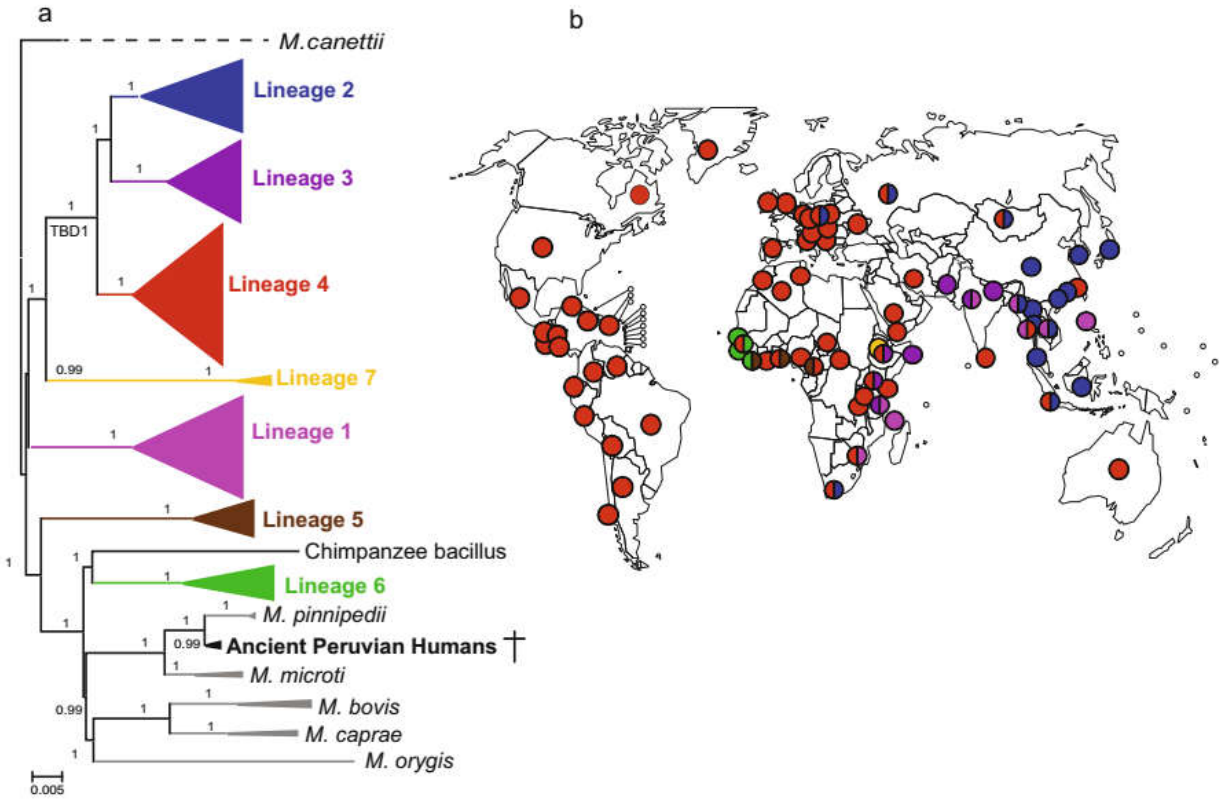

Figure 1.1.. Global phylogeography of the human adapted MTBC. (a) Phylogeny of MTBC lineages, (b) Global distribution of the seven human adapted MTBC lineages (Brites and Gagneux, 2017).

Classification of lineage types in to "modern" or "ancient" is based on the presence or absence of an MTBC-specific deletion (TbD1). TbD1 is a large genomic segment deleted in all modern lineages, but present in ancient lineages (Banuls et al., 2015) (**Figure 1.2**). Modern lineages tend to have spread more recently, are thought to be more transmissible and are generally associated with recent transmission of TB and with epidemics and increased virulence. In contrast, there is a trend in decreased rates of disease caused by evolutionary ancient lineages of MTBCs (Banuls et al., 2015, Comas et al., 2013).

Lineage 7 as a relatively newly discovered lineage within the MTBC which was identified among MTBC strains originating from Ethiopia. Characterization of lineage 7 strains by spoligotyping showed deletions from the 4^{th} to 24^{th} spacers specific to these strains and assigned as international spoligotype types (SIT) 910 and 1729 (Yimer et al., 2013). Based on phylogenic analysis, Lineage 7 is positioned in between the ancient and modern lineages of *M. tuberculosis* (Firdessa et al., 2013, Takiff and Feo, 2015), and underwent recent expansion ~310 years ago (Yimer et al., 2016). Whole genome sequence analysis of lineage 7 strains showed the heterogeneity of the strains (Nebenzahl-Guimaraes et al., 2016), identified more than 800 mutations specific to lineage 7 strains and also identified SNPs in genes possibly related to the unique clinical and growth characteristics of the lineage 7(Yimer et al., 2016). Therefore, lineage 7 is has a considerable interest in terms of studying the epidemiology of TB.

In general, it is noted that the global distribution of the lineages is varied globally and Africa is the only region that presents all the seven MTBC lineages with the biggest genetic diversity in the world (Gagneux, 2012, Firdessa et al., 2013). In the Ethiopian context, lineages 1, 3, 4 and 7 were documented with different geographic distribution in the country (Comas et al., 2015).

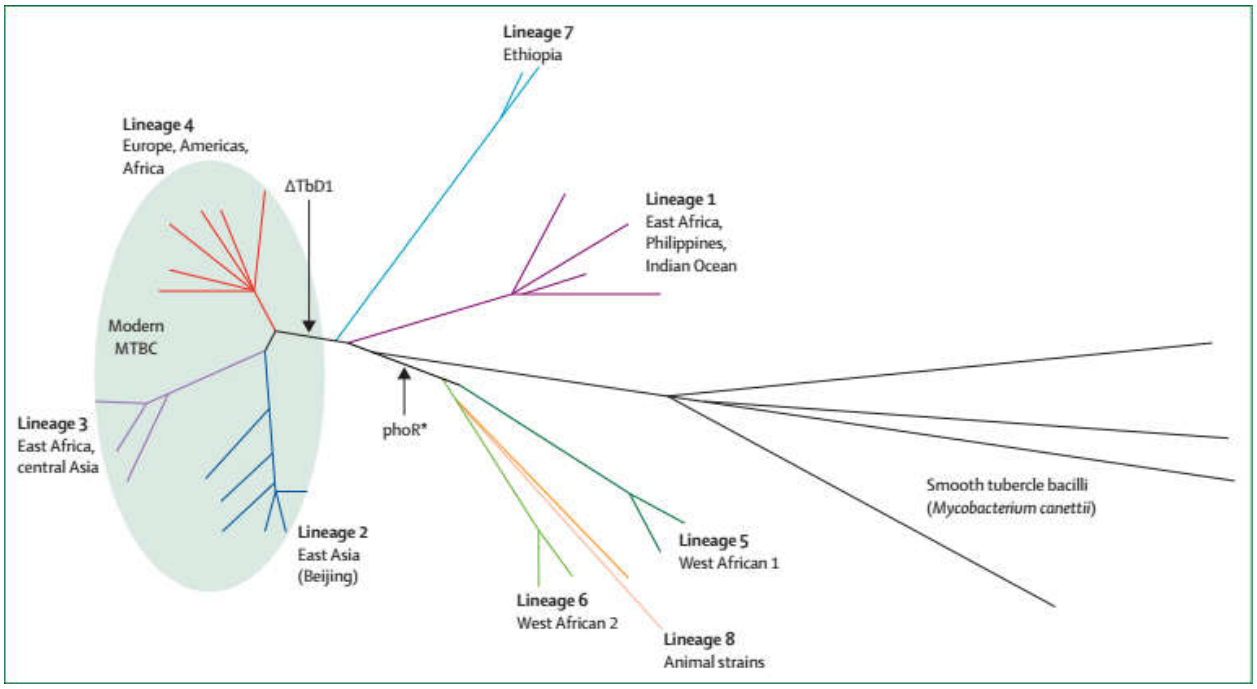

Figure 1.2. Phylogenetic tree of MTBC bacteria (describing modern and ancient MTBCs) (Takiff and Feo, 2015)

Evidences suggest that different lineages have different phenotypic properties such as immunogenicity and virulence (Williams et al., 2005, Reed et al., 2007, Lopez et al., 2003). Clinical studies have also demonstrated lineage-specific effects on the site and outcome of TB infection and disease in various settings (Caws et al., 2008, de Jong et al., 2008, Thwaites et al., 2008). Lineage specific transmissibility of drug-resistant TB has also been demonstrated in the Beijing MTBC strains. Overall, available evidence suggests that strains from different lineages may have an impact on clinical outcomes and transmissibility of MTBC and development and spread of drug resistance TB (Kato-Maeda et al., 2011).

1.3. Epidemiology of Tuberculosis

1.3.1. Global burden of Tuberculosis

TB has been a scourge of humanity throughout recorded history. Even today after the availability of effective drugs for more than half a century, TB is a major cause of morbidity and mortality worldwide. TB remains one of the world's deadliest communicable diseases

and has recently surpassed as the leading cause of infectious disease related mortality worldwide. One-third of the world's population is estimated to be infected with *M. tuberculosis* (Corbett et al., 2003, Nunn et al., 2005) and the socio-economic outcomes of the disease are substantial. Each year, approximately 10 million new cases of TB occur (WHO, 2018) along with an estimated 2 million deaths globally (Banuls et al., 2015). Globally, TB is one of the top 10 causes of death and the leading cause from a single infectious agent ranking above HIV/AIDS. In 2017, TB caused an estimated 1.3 million deaths among HIV-negative people an additional 300,000 deaths from TB among HIV-positive people (WHO, 2018). TB continues to result in unnecessary deaths and in the past 200 years it has killed more people than all other epidemic infections combined and it still kills around 5,000 people per day(Scully, 2013). More than 90% of new TB cases and deaths occur in developing countries, mainly in SSA, South-East Asia and Eastern Europe (Banuls et al., 2015). TB is one of the most challenging communicable diseases for developing countries particularly in SSA including Ethiopia (WHO, 2018).

1.3.2. Tuberculosis in Ethiopia

TB is among the leading causes of morbidity and mortality in Ethiopia (FMOH, 2011). Ethiopia is one of only 14 countries to have a high burden of TB, HIV/TB co-infection and MDR-TB. The annual estimated TB incidence is 164/100,000 persons with a death rate of 24 per 100,000 persons. The treatment success rate for newly registered cases was 90% in 2017 (WHO, 2018). According to the Ministry of Health report, TB is the eighth leading cause of hospital admissions and the third leading cause of hospital deaths in Ethiopia (FMOH, 2011). Ethiopia started implementing DOTS (as a pilot project) within a standardized TB prevention and control program in 1992 (FMOH, 2008). DOTS coverage is estimated at 100% geographical and 95% health facility level (FMOH, 2011). Approximately 10-15% of the annually notified TB cases are co-infected with HIV(FMOH, 2016). According to the first population-based national tuberculosis prevalence survey in Ethiopia, in year 2010-2011, the prevalence of smear-positive TB was 108/100 000 (Kebede et al., 2014).

1.3.3. Tuberculosis in Prison

TB disease burden is higher in prisons compared to the general population. Prisons are often neglected reservoirs for TB disease and can be significant amplifiers of disease both in prison and the community (Valway et al., 1994, Abebe et al., 2011). Transmission of drug-resistant strains, overcrowding, poor living conditions, limited health care, inadequate TB treatment and control strategies, and high rates of HIV infection all contribute to the disproportional burden of TB in prisons (Abebe et al., 2011). The World Health Organization (WHO) estimates (WHO, 2000) the prevalence of TB in prisons to be 10-100 fold higher than the general population. The median estimated fraction of TB in the general population attributable to the exposure in prisons for TB is 8.5% (Baussano et al., 2010).

Globally, close to three million cases of active TB each year are undiagnosed by existing health systems (World Health Organization, 2016), including many in the prison system, especially in sub-Saharan Africa (Drobniewski, 1995, Noeske et al., 2014). Lack of active surveillance and monitoring programs and well-equipped laboratory facilities for TB diagnosis contribute to low case finding among persons in prisons (Biadglegne et al., 2015b). Furthermore, overcrowding of prisons in low to middle-income countries provides a favorable environment for the transmission of *M. tuberculosis*. In high burden TB countries, those who are incarcerated often come from underprivileged communities with higher risk and rates of TB (Maher et al., 1998).

The impact of TB in prisons extends beyond prison walls into surrounding communities (Editors et al., 2010). Failure to control TB in prisons leads to enhanced TB transmission in the community, including drug-resistant disease (O'Grady et al., 2011). Thus, TB control in prisons is a major public health priority. However, there is limited understanding regarding TB epidemiology in African prisons. Previous studies carried out in African prisons reported 10 to 35 times higher TB prevalence in prisoners than in the general population (Noeske et al., 2006, Nyangulu et al., 1997, Habeenzu et al., 2007, Rasolofo-Razanamparany et al., 2000). In many TB high burden settings in low and middle income countries, there is no effective TB control program in place in prisons.

1.3.3.1. Tuberculosis in Ethiopian prisons

There are six Federal and 120 regional prisons and detention centers in Ethiopia (FMOH, 2015). Most prisoners are incarcerated in an overcrowded and poorly ventilated environment. The health service in prisons is often poorly organized, lacks skilled manpower and laboratory facilities for TB diagnosis (Baussano et al., 2010). Even though there is emerging prison TB prevention and control efforts in Ethiopia, it has been limited to a few prisons. Previous studies in the Ethiopian prisons reported point prevalence of TB ranging from 349 to 1913 per 100,000 populations(Abebe et al., 2011, Bayu et al., 2016, Moges et al., 2012, Fuge and Ayanto, 2016, Ali et al., 2015, Adane et al., 2016, Gebrecherkos et al., 2016, Zerdo et al., 2014). However, there are no data on the burden of TB in Hawassa Prison one of the largest prisons in the Southern Ethiopia. Therefore, the aim of the study was to estimate the burden of TB in this prison and assess the value of active TB case finding in a prison setting.

1.3.4. Tuberculosis in rural community

The fight against TB has been bolstered by the development of new molecular diagnostics, drugs, and a recent high-level United Nations meeting addressing the epidemic; however, many challenges to TB control remain. One of the most pressing challenges to eliminate TB is the high number of undetected cases. Only 6.4 of an estimated >10 million cases (64%) were officially notified in 2017, leaving a gap of > 3.5 million cases unreported and potentially undetected. Most of these missed cases occur in low-and-middle-income countries (LMICs) and among vulnerable populations (WHO, 2018). Rural settings are particularly challenging areas to detect and diagnose TB due to limited healthcare services, poor healthcare seeking behavior, and limited awareness and knowledge about TB (Cambanis et al., 2005, Sudha et al., 2003). Understanding the burden of TB in poor rural areas has large implications for TB control and is needed to design optimal case finding strategies (Sudha et al., 2003, Cambanis et al., 2005).

Active case-finding for TB is influenced by individual (care-seeking behavior), social (access to health care), and biomedical (diagnostic capability) factors (Shargie et al., 2006a). Strengthening surveillance and improving diagnostic capacity is recommended to improve case detection (WHO, 2012). Globally, most National TB Programs (NTPs) including in

Ethiopia rely on passive case-finding to detect TB disease. This passive strategy is based on self-presentation of symptomatic patients to the healthcare system and due to both patient and health system factors can result in long delays in diagnosis and subsequently increased disease transmission in the community (Storla et al., 2008, Yimer et al., 2005). Active case finding (ACF) is a systematic search for possible TB cases among high risk groups and facilitates early detection and prompt treatment. In rural communities, ACF can help reach persons with no transport or limited mobility, scarce resources, and persons who rarely seek healthcare (Yassin et al., 2013, Datiko et al., 2015). The Ethiopian NTP relies on passive case finding; however, there is a recognized need to strengthen community screening given variations in disease epidemiology across diverse geographic and cultural settings (Kebede et al., 2014).

1.3.4.1. Tuberculosis in Ethiopian rural community

Ethiopia is one of fourteen countries to be included on all three WHO high burden country lists for TB, TB/HIV and multi-drug resistant TB (MDR-TB). The TB incidence in Ethiopia in 2017 was estimated to be 164 per 100,000 population (WHO, 2018). The prevalence of smear positive PTB was 108 per 100,000 per population according to a national population-based TB survey which was conducted from October 2010 to June 2011, where the vast majority of those identified were newly diagnosed cases that had not been captured by the control program and most (55%) were among the younger age groups (15–34 years) (Kebede et al., 2014). Additional studies across various rural settings in Ethiopia have found a range of smear positive PTB prevalence (from 30 to 174 per 100,000 population) suggesting disease epidemiology varies across different geographical locations of the country (Berhe et al., 2013, Hamusse et al., 2017, Shargie et al., 2006b, Deribew et al., 2012, Yimer et al., 2009, Tadesse et al., 2011). The current study sought to evaluate the utility of a volunteer health development army (HDA) in conducting population screening for active TB in a rural state in Southern Ethiopia.

1.3.5. Molecular Epidemiology of Tuberculosis

Pattern of TB transmission differ greatly between and within countries, as they reflect the interplay of various factors, including effectiveness of TB control strategies, endemicity,

population density and transmissibility of locally relevant *M.tuberculosis* complex strains (Farnia et al., 2004). Interruption of the transmission of *M. tuberculosis* is one of the primary goals of tuberculosis control programs. The ability to track specific strains of *M.tuberculosis* that are circulating in the community improves the understanding of the transmission and pathogenesis of tuberculosis and helps to design intervention measures to control and prevent the disease as well as to interrupt further transmission of *M.tuberculosis* (DeRiemer and Daley, 2004). Molecular epidemiology of TB helps to study TB transmission dynamics and to enhance our understanding of the epidemiology of TB by utilizing molecular typing methods as an adjunct to classical epidemiological approach. It is used in identifying high-risk groups or areas where transmission is ongoing (distinguish between reactivation and recent infection) (Tazi et al., 2002), identifying transmission links, tracking the geographic distribution of specific strains. These data inform public health authorities on patterns of spread and potential areas for action to curb the spread of TB in communities (Jagielski et al., 2016).

Differential clinical outcomes have traditionally been considered to be predominantly associated with host and environmental differences among cases. More recently, strain diversity has also been implicated as a possible causal factor influencing clinical outcomes (Comas and Gagneux, 2009)**.** Since the discovery of DNA polymorphisms in *M. tuberculosis*, molecular typing of strains has become an invaluable tool for the study of epidemiology of TB (Bazira et al., 2010).

Molecular epidemiologic tools support the TB control program by providing data about the population structure of the MTBC strains circulating in the community. They differentiate between infecting strains, describe the diversity of circulating strains, measure the prevalence of endemic strains and identify dominant strains associated with outbreak, severe disease and drug resistance (van Soolingen et al., 1995, Van Soolingen, 2001, Bazira et al., 2010). Such molecular epidemiologic data could help the TB control program by providing better understanding of the transmission dynamics of TB in specific settings and to stimulate

the designing and implementation of appropriate intervention measures in the prevention and control of the disease (Tazi et al., 2002, Jagielski et al., 2016).

Molecular epidemiologic studies on drug resistance are used to examine the nature (e.g., genotype-specific mutations, association of specific mutations with phenotypic resistance) and extent (e.g., prevalence of specific mutations in a population) of drug resistance and patient risk factors (e.g., HIV) for acquiring resistance. Some studies tried to look at the contribution of primary (infection by an already-resistant organism) versus acquired (acquisition of drug resistance within a patient, de novo) drug resistance in specific populations (Lutfey et al., 1996, Xu et al., 1996). Molecular epidemiologic studies of drug resistance have also focused on describing the nature of resistance within a patient to better understand the dynamics of drug-resistant subpopulations resident within a patient (Post et al., 2004).

1.3.5.1. Molecular genotyping methods for MTBC

For a DNA marker to be used for the study of the transmission dynamics of TB, it has to be polymorphic enough to distinguish among unrelated isolates. Additionally, it has to be stable enough to make the connection between isolates that are indeed related. Methodology to determine the genetic polymorphism needs to be simple, affordable, have a rapid turnaround time and the results has to be in a format that can be easily shared between different laboratories (Kato-Maeda et al., 2011). Different genotyping methods have been developed and used in molecular epidemiologic studies of TB. These include, the restriction fragment length polymorphism (RFLP) method using IS*6110* that was introduced in early 1990s and successfully used to identify and track individual isolates of *M. tuberculosis* in the community (van Embden et al., 1993). Later, PCR-based methods such as spoligotyping (Kamerbeek et al., 1997), and mycobacterial interspersed repetitive units (MIRU)-VNTR typing (Mazars et al., 2001) were added as molecular epidemiological tools. Most recently, whole-genome sequencing has been introduced and used to give high resolution in strain differentiation and study community transmission and microevolution of *M tuberculosis*

(Schurch et al., 2010a, Schurch et al., 2010b). Below are the descriptions of each genotyping methods used in the molecular epidemiology of TB.

1.3.5.1.1. IS6110-RFLP

IS6110-RFLP has been considered, until recently, to be the gold standard of molecular epidemiologic studies owing to its discriminatory power and because it has been widely used since the early 1990s (Houben and Glynn, 2009). The genotyping method is based on the variability in the number and position of IS6110 elements in the genome of MTBCs isolates (Kato-Maeda et al., 2011).

IS*6110* RFLP was standardized in 1993 and in brief, after DNA restriction with *Pvu*II endonuclease and electrophoretic separation of the obtained fragments on agarose gels, hybridization by Southern blotting is performed with an IS*6110* probe to generate strain-specific DNA fingerprints, which reflect the variability in the numbers and positions of IS*6110* elements in genomes of MTBC isolates (van Embden et al., 1993).

The main advantage of the IS6110-RFLP method is its high discriminatory power. The main limitation of IS6110 include: it is a labor intensive and time consuming method, furthermore, it has significant technical limitations including the need for 2–3 μg of high quality DNA (and therefore the need of prior culture of the isolates) and the determination of results based on visual inspection of images of band patterns that are difficult to share between laboratories. All these limitations stimulated the search for alternative, PCR-based genotyping methods (Kato-Maeda et al., 2011).

1.3.5.1.2. Spoligotyping

Spacer oligonucleotide typing (spoligotyping) is a PCR-based technique for MTBC strain differentiation based on the structure and polymorphism of the DR locus (Jagielski et al., 2016). It is based on the polymorphism in the direct repeat (DR) locus, which is a member of the clustered regularly interspaced short palindromic repeats (CRISPRs). The CRISPR loci consist of a variable numbers of identical direct repeats (DRs) interspersed with unique

(non-repetitive) spacer sequences or spacers (Zhang et al., 2010). The DR and the spacers together are called direct variable repeats (DVRs). The DR region evolves through IS*6110*-mediated mutation, homologous recombination between repeat sequences that lead to the deletion of a DVR, strand slippage that lead to duplication of DVRs, and point mutations (Aga et al., 2006, Warren et al., 2002).There are 94 spacer sequences; however, only 43 spacers are used in the most common typing methodology (Kamerbeek et al., 1997).

Spoligotyping amplifies the spacers and the result is described as strain-specific patterns (spoligotypes) based on the presence or absence of spacers and will result in different polymorphism (Driscoll, 2009, Kamerbeek et al., 1997). Since spoligotyping results can be presented as a binary system (present/absent) or, after a simple conversion, as an octal numeral, they can be easily interpreted, digitized, and compared among different laboratories (Dale et al., 2001). The databe of spoligotyping patterns is available online in SITVITWEB data base (http://www.pasteur-guadeloupe.fr:8081/SITVIT2/). Spoligotyping was introduced into laboratory practices in the late 1990s (Kamerbeek et al., 1997).

There are two methods currently used to obtain a spoligotype pattern. The first one (the original or conventional method) is based on reverse hybridization where the sequences of each of the spacers are attached to specific areas on a membrane and the PCR products are hybridized to the membrane (Driscoll, 2009). The patterns (presence and absence of spacers) are represented as a binary number and then to an octal number. The second method is based on Luminex technology, where synthetic spacer oligonucleotide probes immobilized on microspheres and detected via fluorochromes attached to the beads and hybridized PCR products. This method offers higher reproducibility due to the elimination of membrane hybridization and avoidance of manual interpretation of the spoligopatterns (Cowan et al., 2004).

Spoligotyping has many important advantages. It is highly reproducible and it needs very little DNA (20–50 ng). It also allows the detection of MTBC bacteria in noninfectious samples without the need for culturing of bacteria; detection and genotyping can be

performed directly on clinical samples (Cafrune et al., 2009). Spoligotyping has proven useful for typing of nonviable cultures, Ziehl-Neelsen smear slides, or paraffin-embedded tissue sections (van der Zanden et al., 1998, Driscoll et al., 1999). Since spoligotyping interrogates more conserved genetic information than, for instance, IS6110-RFLP typing, this method can be used for the identification of members of the MTBC to the species or subspecies level. Furthermore, spoligotyping is much faster than IS6110-RFLP analysis, with the laboratory turnaround time of the former being <48 h (Farnia et al., 2004, Gori et al., 2005).

The main limitation of spoligotyping is the inferior discriminatory power when compared with IS*6110*-RFLP and MIRU-VNTR typing. For example, isolates that have the spoligotype lacking the spacers 1–34 (also known as the Beijing family) may have different IS*6110*-RFLP and MIRU-VNTR polymorphisms (Hanekom et al., 2008). The limited discriminatory power of spoligotyping is due to the fact that it targets a single genetic locus, covering <0.1% of the MTBC genome, unlike IS6110-based RFLP analysis, where IS6110 is distributed over the whole mycobacterial genome. Additionally, convergent deletions in the CRISPR locus occur frequently (Schurch et al., 2011). Spoligotyping, when used alone, is not sufficient for epidemiological studies, but it is sometimes recommended as a first-line screening test, especially when a large collection of isolates is being tested (Krawczyk et al., 2011, Dong et al., 2009, Goguet de la Salmoniere et al., 1997). However, because of its simplicity, binary-result format, and high reproducibility, spoligotyping is widely used for investigations of MTBC molecular epidemiology (Coll et al., 2012).

1.3.5.1.3. MIRU-VNTR typing

Mycobacterial interspersed repetitive unit VNTR (variable number tandem repeats) is considered by some authors to be the new gold standard for *M. tuberculosis* genotyping, as it is highly discriminatory and reproducible (Iwamoto et al., 2007). This genotyping method is based on VNTRs of the genetic elements called MIRUs. VNTRs are tandem-repeat regions, scattered throughout the genome of *M. tuberculosis*, that resemble polymorphic minisatellites in eukaryotic genomes (Frothingham and Meeker-O'Connell, 1998). The

repetitive units are 40–100 base pairs in length and are located in 41 loci scattered throughout the genome of *M. tuberculosis* H37Rv (Supply et al., 2000). The variability in the number of copies of the repeat unit differentiates isolates into distinct genotypes (Kato-Maeda et al., 2011).

The most polymorphic VNTR/MIRU loci have been used to develop MIRU-VNTR typing, a PCR-based method which differentiates between strains by assessing the number and length of tandem repeats at each locus. The principle for MIRU-VNTR typing includes PCR amplification of each locus by using specific primers complementary to the flanking regions and analysis of the resulting PCR products, which are separated by gel electrophoresis (Supply et al., 2006). The discriminatory power of the 24-locus MIRU-VNTR typing system provides a resolution comparable to that of IS*6110*-RFLP profiling (Vadwai et al., 2012). Therefore, 24-locus MIRU-VNTR typing has been suggested to be the new "gold standard" for molecular typing of MTBC strains (Jagielski et al., 2016).

Generally, genotyping based on MIRU-VNTR regions is fast, easy to perform, sensitive, highly reproducible, and discriminative. It can be performed in large-scale genetic or evolutionary investigations for tracking key epidemiological events. MIRUVNTR genotyping provides significantly higher resolution than spoligotyping and a resolution close to or even better than that obtained with IS*6110*-RFLP analysis. Therefore, MIRU-VNTR typing could be used to further investigate strains that were matched by both IS*6110*-RFLP and spoligotyping methods or that had a known epidemiological link (Jagielski et al., 2016). The results of MIRU-VNTR typing are expressed in a simple, digital format in which each digit represents the number of copies at a particular locus. Digitized data allow comparison of the results among laboratories worldwide (Allix et al., 2006). One of the largest publicly available international databases, SITVITWEB (http: //www.pasteur-guadeloupe.fr:8081/SITVIT_ONLINE/) (Demay et al., 2012).

1.3.5.1.4. Whole genome sequencing (WGS)

WGS provides information about the whole genome and this method can identify virtually all varieties of markers detected by classical genotyping methods. It is therefore much more

accurate and precise in detecting variability among strains and provides a wealth of information (Jagielski et al., 2016). Compared with classical genotyping methods such as IS6*110*-RFLP typing, spoligotyping, or 24-locus MIRU-VNTR typing, WGS provides much higher resolution and in-depth knowledge about each strain under study (Jagielski et al., 2016). This is due to the fact that classical genotyping methods only interrogate a small fraction of the genome where as WGS gives access to the complete genome sequence (Niemann and Supply, 2014).

WGS is also useful in delineating outbreaks and tracking transmission routes. When the same strains that were subjected to WGS were examined by classical genotyping methods, they were, in part, not correctly clustered (Jagielski et al., 2016). WGS provides an excellent tool to investigate the transmission and microevolution of mycobacteria (Jagielski et al., 2016). It can also be helpful in exploring important questions about the biology of mycobacteria, including evolutionary mechanisms shaping mycobacterial populations (Pepperell et al., 2013, Choo et al., 2014), antibiotic resistance (Motiwala et al., 2010, Comas et al., 2011), or virulence and immunogenicity (Comas et al., 2010, Coscolla and Gagneux, 2010). Additionally, data from WGS analysis can also allow for estimation of temporal scales of TB epidemics based on reconstruction of SNP based phylogenies. WGS can be further exploited for a wide range of evolutionary and comparative genomic applications (Merker et al., 2015, Niemann and Supply, 2014, Roetzer et al., 2013, Walker et al., 2015).

WGS also has invaluable application on studying of drug resistance. Compared with classical genotyping, WGS simultaneously predicts drug resistance and highly precise phylogenetic identification (Koser et al., 2013). This combination of such diagnostic and epidemiological information in a single assay is a great benefit, especially for *M. tuberculosis*, for which early detection of drug resistance is important.

Analysis of drug resistance based on WGS goes far beyond conventional molecular tests, focusing on known selected mutations in hot spot regions of genes involved in resistance to

first and second-line anti-tuberculous drugs. In principle, WGS captures most, if not all, the gene sequences determining the so-called *M. tuberculosis* resistome, which thus allows interrogation of the entire spectrum of known mutations associated with drug resistance (Koser et al., 2012, Roetzer et al., 2013). WGS at high depth enables to detect the emergence and coexistence of different drug-resistance-conferring mutations before selection and fixation of a final mutant, in possible combination with compensatory mutations (Sun et al., 2012, Merker et al., 2013). Such detection is of clinical relevance as the coexistence of wild-type and mutant subpopulations resulting in hetero resistance might confound the current phenotypic and molecular drug-resistance tests (Merker et al., 2013, Sun et al., 2012), as well as conclusions on transmission or secondary acquisition of drug resistance.

1.4. Drug-resistant TB

1.4.1. General overview

Drug-resistant TB continues to be a public health crisis and remains a major public health concern in many countries (WHO, 2018). In particular, multidrug-resistant TB (MDR-TB), defined by resistance to at least isoniazid (INH) and rifampin (RMP), has profound effects on patient treatment outcomes, since the two most effective anti-TB drugs with the fewest side effects must be replaced by less effective, more expensive and toxic drugs (Chihota et al., 2012). More recently, extensively drug resistant TB (XDR-TB) has been recognized as an even more severe public health problem (Shah et al., 2007). Infection with either MDR or XDR *M. tuberculosis* strains can result in more severe disease, prolonged infectiousness and a poor prognosis (Gandhi et al., 2010). Studies have also showed the spread of MDR-TB among household contact with a prevalence rate ranging from1.8% to 11.2%. Additionally, MDR-TB outbreaks within health care facilities, schools, work places and other confined settings have been reported (Langendam et al., 2013). Therefore, the emergence of MDR-TB and XDR-TB strains poses serious challenges to the control of TB.

Globally, an estimated 3.5% of new cases and 18% of previously treated cases had MDR/Rifampicin resistance -TB in year 2017 and about 8.5% MDR-TB cases were XDR-

TB (WHO, 2018).The prevalence of MDR/RR-TB varies across counties and more than half of MDR-TB cases occurring in India (24%), China (13%) and the Russian Federation (10%) (WHO, 2018). MDR-TB has reached to epidemic level even in some countries (WHO, 2014a). XDR-TB has been reported from 92 countries of which 8 are in SSA including Ethiopia (Wilfred A C Nkhoma et al., 2012).

1.4.2. Drug resistance TB in Ethiopia

Drug resistant TB is an emerging problem worldwide including in Ethiopia. Ethiopia is one of 14 countries to be included on all three WHO high burden country lists for TB, TB/HIV and MDR-TB. WHO estimated the prevalence of MDR-TB among new TB cases in Ethiopia at 2.7 % (95 % CI, 1.6 to 4.1 %) and 14 % (95 % CI: 6.7 to 25 %) among previously treated cases (WHO, 2018). According to the national anti-tuberculosis drug resistance survey in 2014, the prevalence of MDR-TB among new and previously treated TB cases was 2.3% and 17.8% respectively (EPHI, 2014d). Additionally, study reports from different regions of Ethiopia have found the prevalence of MDR-TB among new cases ranged from 1.1 to 5.8 % (Seyoum et al., 2014, Agonafir et al., 2010, Tessema et al., 2012, Abebe et al., 2012) and among previously treated TB from 10.9 to 71.4 % (Agonafir et al., 2010, Tessema et al., 2012, Abate et al., 2012, Nigus et al., 2014).These and other data coming from the country show that drug-resistant TB is a major public health concern of Ethiopia that warrants attention.

Development of drug-resistant TB is largely a man-made problem associated with ineffective TB control programs as a result of inadequate therapy, poor patient compliance, interrupted drug supply and inappropriate treatment regimens (Urassa et al., 2008). In most high-burden countries, MDT-TB is only diagnosed after prolonged treatment with first-line TB drugs and clinician recognition that treatment has failed. Treatment of drug-resistant TB without drug susceptibility testing (DST) result has several potential adverse consequences including patients receiving inadequate treatment which increases the risk of treatment failure or death, amplification of drug-resistance, and patients remain infectious, promoting transmission to close contacts throughout the community (Dorman and Chaisson, 2007). In

the Ethiopian context, DST is not accessible to all TB patients due to inadequate laboratory capacity, inadequate transport network and resource limitations (Biadglegne et al., 2014, FMOH, 2009). It was reported that only 10% of MDR-TB cases in Ethiopia were detected and the patients received treatment (EPHI, 2014c). This makes the situation of drug-resistant TB very challenging in Ethiopia and warrants for the need of urgent expansion of DST services in the country.

1.4.3. Molecular basis of anti-TB drug resistance

The effective treatment of TB started in 1946 with the introduction of streptomycin (STM) (Mitchison and Davies, 2012). However, soon after the first antibiotic was introduced drug resistance emerged mainly due to the use of streptomycin as monotherapy (Wolinsky et al., 1948). Currently, treatment for non-drug-resistant TB consists of a two-stage process including an initial intensive of a 2 month regimen of bacterial eradication, followed by a second 4 months continuation stage devoted to elimination of persistent or latent bacterial organisms using combined drugs. Combination regimens are used to ensure that mutants resistant to a single drug do not emerge and may be explained by the historical reports of treatment using a single drug resulting in the selection of resistant strains and treatment failure. Additionally, with the mycobacterial population within a patient, there may be different populations of bacilli and each can present a different susceptibility profile for anti-TB drugs. Besides, each of the anti-TB drugs has its own effect on clearing the bacteria (Rattan et al., 1998, Mitchison and Davies, 2012, du Toit et al., 2006). Isoniazid (INH), rifampicin (RMP), pyrazinamide (PZA), streptomycin(STM), and ethambutol (EMB) are the first line anti-TB drugs recommended to treat TB (Taniguchi, 2000) and their use started many years ago with streptomycin introduced in 1943, isoniazid in 1952 and rifampicin in 1963 (Frieden et al., 2003). The emergence of strains resistant to either of these drugs causes major concern, as it leaves drugs that are far less effective, have more toxic side effects, and result in higher death rates, especially among HIV-infected persons (Rattan et al., 1998).

Mobile genetic elements such as plasmids and transposons, which are known to mediate drug resistance in various bacterial species, are not thought to be responsible for drug

resistance in *M. tuberculosis* (Zhang and Yew, 2009). Rather, in a population of *M. tuberculosis*, resistance to anti-TB drugs is thought to be due to spontaneous chromosomal mutations that occur at a relatively low frequency, 10^{-6} to 10^{-8} mycobacterial replications. Individual nucleotide changes (point mutations) confer resistance to single drugs, and the sequential accumulation of these mutations in different genes involved results in multi-drug resistance TB (Ozturk et al., 2005, Soini and Musser, 2001). Drug resistance in *M. tuberculosis* incurs a fitness cost that decreases its virulence and transmissibility (Meissner, 1954), however, it has been identified that the bacteria in many cases form compensatory mutations that restore fitness but retain resistance (Comas et al., 2011).

Clinically significant drug resistance in TB may develop during anti-TB treatment (acquired resistance or secondary resistance). Anti-TB drugs impose selection pressure in a population of *M. tuberculosis* in which resistant mutants gradually outnumber susceptible bacilli and emerge as the dominant strains. Factors contributing to this selection pressure include: monotherapy due to irregular drug supply, inappropriate medication prescription and poor patient adherence to treatment (Zhang and Yew, 2009). Once resistant bacillary strains emerge during treatment, these could be transmitted in a community. Those who are infected with drug-resistant strains rather than developing resistance during therapy are said to have primary resistance (Faustini et al., 2006).

INH is one of the key first-line anti-TB drugs and it is only active against metabolically active tubercle bacilli (Zhang and Yew, 2015). INH resistance is mediated by mutations in several genes (katG, inhA, KasA, ndh, the oxyR-ahpC intergenic region, fabG, fadE24, inhA promoter, iniA and the mabA-inhA operon) (Muller et al., 2013, Siu et al., 2011). However, the majority are associated with missense mutations at codon 315 of katG gene, where 60-95% of INH resistance is from a S315T mutation (Miotto et al., 2018). katG gene encodes catalase-peroxidase which transforms INH into its active form (Ramaswamy and Musser, 1998, Hazbon et al., 2006, Kiepiela et al., 2000). Next to katG gene, IHN resistance is mediated in the promoter region of inhA, encoding a putative enzyme involved in mycolic acid biosynthesis. A mutation in the inhA promoter region results in the over expression of

InhA and develops INH resistance via a titration mechanism (Ramaswamy and Musser, 1998, Miotto et al., 2018). Mutations located at the mabA-inhA operon can also lead to INH resistance and are present in 8– 30% of the resistant strains (Siu et al., 2011). Mutations in the other genes are rare and usually coexist with other hotspot mutations in katG and mabA-inhA (Siu et al., 2011). Approximately 10% of IHN resistant strains do not harbor any mutation in katG or inhA genes, suggesting the presence of alternative resistance mechanisms (Zhang and Yew, 2015). In general, it is well documented that mutations in the *inh*A genes confer low-level resistance to INH, while mutations in the *kat*G gene at codon 315 exclusively confer high-level resistance to INH (Banerjee et al., 1994, Morlock et al., 2003, Guo et al., 2006, Sandgren et al., 2009).

RPM is highly bactericidal for both growing and non-growing *M. tuberculosis*. The target of RPM is the β-subunit of RNA polymerase and RPM binding inhibits the elongation of messenger RNA and thus hinders transcription and thereby kills the bacteria (Herrera et al., 2003, Nguyen, 2016). RNA polymerase is composed of four different subunits (α, β, β'and σ) encoded by *rpoA, rpoB, rpoC* and *rpoD* genes respectively. Most RPM resistant *M.tuberculosis* strains harbor resistance associated mutations in the structural region of rpoB encoding for β-subunit of RNA polymerase (Telenti et al., 1993). More than 96% of the rifampin-resistant strains contain a mutation in this 81 bp region of *rpoB*, which is a mutational "hot-spot" region. This region covers codons from 507-533 and it is also termed as the rifampicin resistance-determining region (RRDR) (Ramaswamy and Musser, 1998). The most frequently reported mutation in most studies are in codons 531 and 526 (Somoskovi et al., 2001). Some studies have also reported mutations outside of the hot-spot region of rpoB in rifampicin-resistant *M. tuberculosis* isolates (Heep et al., 2000).

PZA plays a critical role in the current first line anti-TB regimens as it kills persistent tubercle bacilli and it has effective sterilizing activity in acidic environment (Somoskovi et al., 2001). PZA use shortens the duration of treatment from 9 months to 6 months (when used in combination with rifampin). PZA is a pro-drug which is converted to its active form, pyrazinoic acid (POA) by the pyrazinamidase (PZase) encoded by *pncA* gene of

M.tuberculosis. POA is the lethal molecule inhibiting various functions of *M. tuberculosis* in an acidic environment (Sheen et al., 2009) . The mechanism of action of pyrazinamide is through pyrazinoic acid, its active moiety, by disrupting bacterial membrane energetics and inhibiting membrane transport (Zhang et al., 2003). PZA is highly specific activity to *M.tuberculosis* and *M. bovis* is naturally resistant to PZA due to a unique C-G point mutation in codon 169 of the *pncA* gene (Zimhony et al., 2004). Mutations in pncA, resulting in a loss of function of PZase, represent the primary molecular mechanism for PZA resistance in clinical strains (Fu and Shinnick, 2007). Mutations in pncA are the main mechanisms for pyrazinamide resistance in *M. tuberculosis*. Most alterations occur in a 561 bp region of the open reading frame or in an 82 bp region of its putative promoter (Scorpio et al., 1997, Jureen et al., 2008). There is a high degree of diversity of pncA gene mutations among pyrazinamide-resistant strains; however, some pyrazinamide-resistant strains do not show mutations in pncA or its promoter region (Cheng et al., 2000). pncA mutations are diverse in nature and scattered along the entire gene (561 base pairs in length) and additional mutations found in the promoter regions (Somoskovi et al., 2001). PZA susceptibility testing is not done routinely in many countries due to technical difficulties. Thus the extent of PZA resistance globally is largely unknown (Johnson et al., 2006).

EMB has bacteriostatic activity as opposed to the other first-line anti-TB drugs which have bactericidal activity. It is active against multiplying bacteria and it primarily targets an arabinosyltransferase encoded by embCAB operon, which inhibits the arabinogalactan biosynthesis in *M.tuberculosis* cell wall. In *M. tuberculosis*, embB is organized into a 10-kb operon with embC and embA genes named embCAB (Telenti et al., 1997, Sreevatsan et al., 1997b). Resistance towards EMB is generally caused by missense mutations at embCAB operon, in particularly at codons 306, 406 and 497 of embB (Cheng et al., 2014). Among all the EMB resistance-related mutations, the most common one is embB M306Vand it is considered the ethambutol resistance determining region (ERDR). In addition, missense mutation in Rv3806c (ubiA) V188A, A237V, R240C and A249G as well as over expression of the gene were confirmed to cause increased EMB resistance (He et al., 2015).

STM was the first drug introduced for the treatment of TB. Currently, STM is utilized as an alternative first-line anti-TB drug recommended by the WHO (WHO, 2008) and is used in retreatment TB cases together with INH, RIF, PZA and EMB (Brzostek et al., 2004). STM binds to the 30S subunit of bacterial ribosome interacting with the 16S rRNA and S12 ribosomal protein (rrs and rpsL genes, respectively) (Abbadi et al., 2001), inducing ribosomal changes, which cause misreading of the mRNA and inhibition of protein synthesis (Davies et al., 1965). STM kills actively growing *M. tuberculosis* bacilli, but is inactive against non-growing or intracellular bacilli. Point mutations in STM resistant isolates have been reported in both rpsL and rrs genes, and these are the major mechanisms of STM resistance, accounting for 65% - 67% of STM-resistant strains (Ramaswamy and Musser, 1998, Finken et al., 1993, Nair et al., 1993). However, mutations in rpsL (30S ribosomal protein) are the major mechanism of resistance and accounts for around 50% of the resistance. Mutations in rrs also account for approximately 15% of STM resistance. Recently, mutations in gidB, a gene encoding 7-methylguanosine methyl transferase, have been suggested to reduce 16S ribosomal methylation. The mutation can lead to the decrease in the affinity between STM and 16S ribosomal RNA (rRNA)-binding site, thus causing low-level STM resistance (Spies et al., 2008).

In summary, several molecular studies found that *M. tuberculosis* generally acquires drug resistance via de novo nsSNP, small deletions, or insertions in specific chromosomal loci, unlike most other pathogenic bacteria, which often acquire drug resistance via horizontal transfer (Mathema et al., 2006). Understanding the rate of nucleotide mutation in *M. tuberculosis* is thus central to our knowledge of the process of drug resistance evolution (Galagan, 2014). Additionally, understanding of the molecular basis of resistance to anti-tuberculosis drugs is bases for the development of exacting laboratory testing and initiation of timely treatment regimens (Galagan, 2014) .

1.5. Immunity of TB

Immunity to *M. tuberculosis* is an interplay between the innate and adaptive immune response, both cellular and humoral (Scriba et al., 2017). The outcome of human infection with *M. tuberculosis* is dependent on the ability of the immune response to clear or contain the infection. In cases where this fails, the bacterium replicates, disseminates within the host, and elicits a pathologic inflammatory response, and disease ensues. Clinical presentation of TB disease is remarkably heterogeneous, and the disease phenotype is largely dependent on host immune status. Onward transmission of *M. tuberculosis* to new susceptible hosts is thought to depend on an excessive inflammatory response causing a breakdown of the lung matrix and formation of lung cavities. But this varies in cases of underlying immunological dysfunction: for example, HIV-1 infection is associated with less cavitation, while diabetes mellitus comorbidity is associated with increased cavitation and risk of transmission (Scriba et al., 2017, Scriba et al., 2016).

The granuloma, a hallmark histological structure in TB infection, was described as an aggregation of immune cells, majorly macrophages and T lymphocytes, to restrict mycobacterial infection (Williams and Williams, 1983). However, recent studies have shown that the granulomas are actually highly dynamic structures in which neutrophils are one of the predominant cell types (Eum et al., 2010). Recent advances in TB immunity have revealed that granulomatous inflammation in TB infection is highly dynamic and the early influx of neutrophils may lead to excessive inflammation and pulmonary cavitation, which provide niches for MTB not only to survive but also to spread to other sites (Chao et al., 2019).

People infected with TB bacilli are usually asymptomatic during latent infection, and secondary TB develops in 10% of those by endogenous reactivation. Each granuloma contains viable TB bacilli; most likely, throughout the lifetime of the host, the maintenance of the granuloma is a prerequisite to allowing continued protection from the bacilli. Factors disrupting the fine-tuned balance between mycobacteria and the maintenance of the granuloma will inevitably raise the risk of reactivation of the disease (Yasui, 2014).Therefore, the understanding of TB immunology elucidates TB infection and disease as a spectrum rather than dichotomous states (Lewinsohn and Lewinsohn, 2019).

1.6. Diagnosis of TB (Disease and Infection)

TB diagnosis relies on evaluation of clinical symptoms and patient history combined with radiographic examination and detection of bacteria in sputum (Dheda et al., 2017). The presence of AFB in sputum smears by microscopy does not specifically indicate infection with *M. tuberculosis*; microbiological culture and nucleic acid amplification-based tests are required to confirm the presence of *M. tuberculosis* infection. Xpert MTB/RIF, a cartridge-based near-patient diagnostic assay utilizing real-time nucleic acid amplification of *M. tuberculosis* DNA, which also detects drug resistance to the first line drug, rifampicin, is recommended by the World Health Organization for TB diagnosis (Helb et al., 2010, Stevens et al., 2017). Interferon gamma (IFN-γ) release assays (IGRAs), which leverage the specificity of the immune response to *M. tuberculosis*, are the basis of the QuantiFERON®-TB Gold In-Tube and T-SPOT. IGRAs measure IFN-γ produced by antigen-specific T-cells in blood that recognize *M. tuberculosis* antigens (ESAT-6, CFP-10, TB7.7). IGRAs provide increased specificity over traditional Mantoux skin tests that depend on delayed type hypersensitivity reactions to purified protein derivative (PPD), which is not specific to *M. tuberculosis* infection and positive results may be due to BCG vaccination or exposure to environmental mycobacteria. However, IGRAs do not differentiate between active and latent TB and cannot be used to diagnose TB disease (Sia and Rengarajan, 2019).

While sputum-based smear and culture techniques are established worldwide for clinical indication of *M. tuberculosis* infection, collection of sputum, especially from children, can be challenging and is not completely reliable. Therefore, there is interest in developing non-sputum based diagnostic approaches for TB. Detection of urinary lipoarabinomannan in suspected TB cases are being investigated in HIV-infected and uninfected individuals. Blood-based biomarkers discriminating LTBI and ATB are being investigated for potential application to TB diagnostics and treatment response Further understanding the spectrum of antigen-specific responses to *M. tuberculosis* infection can be leveraged to develop diagnostics that can monitor infection and treatment response (Sia and Rengarajan, 2019).

1.7. Treatment of TB (First line and Second lne drugs)

Currently, treatment for non-drug-resistant TB consists of a two-stage process including an initial intensive of a 2 month regimen of bacterial eradication using a four drugs regimen (isoniazid, rifampicin, pyrazinamide, and ethambutol) , followed by a second 4 months continuation stage with isoniazid and rifampicin which is devoted to elimination of persistent or latent bacterial organisms using combined drugs (FMOH, 2016)

Second-line drugs that are used for the treatment of MDR-TB are listed as aminoglycosides; e.g., amikacin (Am) and Kanamycin (Km); polypeptides: e.g., Capreomycin (Cm), viomycin and enviomycin; fluoroquinolones; e.g., ciprofloxacin (Cip), levofloxacin (Lfx), ofloxacin (Ofx), moxifloxacin (Mxf) and gatifloxacin; and thioamides: e.g., ethionamide (Eto), prothionamide and cycloserine (Cs), and P-aminosalicylicacid (PAS) (Biadglegne et al., 2015b). Second-line anti-TB drugs are less potent, need to be administered for a much longer time, are more toxic and are high-cost compared to first-line anti-TB drugs (Biadglegne et al., 2015b).

The treatment guideline for drug-resistant TB has been updated recently (WHO, 2019b). According to the new guideline, most MDR/RR-TB patients can be treated with fully oral drug regimens. These regimens, lasting 18–20 months, should start with a combination of a fluoroquinolone, bedaquiline and linezolid, plus one or more other agents likely to be effective. The classification of medicines to be used in these regimens was updated based on an assessment of their relative benefits and potential harms. Injectable agents should only be used if other options are not possible; two such agents (kanamycin and capreomycin) are no longer recommended. The standardized, shorter MDR-TB regimen (with treatment duration of 9–12 months) can be offered to eligible patients who agree to shorter treatment but this requires a daily injectable agent for at least 4 months (WHO, 2019a).

1.8. Rationale of the study

TB is a major public health problem in Sub Saharan Africa with Ethiopia being one of the most affected countries (Hamusse et al., 2017). With the large-scale introduction of DOTS, the transmission of infection is likely to be reduced due to higher cure and lower relapse

rates. However, the incidence of TB is still very high despite effective DOTS implementation. The problem of HIV and multidrug-resistance aggravates the problem and threatens national TB control programs in several countries including that of Ethiopia (Dye and Williams, 2010, FMOH, 2016, Lange et al., 2018).

In rural settings, access to healthcare is limited; health seeking behavior is poor and the current living condition favors disease transmission. As a result, understanding the burden of TB in rural areas will have important implication for TB control in such settings (Sudha et al., 2003, Cambanis et al., 2005) including Ethiopia where 85% of the population resides in rural setting. Hawassa Zuria Wereda is one of the 9 Woredas in the Sidama zone of the Southern region of Ethiopia with a total population of 153, 190 organized in 23 kebeles. There was no published data on the burden of TB in the area. Moreover, the involvement of voluntary community health workers in the identification of undiagnosed TB in the community had not been evaluated. Therefore, it was important to estimate the burden of TB in the rural settings utilizing voluntary community health workers in the active screening of suspected TB cases in the community.

Understanding the epidemiology of TB and the development and spread of drug resistant TB is limited by scarce molecular epidemiologic data in SSA (Brosch et al., 2002) including Ethiopia. A few molecular epidemiology studies have been conducted in Ethiopia (Bruchfeld et al., 2002, Mihret et al., 2012, Abebe et al., 2012, Tessema et al., 2013, Belay et al., 2014a) and they provided information on the circulating *M. tuberculosis* strains in different study settings and their implication in the transmission of the disease, development and spread of MDR TB. They could serve as a tool to assess the performance of TB control program in the country. However, these already available data were restricted to certain geographic regions of the country and could not give comprehensive information on the molecular epidemiology of the disease in Ethiopia. Therefore, there is a need to have more data on the molecular epidemiology of TB from different parts of the country to better understand the transmission dynamics of the disease in the country, thus the current study will provide data addressing a critical knowledge gap. Besides, much evidence indicates that

the ability of *M. tuberculosis* to spread varies from strain to strain and that different strains have different geographical prevalence. Therefore, it is important to carry out a molecular epidemiology study of the disease in the Southern part of the country in order to get data that will support the TB control program in the prevention and control of TB.

The development and spread of drug-resistant TB is becoming a concern to the national TB control programme of Ethiopia and poses threat to its TB control efforts; and reports coming from the county with regards to MDR TB warrants attention on the problem (Agonafir et al., 2010, Diriba et al., 2013). Shashemene is the major roadside urban center and commercial town and a high TB-HIV co-infection rate (25.7%) had been reported previously in the study area. Additionally, the prevalence of resistant to one or more of the first-line anti-TB drugs was 19.8% and of MDR-TB was 0.9% in the same study area (Arega, 2007 (un-published)). About 10 years had elapsed since the first study was done, moreover the study did not asses the molecular characterization of the strains associated with drug resistance. Therefore, it is important to evaluate the trend of drug resistance and characterize the genetic diversity and drug sensitivity pattern of *M. tuberculosis* strains in this area. Our follow up study will help to measure the program status and provide relevant information that supports the TB control program.

Prisons are increasingly becoming ideal breeding grounds for the concentration and dissemination of TB (including MDR-TB), from which infection is transmitted to the general population. Active transmission of drug-resistant strains, overcrowding and poor living conditions, limited health care, including inadequate TB treatment and control strategies, and the spread of HIV infection, are factors contributing to the disproportional burden of TB in prisons (Todrys and Amon, 2012). While there have been few reports of TB in prisons from Western and Northern parts of Ethiopia, there is no report on TB in prison settings in Hawassa town. Additionally, Hawassa prison is the regional prison center of the southern region of Ethiopia where prisoners from different parts of the region stay. It is the largest prison in the region and there is a long incarceration period that may contribute to a

high risk of TB transmission. Therefore, it would be important to assess the situation of TB and MDR-TB in a prison setting in Hawassa town of the Southern region of Ethiopia.
In general, the study was intended to describe the burden, molecular epidemiology and drug resistance pattern of TB to better understand the transmission dynamics of TB and the development and spread of drug resistance in different settings in Southern Ethiopia. The study provided important information on the DST patterns and genetic diversity of *M. tuberculosis* isolates circulating in Southern Ethiopia and the burden of TB in different settings. The information will support efforts of the control programme in the prevention and controlling of TB in the study settings in particular and the country in general.

1.9. Hypothesis

- ✓ *Mycobacterium tuberculosis* strains circulating in the Shashemene area display higher genetic diversity and a different lineage proportion than those reported for Ethiopia (Firdessa et al., 2013).
- ✓ There is a higher prevalence of TB and MDR TB in the rural settings of Hawassa zuria woreda than the national average
- ✓ There is a higher prevalence of TB and MDR TB in the Hawassa prison center than reported for the Ethiopian prisons
- ✓ The prevalence of MDR TB in Shashemene area is greater than the previously reported prevalence of 0.9% from the same setting (Arega, 2007 (un-published)).

1.10. Objectives

1.10.1. General objective

- ✓ To describe the molecular epidemiology and drug resistance pattern of TB at health facilities (in Shashemene area), in a prison setting (Hawassa prison) and at community level (Hawassa Zuria woreda) in Southern Ethiopia.

1.10.2. Specific objectives

- ✓ To estimate the prevalence of drug resistant tuberculosis among self-presenting pulmonary TB patients seen at health facilities in Shashemene area and compare it to a previous report from the same study area.
- ✓ To determine the prevalence of and factors associated with PTB and MDR TB in Hawassa prison
- ✓ To determine the prevalence of and factors associated with PTB and MDR TB in a community based survey of Hawassa Zuria Wereda using voluntary community health workers.
- ✓ To evaluate the utility of a volunteer health development army (HDA) in conducting population screening for active TB in a rural area of Southern Ethiopia.
- ✓ To characterize the genetic diversity and drug sensitivity pattern of *M. tuberculosis* strains in the study areas

CHAPTER II

MATERIALS AND METHODS

CHAPTER II: MATERIALS AND METHODS

2.1. Study Design and Duration

The study was carried out in three different settings: congregate (in a prison), at health facilities (passive case detection) and community based (house-to-house survey in a rural community). Each study took place in a different time period.

1. A cross-sectional study was conducted to screen prison inmates for pulmonary TB from June 15 through July 13, 2015 and HIV serologic testing was offered from January 13 through February 10, 2016 at the Hawassa Prison, a regional prison in Southern Ethiopia. The study aimed at determining the burden of pulmonary TB using active case finding among prisoners. (Prison study).

2. A cross-sectional study was conducted among new smear positive tuberculosis (SPTB) patients visiting nine TB facilities in and around Shashemene area, Southeast Ethiopia from June 2015 to May 2016. The study aimed at characterizing the drug susceptibility of *M. tuberculosis* strains circulating in the study area. (Health facility-based study).

3. A population-based cross-sectional survey was conducted in six *Kebeles* (the lowest administrative units) in rural community of Hawassa Zuria Woreda, Sidama zone, Southern Ethiopia. The duration of patient screening and data collection was five days for each of the six *kebeles* from May 08, 2016 through June 09, 2016. The main goal of the study was to assess the feasibility and utility of a population screening program for active TB led by Health Development Armies (HDAs). (Community-based study).

2.2. Study Areas

2.2.1. Hawassa prison (Prison study)

Hawassa prison is a regional prison center located in Hawassa town which is located 273 km from the capital city of Addis Ababa, Ethiopia. It has a capacity of approximately 2, 500 inmates and an average stay of 18 months per inmate and an average cell size of 140 m^2.

The prison has a medical clinic that provides general healthcare with the capacity to perform AFB sputum smear microscopy.

2.2.2. Shashemene area (Health facility-based study)

The study was conducted at nine health facilities (two hospitals and seven health centers) in and around Shashemene area, in West Arisi Zone of Oromia Region, Ethiopia. Shashemene is a major urban center and commercial town, located 240 km south of the capital Addis Ababa. The estimated population of the study area including Shashemene and the adjacent rural towns of Wondo Genet, Aje, and Arsi- Negele was around 3 million. All the health facilities included in the study area provide services for the diagnosis and treatment of TB through DOTS clinics. Patients who visited the nine health facilities from the West Arisi Zone and adjoining kebele of Wondo Genet were mapped and fell into seven districts (**Figure 2.1**).

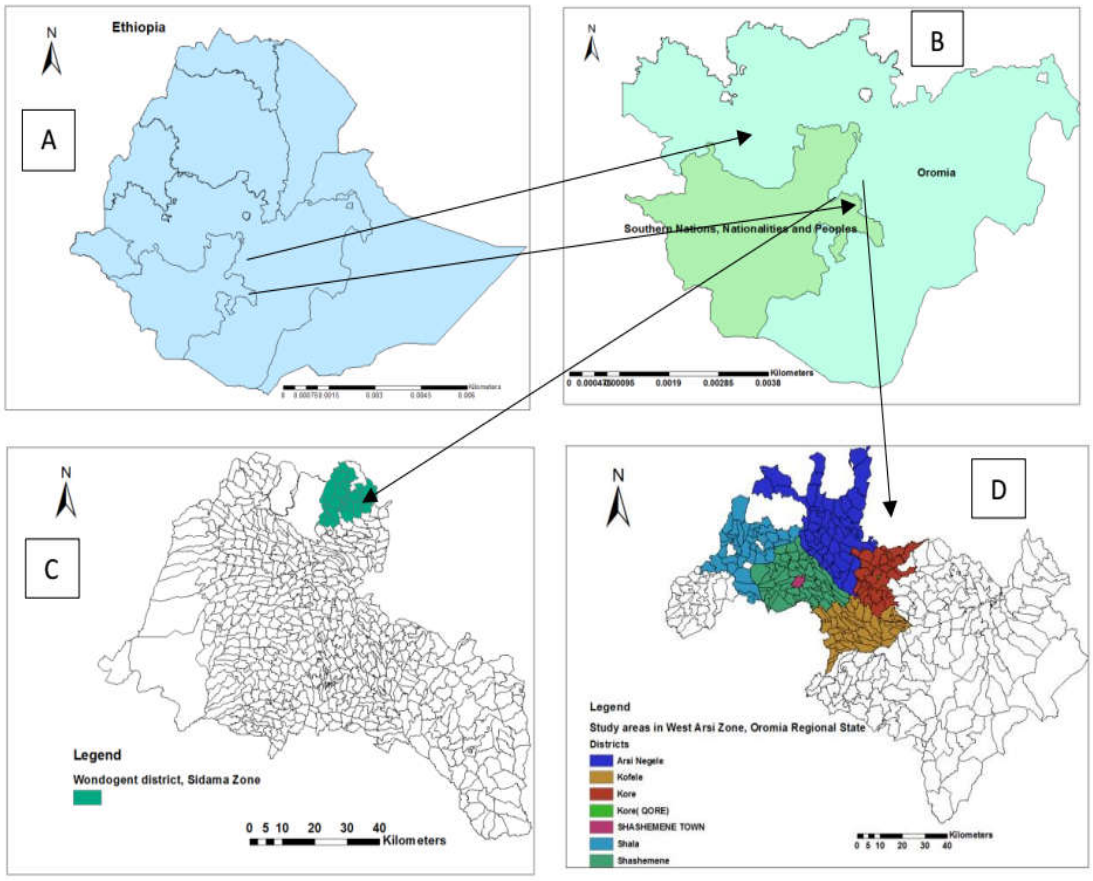

Figure 2.1. Map of the study area (East Arisi Zone, Oromia) with lowest administrative units

2.2.3. Hawassa Zuria Woreda (Community-based study)

Hawassa Zuria woreda (a rural district) is found in the Sidama zone of Southern Ethiopia. Hawassa Zuria woreda has 23 *kebeles* (the lowest administrative units within Ethiopia each with an average population of approximately 5000 persons or 1000 households), and a total population of 153,190 persons, 79,858 of whom were ≥ 15 years (52%). The woreda has one hospital, four health centers, and twenty-three health posts serving the population. Each health center is associated with five satellite health posts and combined they form a primary health care unit (PHCU). The health service coverage of the woreda is 80% (accessible health service is defined as having a health facility within two hours walking distance). Three health centers in the district with functional PHUC were selected for the study (based on accessibility). Then, two *kebeles* from each of the three health centers were selected randomly, thus the study area included six of the twenty-three *kebeles*.

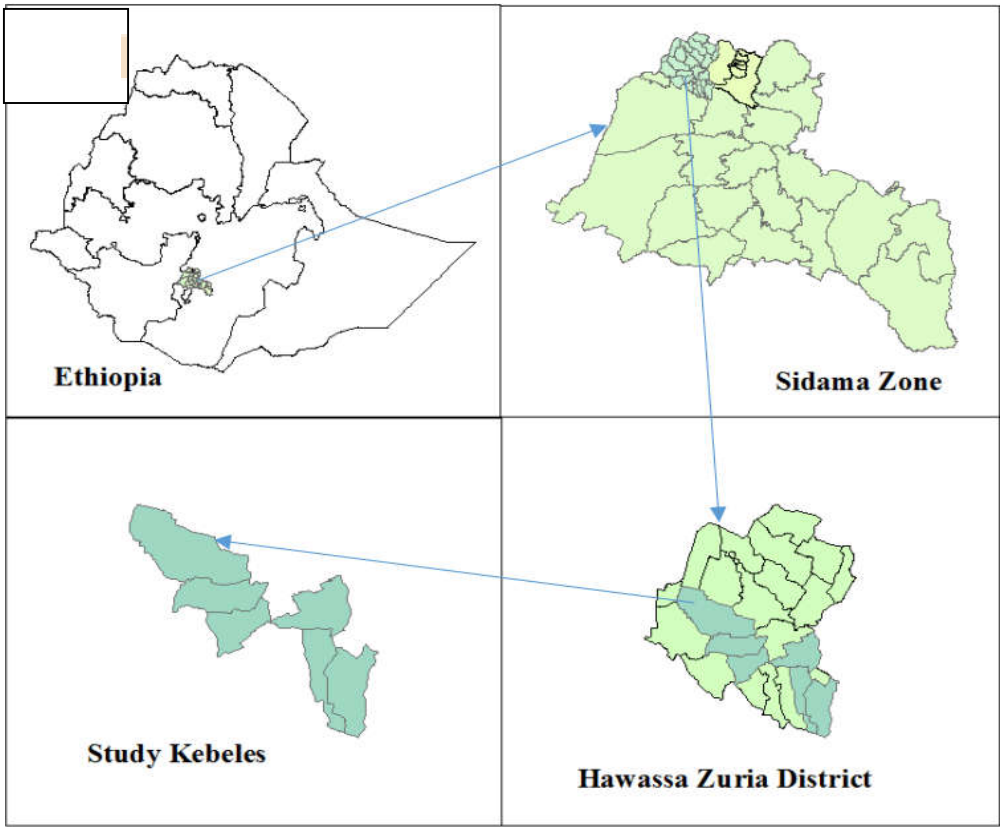

Figure 2.2. Map of Ethiopia, Sidama Zone, and Hawassa Zuria District and study *Kebeles*

2.3. Study Population

2.3.1. Prison study

All prison inmates without a known history of TB who were found in the prison during the study period and consented for the study were enrolled for the survey. At the time of the study, there were 2155 inmates in the prison. A preliminary selection of study subjects was made based on the criteria of cough of 2 weeks or more and consent to participate in the study.

2.3.2. Health facility-based study

Among the TB suspects who were investigated at any one of the nine health facilities during the study period, all newly diagnosed sputum smear positive pulmonary TB patients who consented for the study were enrolled.

2.3.3. Community-based study

Adults and adolescents above 14 years of age residing in the selected six kebeles of the Hawassa Zuria Woreda with cough of two weeks and above and who consented for the study were eligible for the study and therefore, were screened for the presence of active pulmonary TB. All households in the study *kebeles* were surveyed and a total of 24, 517 adults were screened.

2.4 Sample size

2.4.1. Prison study

All the prison inmates without known TB and who consented for the study were screened for the presence of active pulmonary TB. Accordingly, a total of 2068 (96%) inmates were screened for active pulmonary TB. Five PTB patients were already on treatment and they had been identified by passive case detection during the routine diagnosis of TB in the clinic. Additionally, of the 2186 inmates incarcerated during the testing period, 2040 (93%) prisoners without known serostatus agreed to HIV testing and were enrolled for HIV screening.

2.4.2. Health facility-based study

The sample size was determined by taking the prevalence of rifampicin resistance of 1.8% from a previous study (Arega, 2007 (un-published)), 500 new smear positive cases registered during one year in the study setting, a 95% confidence level and a nonresponse rate of 15% resulted in a total sample size of 217 patients. A total of 250 samples were collected. The sample size was calculated based on the sampling method recommended by WHO for drug resistance survey in tuberculosis (WHO, 2009).

Formula used for calculation

$$n(SRS) = \frac{N * z^2 * p * (1-p)}{d^2 * (N-1) + z^2 * p * (1-p)}$$

Where:

- N = total number of new smear positive cases registered during one year in the study setting;
- z = z-value that corresponds to the desired confidence level
- d = absolute precision

p = expected proportion of rifampicin resistance in the target population

2.4.3. Community-based study

The sample size was calculated using the national prevalence of pulmonary tuberculosis of 0.108% (Kebede et al., 2014), 95% CI, a design effect of 2, margin of error of 10%, a non-response rate of 10% and proportion of adults 14years or above to be 55%. This gave a total sample of 16, 500 people and all adults ≥ 15 years in the six kebeles were screened for TB.

Formula used:

$$n = p(1-p)\left(\frac{Z}{E}\right)^2$$

Where:

- z = z-value that corresponds to the desired confidence level
- E = absolute precision
- p = expected proportion of tuberculosis in the target population

2.5 Inclusion and exclusion criteria

The inclusion criteria for the different settings were listed below:

a. The prison study
    - Prisoners without known TB and who had cough ≥2 weeks and voluntary study participation with signed written consent or guardian/parent; assent for the children.
b. The health facility-based study
    - Newly diagnosed pulmonary TB patients and voluntary study participation and signed written consent or guardian/parent; assent for the children.
c. The community-based study.
    - Community members without known TB and had cough ≥2 weeks, ≥15 years of age and voluntary study participation with signed written consent (assent and signed consent by parents or guardians for those under 18 yrs of age).

The exclusion criteria used for the three settings included patients with severe illness unable to provide sputum sample and additionally for the health facility-based study included patients with previous history of anti-TB treatment for more than 4 weeks and for the community study included community members who were not available for screening at time of screening due to travel or hospitalization.

2.6 Sampling technique

The sampling technique employed in the prison study was non-probabilistic sampling (convenience) where all the prison inmates who were found in the study period were surveyed (screened). Similarly, for the health facility-based study purposive sampling was employed, thus consecutive newly diagnosed TB patients attending the nine health facilities during the study period were enrolled. For the community-based study, both probabilistic and non-probabilistic sampling techniques were involved. First, the selection of the three health centers with functional PHCU was made on the bases of accessibility, and then section of the two *Kebeles* from the catchment area of each health center was made randomly.

2.6.1. Operational definitions:

- PTB patient case in the prison study was defined as prison inmate whose sputum sample was positive on Xpert MTB/RIF test (Cepheid, Sunnyvale, CA, USA).
- A confirmed pulmonary TB case for the community-based study was defined as one in whom a sputum specimen was Xpert MTB/RIF test and/or culture positive. Clinical treatment outcomes were defined as per national guidelines (FMOH, 2016).
- Newly diagnosed pulmonary TB patients in health facility-based study referred to patients who have never been treated for TB or have taken anti-TB drugs for less than 1 month. Additionnaly, *M. tuberculosis* isolates that share the same genotype based on spoligotyping considered clustered.

2.7 Data collection

2.7.1. Prison study

All eligible prisoners who consented for the study were enrolled in the study. Enrollment was performed by nurses from the prison clinic and prison's health committee (prison inmates selected by prison authorities to facilitate health work between the inmates and the prison clinic). They provided study information to the prisoners by visiting their cells, asked those interested in participating to come to the prison clinic to receive further details about the study. All study participants had a cough screen performed and those with a positive screen (cough $\geq$ 2 weeks) provided informed consent and were interviewed including for the presence of other symptoms and asked to submit two sputum samples (1 spot and 1 morning). Five persons were already on anti-TB treatment and were excluded except for estimating point prevalence.

HIV screening was carried out after providing pre-counseling education by a trained prison nurse. Additionally, HIV testing was offered and performed for participants diagnosed with active TB cases after obtaining consent.

2.7.2. Health facility-based study

Study participants after they gave written consent for the study, submitted three consecutive sputum samples (spot-morning-spot) per patient at respective health facility in the study

area. Socio-demographic and clinical information was collected for all study participants by a TB clinic nurse at the respective health facilities using a pre-tested standard questionnaire. Data on HIV status was obtained from health facility records.

2.7.3. Community-based study

Prior to the study, meetings were carried out with *kebele* leaders, HEWs and members of the HDA to inform them of study objectives and procedures and to receive input and feedback. Subsequently, trainings were conducted with the field supervisors and HEWs at health posts.

Identification of presumptive TB cases (i.e., those with a positive cough screen) was carried out by members of the HDA. There were 30 to 58 HDAs in each *kebele* depending on population size and approximately 350 HDAs were involved in active TB case finding. Prior to the survey, community mobilization (creating awareness about the study) was done through religious institutions and schools in the community. Afterwards, the HDA conducted house-to-hose visits to identify people who had cough of at least 2 weeks. Individuals with cough $\geq$2 weeks were considered a presumptive TB case and brought to the health post. At the health post, they were evaluated by field supervisors (health professionals who have experience in TB and community work) and HEWs. Those who met study eligibility (cough $\geq$2 weeks, $\geq$15 years of age and voluntary study participation) were interviewed and asked to submit two sputum samples (spot and morning). For all study participants, a pretested (validated) structured questionnaire was used to collect data on patient demographics, clinical presentation, and associated risk factors for the transmission of TB. Two field supervisors and the study principal investigator (YM) monitored the daily data collection process.

2.8 Sample Collection, Handling and Transport

2.8.1. Prison study

For each participant with a positive cough screen, spot and morning sputum samples were collected in the prison health clinic (aseptically in clean screw capped disposable sputum cups). Acid-fast bacilli (AFB) smear microscopy was done by laboratory technician at the prison health clinic. The remaining portions of the samples were transported daily to the

regional public health laboratory that is about 500 meters far using ice. The two sputum samples were pooled individually into 50 ml sterile screw capped universal test tube and stored in -20 freezer until transport to Armauer Hansen Research Institute (AHRI) in Addis Ababa by cold chain.

2.8.2. Health facility-based study

Three consecutive sputum samples (spot-morning-spot) per patient were collected at the respective health facilities in the study area (aseptically in clean screw capped disposable sputum cups). Sputum smears were prepared and examined by an onsite health facility laboratory technologist. The remaining portion of the three sputum samples from AFB smear positive patients were pooled individually into 50 ml sterile screw capped universal test tubes and stored at the diagnostic centers at -20˚C for a maximum of one week until transported by cold chain to AHRI in Addis Ababa, Ethiopia for mycobacterial culture and molecular testing.

2.8.3. Community-based study

Spot and morning sputum samples were collected per presumptive TB cases at the health posts aseptically in clean screw capped disposable sputum cups. Smear for AFB smear microscopy was prepared at the health posts by laboratory technicians assigned for the study. Slides were prepared on the same day of sputum collection and along with the remaining portion of the sputum samples were transported daily to a health center ~25 kilometers away with ice box. Here the slides were stained and examined by an on-site health center laboratory technician. The remaining portions of the two sputum samples were pooled individually into 50 ml sterile screw capped universal test tube and stored in -20 freezer until transported to the Armauer Hansen Research Institute (AHRI) in Addis Ababa on cold chain.

2.9. Laboratory investigations

2.9.1. Sputum microscopy

After sputum smears were prepared on labeled, new, frosted end slides for individual study participant, they were all stained using the standard Ziehl-Neelsen (ZN) hot staining

technique and examined for AFB using regular light microscopy (EPHI, 2014b) by experienced laboratory personnel at health facilities in the respective study settings.

2.9.2. Xpert MTB/RIF assay

Portion of the pooled sputum samples from the prison and community-based studies were tested by Xpert MTB/RIF assay at Shashemene referral hospital located 230 km away from Addis Ababa. The Gene Xpert MTB/RIF system (Cepheid, Sunnyvale, CA, USA) is a real-time PCR-based assay for the detection of MTBC and mutations associated with rifampicin resistance that detects directly in clinical specimens (Shinnick et al., 2015).

2.9.3. HIV Testing

HIV testing was performed according to the national testing algorithm. Briefly, blood samples from finger-pricks were tested first with HIV (1+2) Antibody Colloidal Gold (Shanghai Kehua Bioengineering, Shanghai, China); positive samples were confirmed using Stat-Pak (Chembio, Medford, Brookhaven, NY, USA), while discordant results were resolved using HIV-1/2 Unigold Recombinant Assay (Trinity Biotech, Bray, Ireland).

2.9.4. Mycobacterial culture

The pooled sputum samples were processed within one day based on standard procedures as previously described (WHO, 1998) at AHRI. In brief, the sputum samples were digested and decontaminated using Petroff's method and the processed sample was inoculated into three tubes containing egg-based Löwenstein Jensen (LJ) media (two with glycerol and one with pyruvate) that were prepared according to standard procedure (WHO, 2014b). The inoculated media were incubated at 37^{o}C for at least 8 weeks, with weekly observation for the presence of mycobacterial colonies. Cultures with no growth after the eighth week were considered negative. Mycobacterial growth was confirmed by typical colony morphology and AFB staining. Microscopic examination of the colonies was performed using Ziehl-Neelsen staining method (EPHI, 2014a). Colonies from AFB positive isolates were collected into two cryo vial. One vial was used to prepare heat killed cells for molecular typing with bacteria treated at 80˚C in a sonicator water bath for one hour. The other vial was stored at -80˚C in freezing medium until sub-cultured for drug sensitivity test (DST).

2.9.5. Drug susceptibility testing (DST)

The conventional indirect proportion method was employed to do the DST using 7H10 medium on 24-well tissue culture plates. The DST protocol used in the study was the standard protocol of the TB laboratory of the Armauer Hansen Research Institute (AHRI) which itself was adopted from the guidelines of the World Health Organization (WHO, 2003). The four anti-TB drugs (Isoniazid, Rifampicin, Ethambutol and Streptomycin) were mixed with the media at the recommended concentration and dispensed into 9 wells of the 24 well tissue culture plates and two wells were dispensed with drug free media. A standardized bacterial suspension (a 1.0 McFarland standard*)* was prepared and 10µl of the prepared bacterial suspension was dispensed into each of the drug containing and one drug free media. The remaining well with drug free medium was inoculated with 10µl of 1% (1:100) bacterial suspension. The plate was sealed with par film and incubated in an inverted position at 35˚C in the presence of sufficient humidity. Bacterial growth was checked on day 6, 12 and 19 of culture. Resistance was expressed as the percentage of colonies that grew on critical concentrations of the drugs, i.e. 0.2 µg/ml for isoniazid (INH), 1µg/ml for rifampicin (RPM), 5µg/ml for ethambutol (EMB) and 2µg/ml for streptomycin (STM). The interpretation as resistance was based on the standard criteria for resistance, i.e. 1% for all drugs (Wedajo et al., 2014). For internal quality control, *M. tuberculosis* H37Rv strain sensitive to all anti-TB drugs was processed with the samples. Control strains resistant to the different anti-TB drugs were inoculated into the wells and used as positive controls.

2.9.6. Molecular Genotyping

2.9.6.1. RD-9 deletion analysis

The presence or absence of regions of difference-9 (RD9) was checked on heat-killed culture isolates to identify *M. tuberculosis* from the other species of *M. tuberculosis* complex. RD9 deletion analysis is a polymerase chain reaction (PCR) based analysis and the primers used for RD9 deletion typing were: RD9flankF, 5'-GTG TAG GTC AGC CCC ATC C-3'; RD9intR, 5'-CTG GAC CTC GAT GAC CAC TC-3'; and RD9flankR, 5'-GCC CAA CAG CTC GAC ATC-3'. PCR amplification of the mixtures was performed using a Thermal Cycler according to standard procedures (Parsons et al., 2002). The amplification product was run by electrophoresis in 1.5% agarose gel and the results were interpreted as

M. tuberculosis (RD9) when a band of 396bp was observed. Detection of a band size of 575 bp was considered to be positive for the other members of *M. tuberculosis* complex species (*M. bovis* or *M. africanum).*

2.9.6.2. Spoligotyping

M. tuberculosis isolates confirmed by RD9 deletion analysis were further characterized by spoligotyping according to standard procedure (Kamerbeek et al., 1997). The analysis detects the polymorphism in the direct repeat (DR) locus of the mycobacterial genome. In briefly, the direct-repeat (DR) region was amplified with primers DRa and DRb which are derived from this region. The reaction mixture was amplified with PCR and the amplified product was hybridized to a set of 43 immobilized oligonucleotides, each corresponding to one of the unique spacer DNA sequences within the DR locus (inter-DR spacer). After hybridization, the DNA was detected by the enhanced chemiluminescence and by exposure to X-ray film as specified by the manufacturer. Each hybridization pattern (spoligotype) is represented as a 43-digit binary vector that may be translated to a 15-digit octal code. Individual spoligotyping patterns were compared with the recent International Spoligotyping Database (SITVITWEB, http://www.pasteur-guadeloupe.fr:8081/SITVIT2/). Spoligotyping International Types (SIT) and sub-lineages (clades) were assigned according to signatures provided in SITVITWEB data base. An isolate was defined as a shared type if the same spoligotype was found in the database. If no matching spoligotype was found in the database, the isolate was defined as orphan (new). Lineage types were assigned using a protocol for classification and analysis of MTBC lineages (Shabbeer et al., 2012).

2.9.6.3. Whole genome sequencing (WGS)

Genomic DNA was extracted from isolates which were grown on LJ solid medium using standard methods at AHRI (chloroform method) (Larsen et al., 2007). The extracted DNA samples were shipped to London School of Hygiene and Tropical Medicine (LSHTM). Whole-genome sequencing was performed at LSHTM on an Illumina MiSeq instrument using reads of 300bp in length in the paired end modus. Raw sequence data were de novo assembled. They were also aligned to the H37Rv reference genome (Genbank accession number: NC_000962.3) using the BWA mem algorithm (settings: –c 100 –T 50). The

SAMtools/BCFtools (default settings) and GATK software were used to call SNPs and small indels. The GATK parameters used are "-T UnifiedGenotyper -ploidy 1 -glm BOTH -allowPotentiallyMisencodedQuals 2". The overlapping set of variants from the two algorithms was retained for further analysis. Alleles were additionally called across the whole genome (including SNP sites) using a coverage-based approach. A missing call was assigned if the total depth of coverage at a site did not reach a minimum of 20 reads or none of the four nucleotides accounted for at least 75% of the total coverage. Samples or SNP sites having an excess of 10% missing genotype calls were removed. Delly2 software was used to identify large deletions.

2.10. Quality control /Reference Strains

2.10.1. Sputum microscopy

All health facilities were provided with new frosted end slides and same lot of staining solutions and were used throughout the study. Quality control of the staining solutions was made by testing the lot with known positive and negative sputum smears at AHRI.

For the prison study, blind rechecking of stained slides was carried out at AHRI by a laboratory technician who was blinded for the initial readings at the study area (Hawassa prison) and Xpert result. The AFB sputum microscopy results concurred with the quality control readings at AHRI.

2.10.2. Culture

Known reference strain (H37Rv) of mycobacterium was used for quality control of the culture procedure.

2.10.3. DST

For internal quality control, *M. tuberculosis* H37Rv strain sensitive to all anti-TB drugs was processed with the samples. Additionnaly, control strains resistant to the different anti-TB drugs were inoculated into the wells where the respective anti-TB drugs had been added.

2.11. Data analysis (Data management)

All data were double entered into an online REDCap database (Harris et al., 2009) and analyzed using STATA v.1software. In univariate analysis, differences in categorical variables were tested using the Chi-square test, and for continuous variables a two-sample t-test was used. A multivariable logistic regression model was used to evaluate the independent association of potential risk factors with TB diagnosis. Model building and selection was based on the purposeful selection of covariates strategy as previously described, based on epidemiological findings in the univariate analysis and biological plausibility(Hosmer and Lemeshow, 2000). A p-value of <0.05 was considered significant.

2.12. Spatial analysis

Mapping of TB lineage and strain clusters was made using geographic information system (GIS). First, the proportion of different types of TB lineages was computed (stratified) by district to look for variations in geographic distribution of lineages. Second, clustered strains were mapped by geographic locations. ArcGIS software (10.2) was used for mapping the geographic distribution of lineages and clustered strains by district and clustered strains were further mapped by kebeles. The shape file of study districts and kebeles were obtained from Central Statistics Agency of Ethiopia (CSA). A geographic projection of the World Geodetic System (WGS), Universal Transverse Mercator (UTM) Zone 37 N was used for analysis. The data of attributes (number and proportion of TB cases, lineages and TB strains) were geo-linked for each district and kebele with the geographic data (shape file) using feature identification.

2.13. Ethical consideration

The study was approved by Addis Ababa University, AHRI Institutional Review Boards and the Ethiopian National Ethics Review committees. Due to the difference in the study settings, specific ethical considerations were employed.

For the prison study, study permission was also obtained from the Southern Ethiopia Regional Health Bureau and prison administration. Patients with active TB started treatment in the prison clinic. Newly diagnosed HIV positive participants were linked to a nearby health institution providing HIV care.

For the community-base study, study permission was also obtained from the Southern Regional Health Bureau, Zonal Health Department and the woreda health office. Patients diagnosed with active TB were referred to their catchment health center and hospital for treatment.

For the health facility-base study, study permission was also obtained from the Oromia Regional Health Bureau, Western Arisi zone Health Department, Southern Regional Health Bureau and Sidama Zone Health Department.

CHAPTER III

RESULTS

CHAPTER III. RESULTS

The following section presents the results of the study findings from the three settings; prison, health facility and community-based studies in an orderly manner.

3.1. Prison study

3.1.1. Sociodemographic characteristics

Among 2155 inmates, a total of 2068 (98%) consented to participate and had a cough screen performed. From this group, there were 372 (18%) inmates who reported a cough ≥ 2 weeks (**Figure 3.1.1**). Among those with a positive cough screen, the median age was 23 years (inter quartile range ([IQR] 20-28 years), 362 (97%) were male and 10 (3%) were female. The majority of prisoners (n=329, 88%) had no prior history of incarceration and most were from an urban area (n=235, 63%) (**Table 3.1.1**). There were 293 (73%) persons who reported having a fever, 315 (85%) night sweats, and 241 (65%) weight loss. With regards to prison characteristics, the median number of prisoners per cell was 162 ([IQR] 14 – 360) and the median duration of imprisonment at the time of screening was 10 months ([IQR] 0.5-2years).

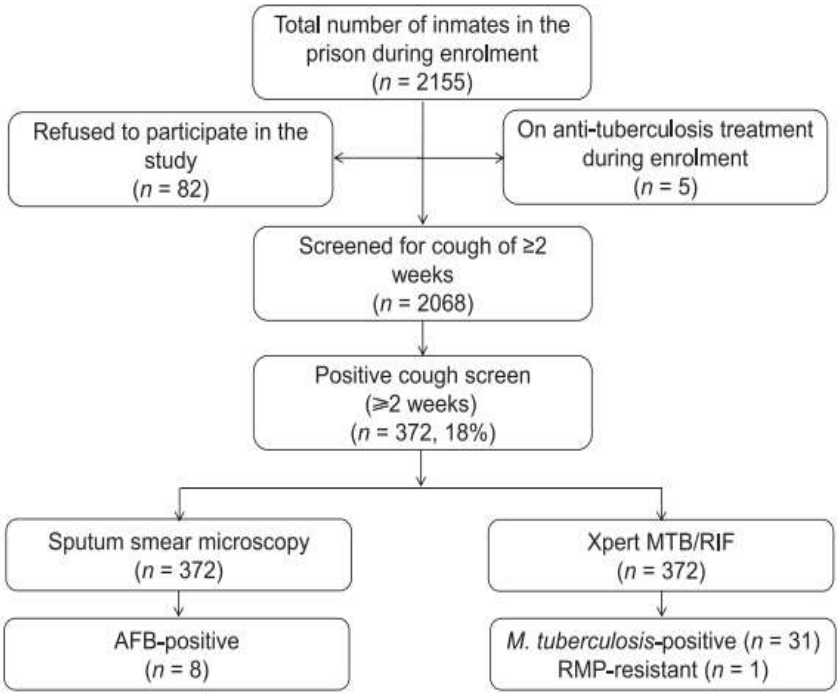

Figure 3.1.1. Study diagram, Prison study. AFB=Acid-fast-bacilli; RMP=Rifampicin

Table 3.1.1. Predictors of having pulmonary TB among persons with a positive cough screen

Characteristic	Total (n=372 (%)	No TB (n=341)	TB (n=31)	Univariate analysis	
				OR (95% CI)	*P*-Value[a]
Sex (Male)	362 (97)	331 (97)	31 (100)		
Age (year), mean	26	26	24		0.08[b]
Illiterate	322 (87)	294 (86)	28 (90)	1.49 (0.43-5.10)	0.52
Unemployed	346 (93)	319 (94)	27 (87)	0.46 (0.14-1.44)	0.18
Not married	209 (56)	192 (56)	17 (55)	1.06 (0.50-2.22)	0.87
Duration of cough in weeks					
2- 4	93(25)	78 (23)	15 (48)		
>4	279 (75)	263 (77)	16 (52)	3.16 (1.49-6.68)	0.003
Fever	273 (73)	247 (72)	26 (84)	1.97 (0.73-5.30)	0.17
Night sweats	315 (85)	289(85)	26 (84)	0.93 (0.35-2.64)	0.89
Loss of appetite	235 (63)	213 (62)	22 (71)	1.46 (0.65-3.28)	0.35
Weight loss	241 (65)	219 (64)	22 (71)	1.36 (0.60-3.05)	0.45
Chest pain	338 (91)	308 (90)	30 (97)	3.21 (0.42-24.3)	0.13
Shortness of breath	252 (68)	228 (67)	24 (77)	1.69 (0.71-4.06)	0.23
Previous imprisonment	43 (12)	42 (12)	1(3)	0.23 (0.03-1.78)	0.16
Previous TB treatment	34 (9)	31 (9)	3 (10)	1.07 (0.30-3.72)	0.91
Tobacco use (smoking cigarettes) at time of incarceration	110 (30)	104(31)	6 (19)	0.54 (0.21-1.37)	0.19
Chewing chat	171 (46)	159 (47)	12 (38)	0.72 (0.34-1.53)	0.39
Incarceration period in years					
≤ 1	180 (48)	161 (47)	19 (61)		
1-3	113 (30)	106 (31)	7 (23)	0.55 (0.22-1.37)	0.20
>3	79 (21)	74 (22)	5 (16)	0.54 (0.19-1.49)	0.28
Contact with known TB patient in the prison	90 (24)	83 (24)	7 (23)	0.90 (0.37-218)	0.82
Presence of coughing people in the cell	191(51)	175 (51)	16 (52)	1.01 (0.48-2.11)	0.97
No. of prisoners per cell					
≤100	35 (9)	32 (9)	3 (10)		
>100	337 (91)	309 (91)	28 (90)	0.96 (0.27-3.35)	0.95

CI- confidence interval; OR-odd ratio; TB-tuberculosis

a- *p*-value for Chi-square test unless otherwise stated; b-*p*-value for two-sample t-test

3.1.2. Pulmonary tuberculosis and HIV infection

Among those with a positive cough screen, 8 (2%) had a positive AFB sputum microscopy result and 31 (8%) of 372 had a positive Xpert TB/RIF test result and thus had active pulmonary TB disease per the study definition. The results of the AFB sputum microscopy were concurred with the quality control readings at AHRI. All samples that were positive on smear microscopy also had a positive Xpert TB/RIF test. By considering the 5 PTB cases which were already on anti-TB treatment at the initiation of the study, the overall point prevalence of PTB among those incarcerated was 1789 per 100,000 persons. Among the 31confirmed TB cases, 3 had a prior history of TB treatment. The median time in prison for the 31 confirmed TB cases was 8 months and the majority (n=19, 61.3%) had been imprisoned for ≤ 1 year; 28 (90%) were living with > 100 inmates per cell. The one TB case that had rifampicin resistance by Xpert was confirmed as MDR TB by culture and drug susceptibility testing and was resistant to all of the four first line drugs tested (isoniazid, rifampicin, streptomycin and ethambutol). The person with MDR-TB had a history of previous TB treatment.

For the HIV screening, a total of 2186 inmates were incarcerated during the study time and 2040 (93%) agreed to HIV testing. Among the 2040 inmates tested, nine (0.4%) were HIV seropositive. Of the 31TB patients identified by Xpert, HIV test results were obtained only for 16 of the TB cases and none were HIV seropositive.

3.1.3. Association between exposure variables and PTB

The duration of cough was the only variable that was statistically significant in univariate analysis. In multivariate analysis, the presence of a >4 weeks of cough was independently associated with an increased risk of having PTB (OR = 3.34, 95% CI 1.54-7.23) (**Table 3.1.2**).

Table 3.1.2. Multivariate analysis of predictors of pulmonary tuberculosis among prison inmates with a positive cough screen

Characteristics	Multivariate analysis	
	aOR (95% CI)	*P*- Value
Duration of cough in weeks		
2-4	1.00	
≥4	3.34 (1.54-7.23)	0.002
Previous imprisonment	0.32 (0.04-2.50)	0.28
Tobacco use	0.63 (0.24-1.64)	0.35
Incarceration period in years		
≤ 1	1.00	
1-3	0.48 (0.19-1.23)	0.13
>3	0.52 (0.18-1.51)	0.23

aOR=adjusted odds ratio; CI=Confidence interval

3.2. Health facility-based study

The overall work flow of the study is depicted on **Figure** 3.2.1

3.2.1. Sociodemographic characteristics

Among 250 newly diagnosed sputum smear positive TB patients enrolled, 145 (58%) were male and 143 (57%) from urban areas. The median age was 25 years (interquartile range [IQR] 20-30) and majorities (86%) of the study participants were in the age group of 15-44 years. One hundred and twenty-nine (52%) were married, 195 (76%) had educational level of primary school and above. Farmers, students and house wife altogether account 70 % (174) of the study participants. (**Table 3.2.1**). TB-HIV co-infection was 10 (4%).

Table 3.2.1. Sociodemographic characteristics and clinical variables of study subjects

Characteristics	**Number**	**Percentage (%)**
Sex		
Male	145	52
Female	105	48
Age in years		
<14	14	5.6
15-34	193	77.2
35-44	23	9.2
45-54	9	3.6
≥ 55	11	4.4
Location		
Urban	107	42.8
Rural	143	57.2
Marital status		
Single	109	43.6
Married	129	51.6
Other	12	4.8
Education		
Primary school and above	195	78.0
Illiterate	55	22.0
Occupation		
Farmer	79	31.6
Student	57	22.8
House wife	38	15.2
Government employee	9	3.6
Others	67	26.8

Clinical variables		
Fever	213	85.5
Night sweat	220	88.0
Loss of appetite	223	89.2
Weight loss	232	92.8
Chest pain	208	83.2
HIV serostatus		
Positive	10	4.0
Negative	236	96.0
Not tested	4	1.6

3.2.2. Genetic diversity of strains

All 250 AFB positive sputum samples underwent culture testing and 230 (92%) were positive, 8 (3.2%) were contaminated and 12 (4.8%) were not grown on culture (**Figure 3.2.1**). The 230 isolates were all identified as *M. tuberculosis* by RD9 deletion analysis Spoligotyping analysis found a total of 65 spoligotype patterns, of which 36 (55%) of them were registered in the international data base and 29 (45%) were new patterns (orphans). With regards to lineage distribution, 187 of the isolates (81%) belonged to the Euro-American lineage (L4), 31 (14%) to East-African-Indian (L3) and 8 (4%) to Lineage 7 (Ethiopian lineage) and 4 strains could not be assigned to any of the lineages. The predominant clade (sub-lineage) was T1 (51, 22%), followed by T3-ETH (48, 21%), H3 and CAS1-Delhi (23, 10%) each. The most dominant shared types were SIT149 (48, 21%) and SIT53 (44, 19%) and orphan strains (37, 16%). One hundred and ninety-three (84%) of the isolates were clustered into 29 spoligotype patterns and the remaining strains fell into single spoligotype. Cluster size varied from 2 to 48 strains per cluster. Of the clustered 193 strains, 179 (93%) of them were registered in the international data base and 14 (7%) of them were orphans. Sixty-two (27%) of the strains were not assigned for clade in the SITVITWEB database (**Table 3.2.2**).

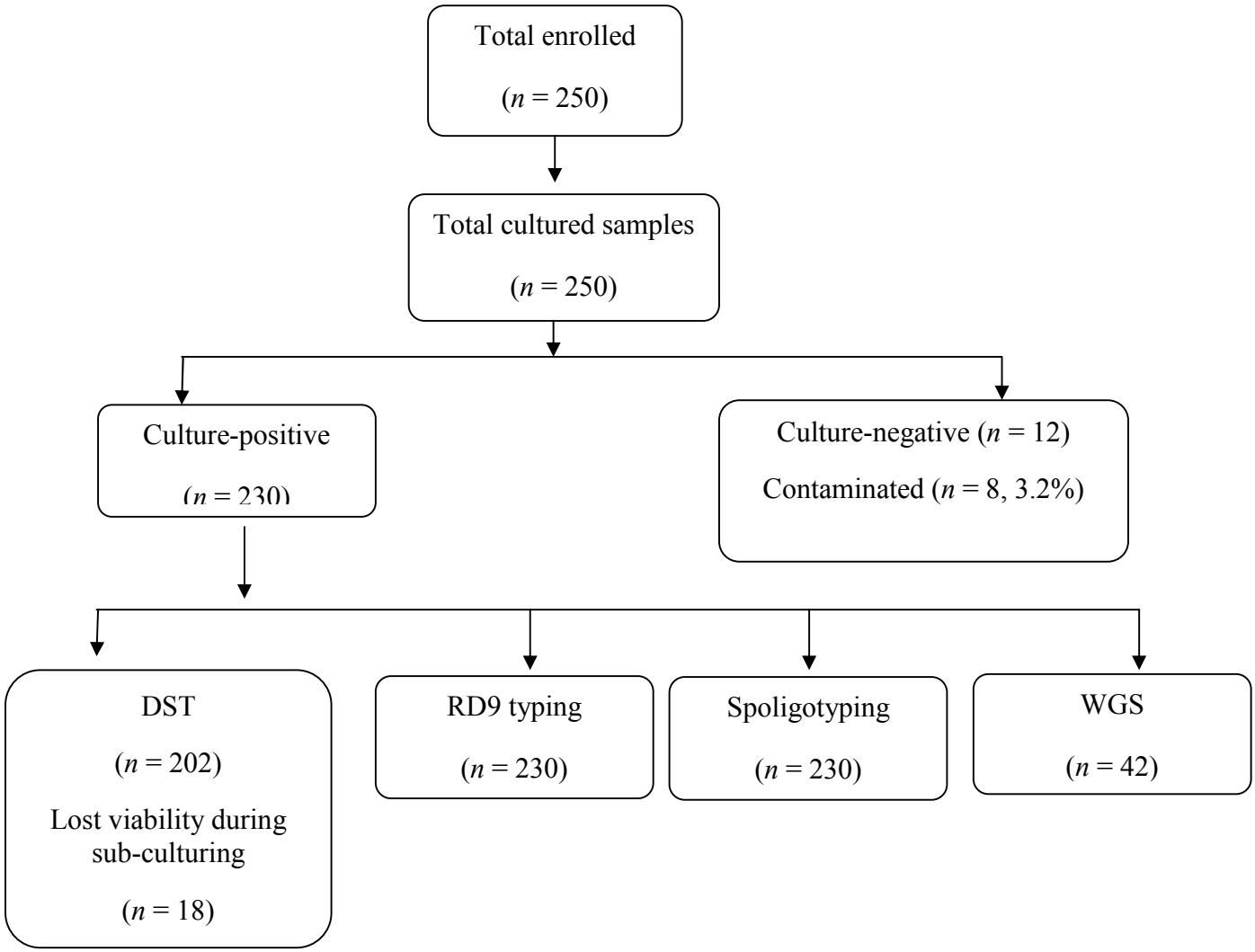

Figure 3.2.1. Study Diagram, Health facility-based study.

DST-drug susceptibility testing, RD9-region of difference-9, WGS-whole genone sequence

Table 3.2.2. Spoligotyping result of 230 isolates, Southern Region of Ethiopia

Lineages, Sub lineages (clades)	SIT (No. of samples. % of the total sample)
Lineage 4, T1 (n=51)	SIT 53 (n=44, 19%)
	SIT 358 (n=4, 1.74%)
	SIT 334 (n= 2, 0.87 %)
	SIT 205 (n= 1, 0.43 %)
Lineage 4, T3- ETH (n=48)	SIT 149 (n=48, 20.9%)
Lineage 4, T2 (n= 2)	SIT 52 (n=2, 0.87%)
Lineage 4, Ambiguous: T2X1 (n=2)	SIT 336 (n=2, 0.87%)
Lineage 4, T3 (n=12)	SIT 37 (n=10, 4.4%)
	SIT 121 (n=2, 0.87)
Lineage 4, Ambiguous: T3T2 (n=1)	SIT 73 (n=1, 0.43%)
Lineage 4, H3 (n=23)	SIT 134 (n=1, 0.43%)
	SIT 49 (n=1, 0.43%)
	SIT 669 (n=10, 4.4%)
	SIT 390 (n=2, 0.87%)
	SIT 394 (n=2, 0.87%)
	SIT 777 (n=7,3.0%)
Lineage 4, H4 (n=1)	SIT 35 (n=1, 0.43%)
Lineage 4, LAM10-CAM (n=1)	SIT 838 (n=1, 0.43%)
Lineage 4, sub-family not assigned (n=47)	SIT 4 (n=5, 2.2%)
	SIT 159 (n=1, 0.43%)
	SIT 156 (n=4, 1.74%)
	SIT 46 (n=3, 1.3%)
	SIT 1410 (n=2, 0.87%)
	SIT 602 (n=3, 1.3%)
	Orphan (n=29, 12.6%)
Lineage 3, CAS1-Delhi (n=23)	SIT 25 (n=6, 2.6%)
	SIT 26 (n=11, 4.8%)
	SIT 247 (n=1, 0.43%)
	SIT 1198 (n=1, 0.43%)
	SIT 1314 (n=1, 0.43%)
	SIT 2359 (n=2, 0.87%)
	SIT 485 (n=1, 0.43%)
Lineage 3, CAS2 (n=1)	SIT 1979 (n=1, 0.43%)
Lineage 3, sub-family not assigned (n=7)	Orphan (n=7, 3.0%)
Lineage 7	SIT 910 (n=8, 3.5%)
Lineage unknown, MANU2 (n=2)	SIT 54 (n=2, 0.87%)
Lineage not assigned (n=4)	No described patterns (n=3, 1.3%) Orphan (n=1, 0.43%)

3.3.3. Mapping of TB lineage and strain clusters

Seven districts (6 from West Arsi, Oromia region and one district from Sidama Zone, SNNPR) were included to look for the geographic distribution of lineages and clustered strains. The spatial distribution of lineages identified in the study was presented in **Figure 3.2.2**

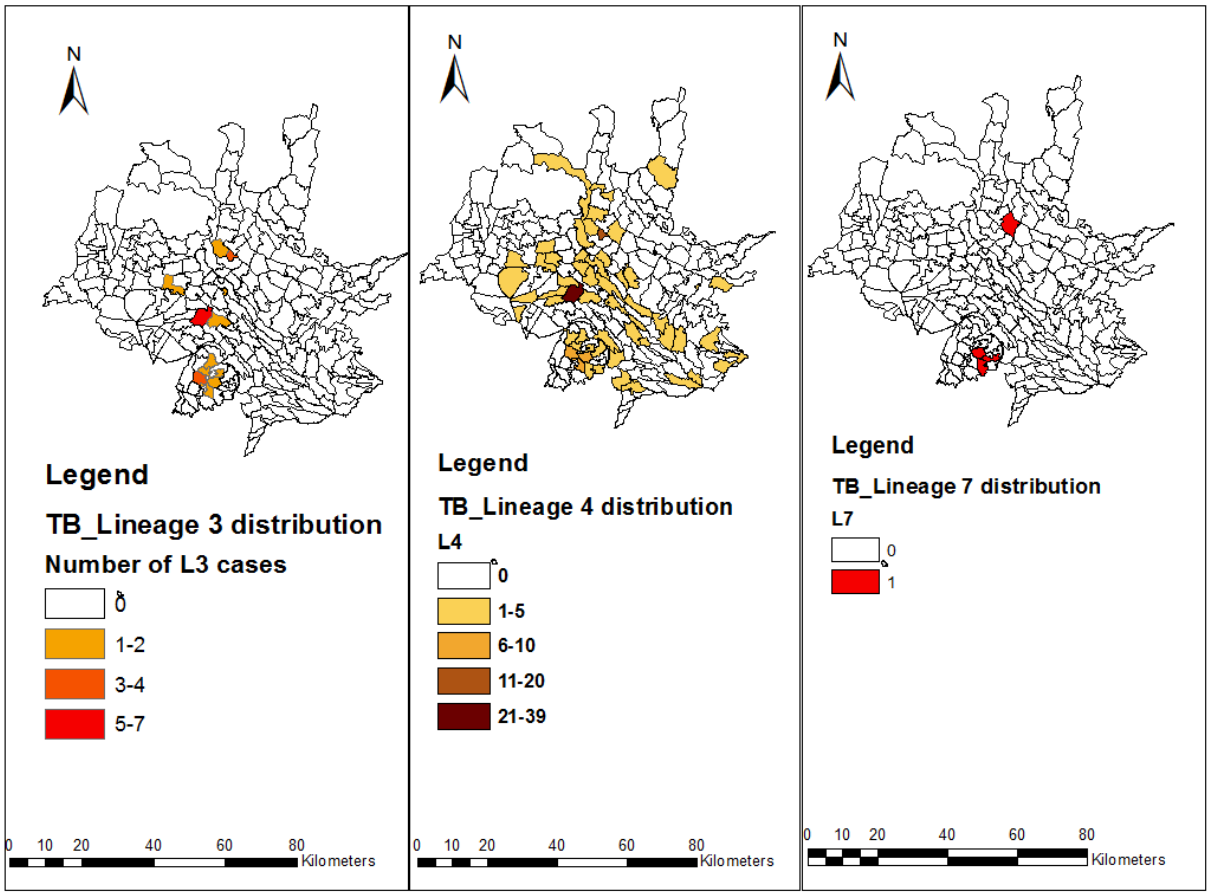

Figure 3.2.2 Spatial distribution of TB lineages, West Arisi zone and Wondo genet districts

Using GIS, it was possible to map the geographic location of clustered strains. Accordingly, SIT 149 is a widely distributed clustered strain both at district and kebele levels. The distribution of clustered strains varies within kebeles in the study area, and the highest proportions of clustered strains were observed in Wendo Genet district of Sidama Zone with SIT 149 (6.52%), SIT 699 (3.04%), and SIT 25 (2.61%). Shashemene town also had a

higher proportion clustered strains such as SIT 149 (4.35%), SIT 53 (4.8%) than other districts. Overall, clustered strains showed a varying distribution across districts and the districts such as Wondo Genet had all types of TB clusters (**Figure 3.2.3**). The data was further analyzed at *Kebele* level within districts and the distribution of strain clusters also vary across *Kebeles* in each district. Some *Kebeles* had all types of strain clusters (**Figure 3.2.4 (A) and 3.2.4 (B)**).

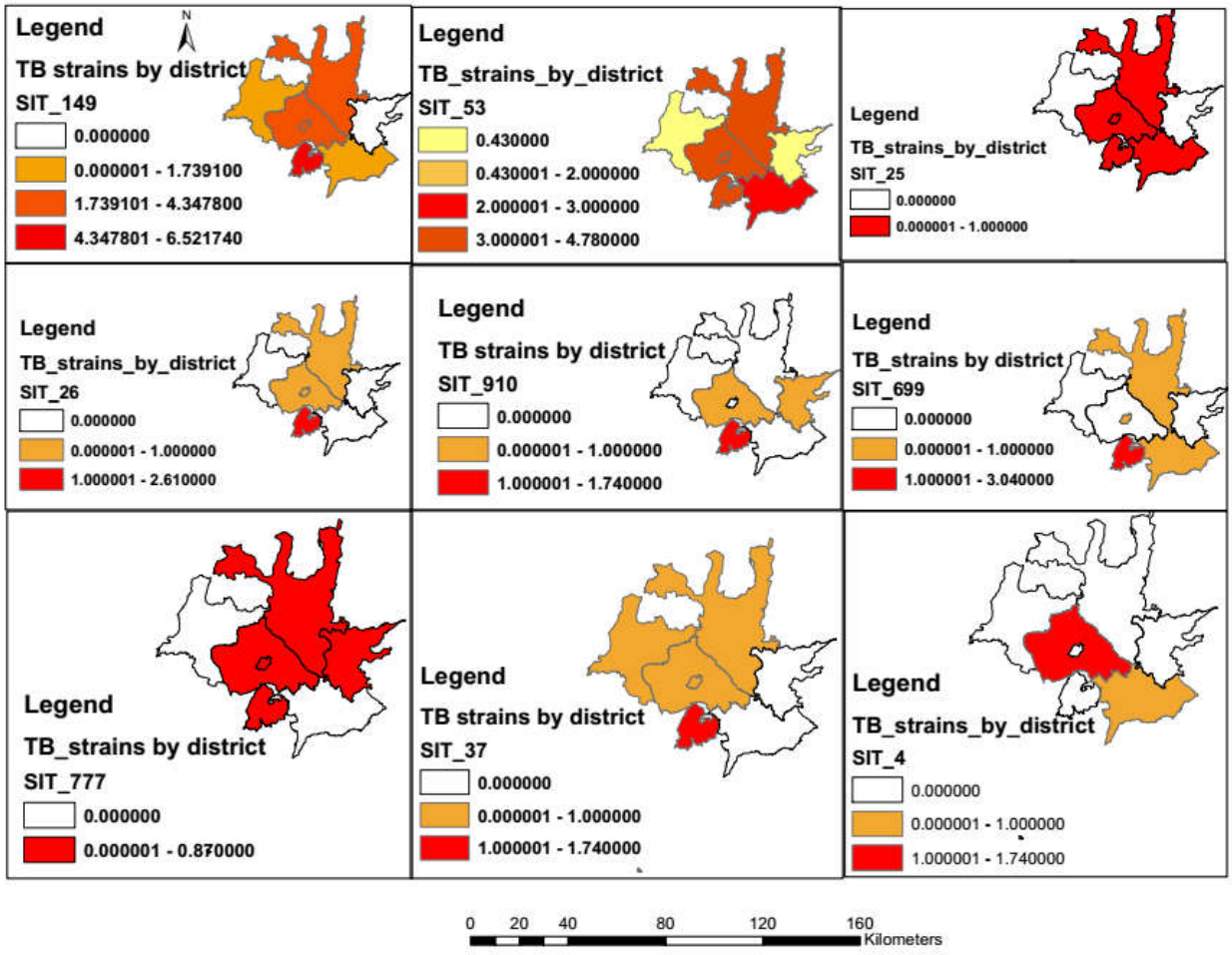

Figure 3.2.3. Spatial distribution of clustered strains by district, West Arisi zone and Wondo genet districts

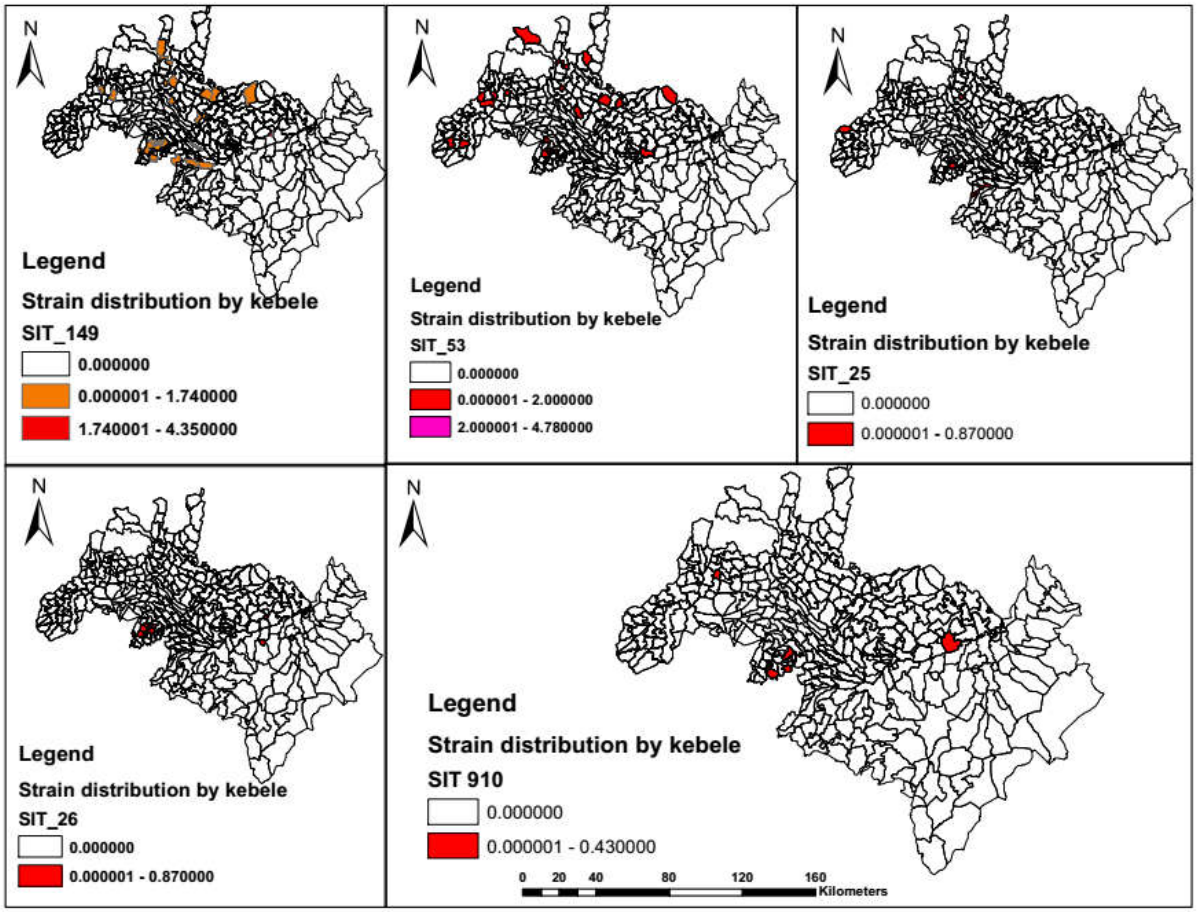

Figure 3.2.4 (A). Spatial distribution of clustered strains by Kebeles, West Arisi zone and Wondo genet districts

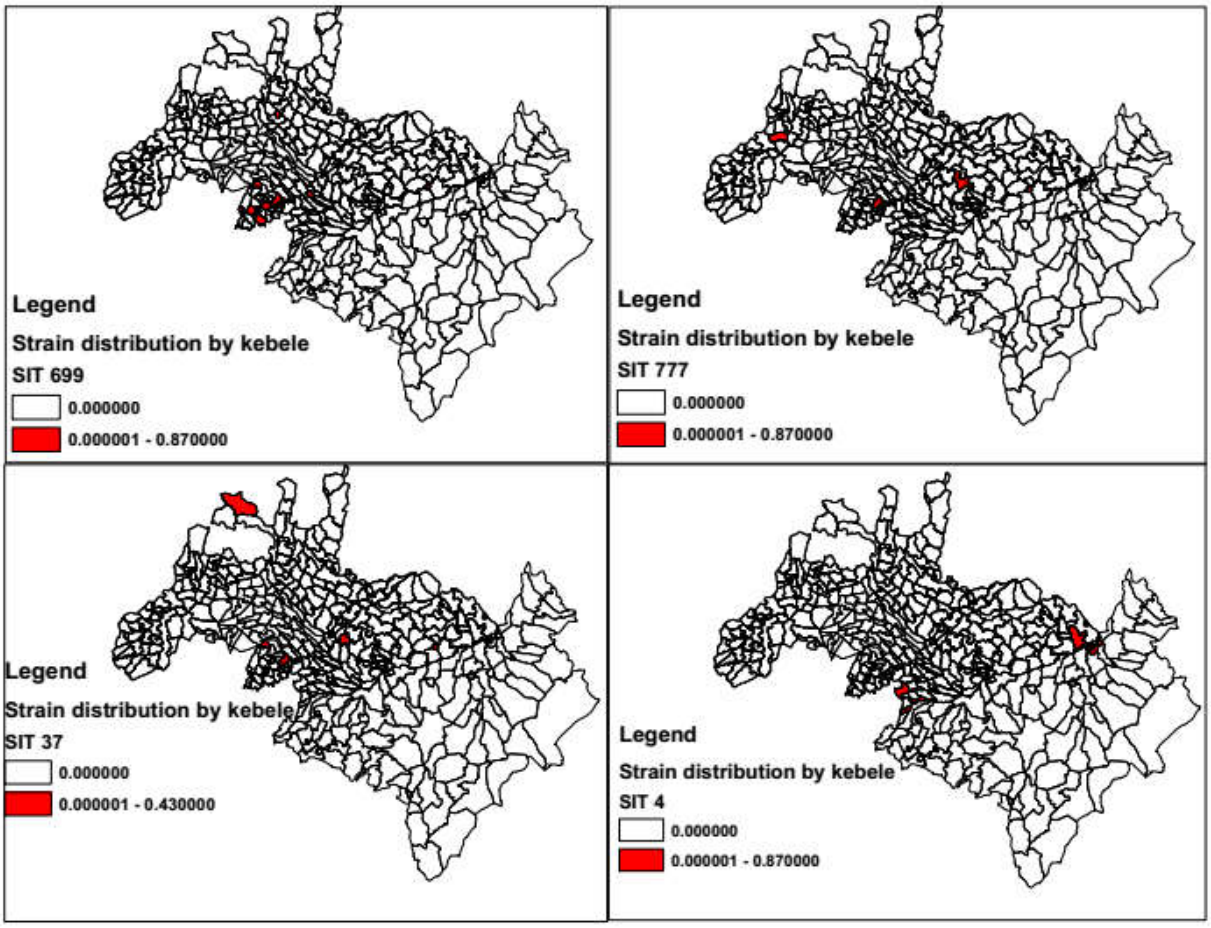

Figure 3.2.4.(B). Spatial distribution of clustered strains by Kebeles, West Arisi zone and Wondo genet districts

3.2.4. Drug Susceptibility profile

Drug susceptibility test was carried out on 202 out of 230 *M. tuberculosis* isolates for the first line drugs: INH, RPM, EMB and STM. A total of 29 (14.3%) isolates were found to be resistant to any of the drugs tested. Any resistance to one drug was most frequently observed for INH, 26 (12.8%) of all isolates tested followed by ETB, 6 (2.9%) and STM, 4 (1.9%). The highest monoresistance was observed for INH, 22 (10.9%) followed by EMB, 6 (2.5%) and STM, 4 (0.5%). There was one case of monoresistance to RPM (0.3%). Combined drug resistance was observed for INH and EMB (1, 0.5%) and INH and STM (3, 1.4%). No MDR-TB was reported in the current study (**Table 3.2.3**).

Table 3.2.3. Resistance to first-line anti-TB drugs

	Number	Percentage (%)	95% CI
Total tested	202		
Any resistance	29	14.3	9.83 – 19.96
Any Resistance to individual drug			
Any INH	26	12.8	8.58 – 18.28
Any RPM	1	0.5	0.12 – 2.72
Any EMB	6	2.9	1.09 – 6.35
Any STM	4	1.9	0.45 – 4.99
Monoresistance			
INH only	22	10.9	6.92 – 16.02
RIF only	1	0.5	0.01 – 2.72
STM only	1	0.5	0.01 – 2.72
EMB only	5	2.5	0.80 – 5.68
Resistance to only drugs			
INH+RIF only	0	0	
INH + EMB only	1	0.5	0.01 – 2.72
INH + STM only	3	1.4	0.30 – 4.27
Resistance to four drugs			
INH+RIF+STM+EMB	0	0	

3.2.5. Genotyping of drug resistant strains

Genotyping of the drug resistant strains showed that SIT 149 (T3-ETH) was the dominant strain (9/43) among the drug resistant isolates and different SITs were also documented to be related with drug resistance. (**Table 3.2.4**)

Table 3.2.4. Strain types of *M. tuberculosis* involved in drug resistance

SIT No., Sub-family (n)	Resistance to				Total (n, %)
	INH (n, %)	RIF (n, %)	EMB (n, %)	STM (n, %)	
T					
149 (T3-ETH) (43)	7 (16)	-	1(5)	1(2)	9 (21)
37 (T3) (10)	1(10)	-	-	-	1 (10)
53 (T1) (36)	2 (6)	-	1(3)	-	3 (8)
205 (T1) (1)	-	-	1(100)	-	1(100)
Haarlem					
390 (H3) (2)	2 (100)	-	-	-	2 (100)
394 (H3) (2)	1(50)	-	-	-	1(50)
699 (H3) (8)	1(13)	-	-	-	1(13)
CAS					
25 (CAS1-Delhi) (5)	-	1(20)	-	-	1(20)
26 (CAS1-Delhi) (9)	1(11)	-	-	-	1(11)
485 (CAS1-Delhi) (1)	-	-	1(100)	-	1(100)
LAM					
838 (LAM10-CAM) (1)	-	-	1(100)	-	1(100)
Sub-family not assigned					
4 (5)	3 (60)	-	-	-	3(60)
Orphan (30)	4 (13)	-	-	-	4(13)

3.2.6. Mutation analysis of drug resistance strains by WGS

WGS analysis was performed on 42 *M. tuberculosis* isolates and of these 39 had phenotypic DST results. Among these, in 69% (27/39) of them, phenotypic DST results were in concordance with WGS result; 67% (26/39) were sensitive to anti-TB drugs by WGS; 10% (4/39) of the isolates resistant to anti-TB drugs by phenotypic DST were sensitive by WGS, 18% (7/39) of the isolates which were sensitive by phenotypic DST showed resistance in WGS. One isolate which was INH resistant by phenotypic DST was also INH resistant by WGS and one isolate which was resistant to INH and STM by phenotypic DST was found to be INH resistant by WGS. Overall, of the 42 *M. tuberculosis* isolates which underwent WGS, drug resistance mutations were identified in 9 (21%) of them (**Table 3.2.5**). The analysis indicated that the majority (5/9) of the drug resistance mutations were for INH, where the majority of the mutations were on katG genes (katG_315S>315T, two in number) and katG_735D>735A). Additionally, oxyR'-ahpC_-4A>G and Rv1482c-fabG1_-17G>T mutations were also reported. Similarly, two RPM resistance cases were reported by WGS and the mutations were on rpoB_428S>428I and rpoC_735D>735N genes. Drug resistance mutations were identified both in the first- and second-line drugs. Additionally, the drug resistance mutations ranged from single to multiple on a single *M. tuberculosis* isolate.

Table 3.2.5. Mutation analysis of drug resistance strains by WGS

Isolates	Resistance	Drug resistance mutations (codon number)						
		RPM	CAR	INH	PAS	PZA	ETH	STM
ab003_S1	PZA, STM	-	-	-	-	pncA_61T>61P	-	rrs_514A>T
ab004_S2	RPM	rpoC_735D>735N	-	-	-	-	-	-
an055_S4	INH	-	-	oxyR'-ahpC_-4A>G	-	-	-	-
bu251	RPM,CAR, PAS	rpoB_428S>428I	tlyA_236N>236K	-	thyA_91G>91R	-	-	-
SR0010	CAR	-	tlyA_236N>236K	-	-	-	-	-
WG1005	INH, ETH, STM	-	-	Rv1482c-fabG1_-17G>T	-	-	Rv1482c-fabG1_-17G>T	rpsL_88K>88R
wg157_S8	INH	-	-	katG_315S>315T	-	-	-	-
wg804_S12	INH	-	-	katG_735D>735A	-	-	-	-
wg815_S4	INH	-	-	katG_315S>315N	-	-	-	-

INH=Isoniazid, PRM=Rifampicin, CAR= Capreomycin, PAS= Para-aminosalisylic-acid, PZA= Pyrazinamide, ETH= Ethiona

3.2.7. Phylogenetic tree of *M. tuberculosis* strains

Phylogenetic tree was constructed based on the WGS analysis of 42 *M. tuberculosis* strains selected randomly from isolates of the study area. The tree showed the presence of 3 lineages (L3, 4 and 7) and lineage 7 being the oldest strain among the other lineages reported in the study (lineages 3 and 4) (**Figure 3.2.5**). Additionally, the drug resistance profile of the strains was depicted along with the tree.

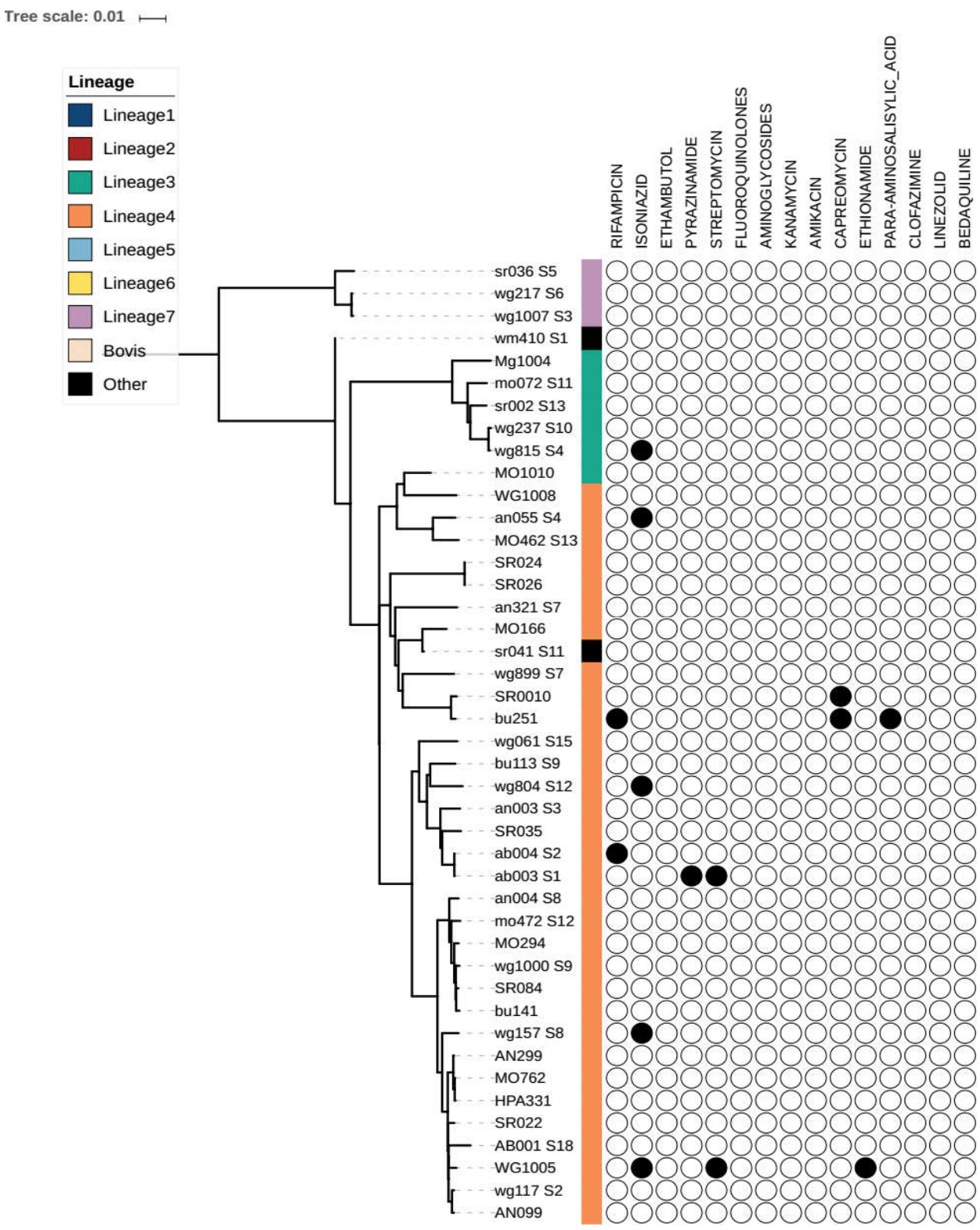

Figure 3.2.5. Phylogenetic tree of 42 *M. tuberculosis* isolates and drug resistance profile by WGS

3.3. Community-based study

The overall work flow of the study is depicted on **Figure 3.3.1**

3.3.1. Sociodemographic characteristics

All 24,517 adults in the six *kebeles* had a cough symptom screen for TB performed during the one-month study period and 544 (2.2%) were found to have cough of ≥2 weeks (**Table 3.3.1**). All patients with prolonged cough submitted two sputum samples. Among the 544 adults with a positive cough screen, the median age was 36 years (interquartile range [IQR] 29-48) and the majority were female (n=354, 65%) There were 152 participants (28%) with a history of contact to a TB patient and 160 (29%) who reported previous anti-TB treatment (**Table 3.3.3**). There were high rates of reported symptoms including fever (80%), night sweats (87%), weight loss (85%) and chest pain (81%).

Table 3.3.1. Distribution of population and confirmed tuberculosis cases by *Kebeles* of Hawassa Zuria Wereda, Ethiopia

Kebeles	No. of house holds	Total population			≥15 years			Positive Cough Screen			Confirmed TB		
		Total	Male	Female	Total	Male	Female	Total	Male	Female	Total	Male	Female
1	1,272	6,231	3103	3128	3,248	1,618	1,630	77	27	50	3	2	1
2	1,508	7,390	3680	3710	3,852	1,918	1,934	91	28	63	7	5	2
3	1,976	9,681	4821	4860	5,047	2,513	2,534	131	35	96	10	3	7
4	1,127	5,534	2756	2778	2,885	1,437	1,448	46	13	33	3	2	1
5	2,436	11,447	5701	5746	5,967	2,972	2,995	113	48	65	6	2	4
6	1,373	6,749	3361	3387	3,518	1,752	1,766	86	39	47	5	3	2
Total	**9,692**	**47,032**	**23422**	**23,609**	**24,517**	**12,210**	**12,307**	**544**	**190**	**354**	**34**	**16**	**18**

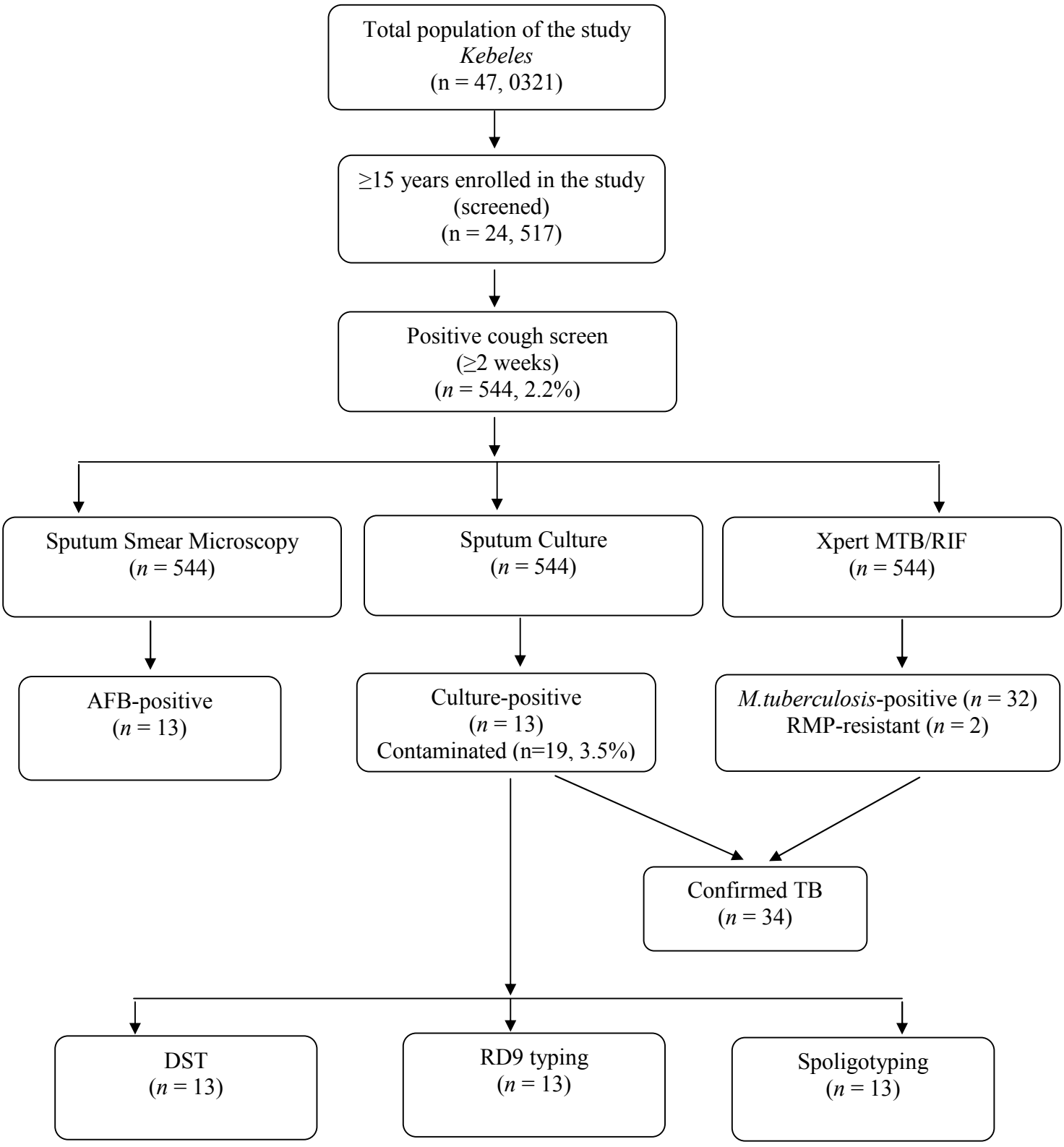

Figure 3.3.1. Study Diagram, Community-based study

AFB=Acid fast bacilli, RPM=Rifampicin, DST=Drug susceptibility testing, RD9=Region of difference 9

3.3.2. Prevalence of pulmonary tuberculosis

A total of 34 (6%) persons with a positive cough screen were determined to have pulmonary TB. All 34 cases were confirmed by Xpert MTB/RIF (n=32) and/or a positive culture result (n=12). Only 13 of the 34 cases (38%) had a positive AFB sputum smear microscopy result (**Table 3.3.2**). Two culture positive cases had a negative Xpert MTB/RIF test and negative sputum smear microscopy results. Two cases were rifampicin resistant by Xpert MTB/RIF testing with one of the cases having a prior history of anti-TB treatment. During the study period, only one case of a patient on anti-TB treatment was identified who was not included in our calculated TB prevalence. The overall point prevalence of confirmed pulmonary TB cases was 139 per 100,000 population (95% CI: 96 - 194) (**Table 3.3.2**).

Table 3.3.2. Distribution of confirmed tuberculosis cases by *Kebeles*, Hawassa Zuria Wereda, Ethiopia

Kebeles	**≥15 years**	**AFB positive**	**Culture positive**	**Xpert positive**	**Confirmed TB**	**Rate**	**95% CI**
1	3,248	1	1	3	3	92	19.05-269.69
2	3,852	3	3	7	7	182	73.09-374.06
3	5,047	4	4	9	10	198	95.05-364.08
4	2,885	1	1	3	3	104	21.45-303.59
5	5,967	2	2	5	6	101	36.91-218.73
6	3,518	2	2	5	5	142	46.16-331.36
Total	**24,517**	**13**	**13**	**32**	**34**	**139**	**96.06-193.74**

AFB =Acid Fast Bacilli; TB=Tuberculosis; CI =Confidence interval

Almost three fourths (25/34, 74%) of the confirmed TB cases were newly diagnosed while 9/34 were previously treated cases. There was similar distribution among females (53%) and males (47%) (**Table 3.3.3**). None of the 31 TB cases who had HIV testing performed had a positive result. A treatment outcome was available for 29 cases; 28 of whom were cured and one had completed treatment. Five persons with TB moved out of their *Kebeles* and outcomes were not available.

3.3.3. Association between exposure variables and PTB

In univariate analysis, longer duration of cough, older age and close contact to a known TB case was associated with an increased risk of having confirmed TB among persons with a positive cough screen (**Table 3.3.3**). In multivariate analysis, a cough of > 4 weeks (aOR = 4.23, 95% CI 1.94-9.23) was associated with risk of having bacteriologically confirmed TB while older age (aOR = 0.047, 95% CI 0.005-0.43) was associated with a reduced risk bacteriologically confirmed TB among those with a positive symptom screen (**Table 3.3.4**).

3.3.4. Drug susceptibility testing (DST)

First line DST was carried out for the 13 isolates identified by culture and all these isolates were susceptible to tested drugs. The two rifampicin resistant isolates that were identified by Xpert MTB/RIF test were not isolated by culture and so that drug susceptibility was not done for them.

3.3.5. Genetic diversity of strains

A total of 6 spoligotype patterns were identified among the 13 *M. tuberculosis* isolates that underwent genotyping, of which 9 (69%) of them were registered in the SITVIT2 database and 4 (31%) were new patterns (orphans). All of them belonged to Euro-American lineage (lineage 4) and the most dominant shared types were SIT149 (4, 31%) and SIT53 (3, 23%). Nine out of the 13 strains were grouped in 3 clusters (≥2 strains/cluster). The predominant clade (sub-lineage) was T1 (4, 23%), followed by T3-ETH (4, 31%), H3 (1, 6.9%).

Table 3.3.3. Predictors of pulmonary TB among persons with a positive cough screen, Hawassa Zuria Wereda, Ethiopia

Characteristic	Total (n=544) n (%)	No TB (n=510) n (%)	TB (n=34) n (%)	Univariate analysis	
				OR (95% CI)	*P*-Value
Female sex	354 (65)	336(66)	18 (53)	0.58(0.28-1.17)	0.12
Mean age (year)	38	38	31		
Age category in year					
15-24	68(12)	61(12)	7 (22)		
25-34	143(27)	132 (26)	11(34)	0.72 (0.26-1.94)	0.52
35-44	159 (29)	150 (29)	9 (28)	0.52 (0.18-1.46)	0.21
45-54	94 (17)	90 (18)	4 (13)	0.38 (0.10-1.38)	0.14
≥55	80 (15)	79 (15)	1(3)	0.11 (0.01-0.92)	0.04
Illiterate	401(74)	383(75)	18 (53)	0.37(0.18-0.75)	0.006
Unemployed	533 (98)	501(98)	32(94)	0.28(0.05-1.38)	0.12
Married	470 (86)	440 (94)	30 (88)	0.83(0.28-2.45)	0.74
Duration of cough in weeks					
2- 4	333(61)	321 (63)	12 (35)		
>4	211 (39)	189 (37)	22 (65)	3.11 (1.50-6.43)	0.002
Symptoms					
Fever	437 (80)	409 (80)	28 (82)	1.15 (0.46-2.85)	0.76
Night sweats	472 (87)	443(87)	29 (85)	0.87 (0.32-2.34)	0.79
Loss of appetite	288 (53)	268 (53)	20 (59)	1.28 (0.63-2.61)	0.47
Weight loss	464 (85)	433 (85)	31 (91)	1.83(0.54-6.15)	0.34
Chest pain	439 (81)	411 (81)	28 (82)	1.12 (0.45-2.78)	0.80
Shortness of breath	315 (56)	294 (58)	21 (62)	1.18 (0.58-2.42)	0.63
Previous anti-TB treatment	160 (29)	151 (30)	9 (26)	0.85 (0.39-1.87)	0.69
Contact with TB case	152 (28)	137 (28)	15 (44)	2.02 (1.00-4.10)	0.049
Presence of TB patient in the family	89(16)	80 (16)	9 (26)	1.99 (0.85-4.21)	0.11
Absence of window in the home	490 (90)	457 (90)	33 (97)	3.82(0.51-28.5)	0.19
Alcohol use	13 (2)	11 (2)	2(6)	2.83 (0.60-13.3)	0.18

TB= tuberculosis; OR=odds ratio; CI=confidence interval.

Table 3.3.4. Multivariate analysis of risk factors for pulmonary tuberculosis among persons with a positive cough screen, Hawassa Zuria Wereda, Ethiopia (n=544)

Characteristics	Multivariate analysis	
	aOR (95% CI)	*P* Value
Age category in year		
15-24	1.00	
25-34	0.70 (0.24-2.07)	0.528
35-44	0.29 (0.09-0.96)	0.043
45-44	0.22 (0.05-0.86)	0.031
≥55	0.047(0.005-0.43)	0.007
Duration of cough in weeks		
2-4	1.00	
≥4	4.23 (1.94-9.23)	<0.001
Close contact with known TB patient		
No	1.00	
Yes	1.99 (0.93-4.26)	0.073

aOR –Adjusted odd ratio, CI=Confidence interval

CHAPTER IV

DISCUSSIONS

Chapter IV. Discussions

This section discusses the study findings of the three study settings, in the order of prison, health facility and community-based studies. The limitations and conclusion and recommendations of the studies will follow the same order and finally closed with summary of the PhD project.

4.1. Discussions

4.1.1. Prison study

Utilizing an active TB case finding strategy combining symptom screening and molecular diagnostic testing, 31 previously undiagnosed cases of active pulmonary TB were detected in a large Ethiopian prison using Xpert MTB/RIF. Along with the five previously known cases of TB, a TB prevalence of 1789 per 100,000 in the prison population was detected. This prevalence is more than 16 times higher than the prevalence found in the general Ethiopian population (Kebede et al., 2014). The results highlight the utility of active TB case finding utilizing a cough screen and Xpert RIF/MTB testing among high risk populations including persons incarcerated in prisons in a high TB burden country.

The prevalence of TB at the Hawassa Prison was high despite a low HIV seroprevalence (0.4%) among those incarcerated. None of those persons found to have PTB in the current study were HIV seropositive. The HIV prevalence among prison inmates in the current study is lower than in previous reports from prisons in other areas of Ethiopia including Gondar (7.6%) (Moges et al., 2012), Tigray (4.4%) (Adane et al., 2016), and in 13 prisons in the country (4.4%) (Ali et al., 2015). The lower prevalence of HIV infection in the current study might reflect lower HIV prevalence in the southern region compared to other parts of Ethiopia (EPHI, 2015). Stigma in general is one of the major factors in hindering people from seeking health care services in the country, however, in a prison setting the acceptance rate for the HIV screening was high (93% agreed to HIV testing).

Delays in diagnosis and incomplete treatment of TB are major challenges in most prison settings in resource-limited countries. These could be related to the limited availability of health care services in the prisons and lack of TB diagnostics in many prison settings

(Biadglegne et al., 2015b, O'Grady et al., 2011). In many high burden, low and middle income countries, TB control activities in prisons are not well integrated into national TB control programs (Biadglegne et al., 2015b), including in Ethiopia (FMOH, 2015). In prison settings, the use of diagnostic tools with high sensitivity and specificity is recommended (Valenca et al., 2015). The current study highlights the utility of active TB case finding that utilizes a rapid molecular diagnostic test. Prior to the current study, there was no ongoing surveillance for TB in the prison, and the only available diagnostic tool in the prison, AFB smear microscopy, was insensitive in the current study and did not detect 75% of TB cases that were identified by Xpert MTB/RIF. The current study provides important data to support an active TB case finding strategy that uses a cough symptom screen plus Xpert MTB/RIF in prison settings in order to increase the case detection, identify drug resistant TB, and improve TB control activities by allowing separation of those with active PTB from other inmates.

The prevalence of TB in the Ethiopian prisons has been reported to range from 349 to 1913 per 100,000 prison populations (Abebe et al., 2011, Ali et al., 2015, Adane et al., 2016, Moges et al., 2012, Bayu et al., 2016, Fuge and Ayanto, 2016, Gebrecherkos et al., 2016, Zerdo et al., 2014). The observed PTB point prevalence in the current study (1789 per 100,000), although within the above range was higher than that reported from most previous Ethiopian studies (Ali et al., 2015, Adane et al., 2016, Fuge and Ayanto, 2016, Bayu et al., 2016, Gebrecherkos et al., 2016, Moges et al., 2012, Zerdo et al., 2014). The difference in the prevalence of TB in Ethiopian prisons could be due to the methodological differences employed in the studies for screening and diagnosis of cases, differing prevalence of HIV co-infection among those incarcerated in different regions and differences in the burden of the disease in the study areas. Studies conducted in the sub-Saharan African prisons also reported high prevalence of PTB ranging from 5.1% to 47.7% positivity (Rutta et al., 2001, Koffi et al., 1997, Nyangulu et al., 1997). The high prevalence of TB in prison settings can impact TB transmission in communities as well as in prison settings themselves. It can amplify TB transmission after release from prison where former inmates can transmit TB to contacts in the community (Baussano et al., 2010, Editors et al., 2010).

Prisons can also be an important source of spread of drug-resistant TB (Rutta et al., 2001) and high levels of MDR TB and XDR TB have been reported in prisons globally (Biadglegne et al., 2015b). In a study conducted in Zambia (Habeenzu et al., 2007), resistance to at least one anti-TB drug was observed in 40 (23.8%) cases and 16 (9.5%) were MDR-TB. The current study identified one case of rifampicin resistant TB using Xpert MTB/RIF test. This case was confirmed to be MDR TB by culture and drug susceptibility testing. A recent study (Ali et al., 2016) also reported a 9.5% of MDR TB cases in Ethiopian prison settings. These findings highlight the emergence of MDR TB in the prison settings and further emphasize the need for strengthening TB control activities in prison settings in Ethiopia.

The study was cross sectional in nature and thus not designed to determine the site of acquisition of infection with *M. tuberculosis* (i.e., prison vs. community) among those found to have active TB disease. The number of persons per cell was high and the median length of incarceration among those with TB was 10 months; 61% of those found to have TB by Xpert were incarcerated for ≤ 1 year. A study from a prison in Gondar, Ethiopia (Moges et al., 2012) reported that an incarceration range of 2-6 months was associated with TB. Further studies are needed to further evaluate the site of transmission and the impact of screening persons at the time of incarceration as an additional TB control measure. Further studies are also needed to identify the frequency of active TB case finding in prison settings.

4.1.2. Health facility-based study

The study revealed a heterogeneous pool of *M. tuberculosis* strains with several clusters including lineage 7 strains circulating in Southern Ethiopia. A high proportion of INH resistance was reported in the study area and SIT 149 (T3-ETH) was the most dominant strain among drug resistant cases. The findings suggest the ongoing transmission of TB, including of drug resistant TB in the Southern part of Ethiopia and calls for surveillance and wider monitoring of DST and improved control responses.

In the current study, the majority of the isolates (81%) belonged to the Euro-American lineage (L4) followed by East-Africa-Indian (L3), 14% and the Ethiopian lineage (L7), 4%. A recent study in southern Ethiopia (which was geographically close to our study) reported that 84% of the isolates were L4 and 3% of them were L3 (Molina-Moya et al., 2018). Studies from other parts of the country reported variable proportion of lineage types in different geographic areas of Ethiopia (Firdessa et al., 2013, Nuru et al., 2015, Bedewi et al., 2017a). Overall, L4 is more widely distributed and more predominant than all other lineages combined (Tulu and Ameni, 2018, Comas et al., 2015). On the other hand, a higher proportion of L3 (25-35%) was reported in northern Ethiopia than elsewhere (Nuru et al., 2015, Firdessa et al., 2013). In general, it was noted that the geographic distribution and proportion of lineages varied across the country. The wider implication of this on the dynamics of the transmission of TB and drug resistance in the respective geographic localities is an area that has yet to be investigated well.

Lineage 7 accounted for 4% in the current study. One case of Lineage 7 was recently reported from the southern part of Ethiopia (Molina-Moya et al., 2018) and 6 cases (2%) from the southwest (Tadesse et al., 2017). Lineage 7 was first reported from Woldia area of Amhara region, Ethiopia with 13% of prevalence rate (Firdessa et al., 2013). Other studies from Amhara region (Biadglegne et al., 2015a, Yimer et al., 2015b) have reported prevalence rates of 10% and 16%. So far, lineage 7 has been prominently reported from the northern part of Ethiopia. The additional report of lineage 7 in the current study suggests its broader occurrence, including in the southern parts of the country. Considering the pre-modern split of this lineage in the phylogenetic tree of *M. tuberculosis* and its localization to

Ethiopia only, further investigations into its epidemiology would be of much interest. The spoligotype data on lineage 7 were further confirmed by WGS and the report of this strain in the Southern part of Ethiopia adds knowledge to the epidemiology of TB in the country. Additionally, from the phylogeny tree it is noted that lineage 7 is closer to the root of the MTBC phylogeny indicating an earlier divergence from the MTBC common ancestor, implying it is the oldest strain. This notion is supported by the recent report by Yimer et al (Yimer et al., 2016) indicating that the lineage underwent recent expansion ~310 years ago. Phylogenetic analysis also confirmed the result of the spoligotyping in that the isolates were distributed into three of the seven currently defined lineages of *M. tuberculosis* complex.

The most common SITs in the present study were SIT149 (21%), SIT53 (19%) and SIT 26 (5%). Studies from northern Ethiopia reported SIT 149 (22.6), SIT 53 (8.3) % and SIT 50 (7.4%) (Esmael et al., 2014) , SIT 25 (18.6%), SIT 53 (10.9%) and SIT 149 (5.9%) (Debebe et al., 2014). The most common SITs from Central Ethiopia (Bedewi et al., 2017b) were SIT 53 (15%), SIT 49 (13%) and SIT 54 (12%), and from Southern part of Ethiopia were SIT53 (17%) and SIT149 (12%) (Molina-Moya et al., 2018). It was noted that the geographic distribution and proportion of SITs varied across the country and this would have a wider implication on the dynamics of the transmission of TB and drug resistance in their respective geographic localities. Most studies in Ethiopia indicated that SIT149 was widely distributed in the country (Tulu and Ameni, 2018). SIT 149 is also designated as T3-ETH by its clade name (Brudey et al., 2006, Belay et al., 2014b). Previously it was also referred as ETH-3 and more recently as L4.2.ETH1 (Comas et al., 2015).

The predominant clade (sub-lineage) identified in the current study was T1 (22%), T3-ETH (21%), H3 and CAS1-Delhi (10%) each. Similarly an earlier study in the country reported T3-ETH (22%), T1 (17.7%) and of CAS1-Delhi (13%) (Mihret et al., 2012) and a considerably high proportion of Dehli/CAS (38.9%) was reported from northern Ethiopia (Tessema et al., 2013). In African settings, CAS family was prevalent in Sudan (Sharaf Eldin et al., 2011, Kibiki et al., 2007, Githui et al., 2004). In Ethiopia, the T3-ETH is present in high proportion (Tulu and Ameni, 2018) and it is believed to be specific to Ethiopia and this SIT is rarely reported in other countries (Brudey et al., 2006). The CAS1-Delhi family

(SIT25 and SIT26) is localized in the Middle East and Central Asia mainly in India (Bhanu et al., 2002). It is hypothesized that East-African Indian ancestral strains spread back from Asia to Africa through India as a result of human migration (Cruciani et al., 2002).

Clustering of strains could suggest the presence an on-going transmission of *M. tuberculosis* infection in the specific geographic region and the high clustering rate relates to a high transmission rate (Bedewi et al., 2017a, Easterbrook et al., 2004, Nuru et al., 2015). In the current study, even if it should be complemented by higher discriminatory methods such as variable number of tandem repeats (VNTR) typing or other methods, 85% of the isolates were clustered and this high clustering rate of strains could suggest the role of these strains in the ongoing transmission of TB in the study areas.

Positioning of clustered strains using GIS mapping is helpful to describe the epidemiological links of Mtb strains in specific geographical localities (Tulu and Ameni, 2018). This information could be utilized to design targeted TB control measures. In the current study, geospatial analysis demonstrated variable distribution of strain clusters in the different districts of the study area suggesting areas affected with possible recent transmission. Strengthening of the TB control program in such settings is recommended in order to prevent ongoing active transmission of the disease. Clustering of strains is a marker for recent transmission and can also serve to evaluate the performance of the TB control program (Small et al., 1994) and help determine where to target interventions.

In the current study, 14% of the newly diagnosed TB patients were resistant to ≥1 first-line anti-TB drugs. In terms of the burden of the problem, this prevalence could be considered as significant. However, the result is lower than the prevalence rates reported in other parts of the country such as 23% (Tilahun et al., 2018) in Central Ethiopia and 23% in Eastern Ethiopia (Seyoum et al., 2014), but relatively higher than the prevalence rate of 11% reported in Northern Ethiopia (Tessema et al., 2012) and 9 % in Southern Ethiopia (Wondale et al., 2018). Compared to a similar study conducted in this same study area in 2006 (Arega, 2007 (un-published)), the prevalence reported in this study (14%) is relatively lower than that of the previous one, 20%. The difference in the prevalence rates observed in different parts of the country could be due to differences in TB control program performance

but also, more simply, due to study-related factors such as study design (population differences, methodology employed in the studies, sample size, study participant selection methods) or study periods. In addition to active case finding, it is essential for programs to build capacity for DST in order to implement recommended early detection and effective treatment of drug resistance to curb its spread (Tilahun et al., 2018).

Using WGS, the current study highlighted the genotypic drug resistance profile of selected *M. tuberculosis* isolates and tried to compare it with conventional DST. In this study, 10% (4/39) of the isolates resistant to anti-TB drugs by phenotypic DST were sensitive by WGS whereas 18% (7/39) of the isolates which were sensitive by phenotypic DST were resistant by WGS. In a study that compared the phenotypic DST with genotypic resistance detected by WGS (Schleusener et al., 2017), it was reported that false-susceptible DST results were caused by missing mutations in the resistance catalogues employed for data interpretations; on the other hand false-resistance identified by WGS was caused by the misclassification of polymorphisms as resistance mutations, suggesting the challenge in the interpretations of genotypic drug resistance by WGS.

In general, phenotypic DST is the gold standard for *M. tuberculosis* drug resistance determination (Iketleng et al., 2018). It produces reliable results, in particular for the two major ant-tubercular drugs, rifampicin and isoniazid. For ethambutol the results are less reliable (Madison et al., 2002) and DST for this drug is not considered a priority by the WHO. Pyrazinamide testing has been reported as highly challenging by several laboratories and results may not be fully reliable (Piersimoni et al., 2013). However, technical issues related to the methodology used for DST, quality of media and drugs, experience of the staff can strongly affect the reliability of the test (Cirillo et al., 2017). On the other hand, WGS allows for the interrogation of the entire *M. tuberculosis* genome for mutations conferring drug resistance. Mutations occurring outside the genes known to be associated with drug resistance can be identifed from TB whole genomes (Iketleng et al., 2018) and this drug resistance might not be detected by the phenotypic DST. However, interpretation of genotypic resistance detected by WGS is challenging.There is no catalogue of tuberculosis

mutations predicting susceptibility. Rules to interpret WGS data on drug resistance need to be well established.

In general, using WGS the current study reports the diversity of mutations found within the genomes of nine clinical *M. tuberculosis* isolates representing varying resistance profiles. With the limited number of isolates, mutations that were found to be involved in the first line (INH, RPM, STM and PZA) and second line (CAR, PAS and ETH) drugs were identified. Further work might help to generate more data on mutation analysis of drug resistance strains in the study setting in order to better understand the drug resistance mechanism.

MDR-TB was not reported in the current study, even though two cases (0.9%) of MDR-TB were reported in a previous study in the same study area (Arega, 2007 (un-published)). Earlier studies in different parts of the country reported MDR-TB among newly diagnosed TB patients as 1.1% in Eastern Ethiopia (Seyoum et al., 2014),1.2% in Central Ethiopia (Tilahun et al., 2018) and 5% in Northern Ethiopia (Tessema et al., 2012). In the recent systematic review on MDR-TB in the country (Girum et al., 2018), the pooled prevalence of MDR-TB among newly diagnosed TB cases was 2.18% (95% CI 1.44–2.92%) with range of 0% to 11.8% MDR-TB among newly diagnosed TB cases (Maru et al., 2015, Hussein et al., 2013). It is noted that the prevalence of MDR-TB varies over time and in different populations (Lukoye et al., 2013, Massi et al., 2011). In general, data on drug resistance among newly diagnosed pulmonary TB cases is a good epidemiological marker to trace the transmission of drug resistant strains in the community (Villa-Rosas et al., 2015, Kamal and Javaid, 2015), thus supporting the effort of the TB control program in designing intervention strategies for the prevention and control of drug resistant TB in the country.

Linking strain typing data with data on drug resistance can be a useful way to monitor the spread of individual drug-resistant clones in communities (Jagielski et al., 2016). T3-ETH (SIT 149) was the most prevalent spoligotype (21%) among drug resistant strains in this series. Other studies have reported similar findings. Fifty percent (12/24) of the drug resistant *M. tuberculosis* isolates were SIT 149 in a collection dating from 2006-2010 (Bekele et al., 2018). Similarly, in previous studies in the country (Agonafir et al., 2010,

Diriba et al., 2013), T3-ETH (SIT 149) was associated with MDR-TB. In general, T3-ETH (SIT 149) is recognized as a predominant spoligotype cluster in Ethiopia most frequently associated with drug resistance, more so than other spoligotypes in the country (Yimer et al., 2015a). However, as it was indicated by Bekele and his colleagues (Bekele et al., 2018), the observed association between T3-ETH (SIT 149) and development of drug resistance may not necessarily indicate that these strains are more prone to be drug-resistant but could rather be a consequence of their high prevalence in the population. This idea is also supported in a recent review (Panwalkar et al., 2017) which showed that the correlation between genotypes and TB drug resistance was still uncertain. Further analysis on SIT149 identified genotype SIT149: A, a potential MDR-TB clone circulating in the Ethiopian highlands probably contributing to the spread of MDR-TB in the area that warrants further attention (Bekele et al., 2018).

Other strains were also identified in the study in relation to drug resistant TB, including T1, H3 and CAS1-Delhi. In previous studies in the country (Agonafir et al., 2010, Diriba et al., 2013), CAS1-Delhi and CAS1-Kili strains were associated with MDR-TB. Additionally, in a study conducted in Northern Ethiopia (Tessema et al., 2013) it was shown that there was a significant association between Haarlem family and drug resistance TB, including MDR TB.

4.1.3. Community-based study

Utilizing a large volunteer healthcare workforce in rural Southern Ethiopia, we were able to carry out a massive population-based screening program for active TB among > 24,000 adults in a short time period (~1 month) and were able to detect 34 previously undiagnosed active TB cases, primarily through the use of Xpert MTB/RIF. The current study demonstrates the feasibility of a large TB screening program using community health volunteers doing the initial symptom screen and referrals and paid community health workers for further testing and confirmation. The high prevalence of previously undiagnosed TB identified in the current study highlights the hidden burden of TB in rural settings and the need for additional active screening programs. In this setting, it was shown that an approach using community health workers can carry out an impressive large-scale screening program and this may be a useful approach to consider for other similar rural LMIC settings.

Innovative approaches using community health workers are growing in number aimed at increasing case detection rate (Yimer et al., 2009) and in this regard practical changes were observed in Southern Ethiopia by applying a community-based TB intervention. Community-based interventions at the village level using female community health workers (HEWs) made TB diagnostic and treatment services more accessible to the community and significantly improved TB diagnosis and treatment in rural settings of Southern Ethiopia (Datiko and Lindtjorn, 2009, Datiko et al., 2017, Yassin et al., 2013). In contrast to these existing studies in Ethiopia, and as part of the innovative approach, the current study used Health Development Armies (HDAs) in identifying symptomatic TB individuals in the community. Using HDAs, a very high number of TB cases was identified in a short period of time. Involving HDAs helped to reach the entire community and trace the symptomatic cases easily. HDAs live in the community and come across symptomatic neighbors in their daily routines. They also participate in community meetings and work closely with the HEWs on health-related issues. They are not paid but contribute voluntarily to improving the health of the community. A similar approach has been reported from among others in Uganda where voluntary Village Health Teams (VHT) are involved in improving and promoting health at the community level (O'Donovan et al., 2018).

Improved screening is inadequate without appropriate diagnosis and treatment. Linking the HDAs with a rapid molecular diagnostic tool such as Xpert MTB/RIF has proved to be a successful approach in detecting TB suspects early for rapid diagnosis and treatment, thus reducing the burden as well as the adverse social and economic consequences of TB. The HEP in Ethiopia employs salaried staff and has continued to be productive for over a decade and a half. The HDA extension is on the other hand relatively new and relies heavily on volunteer women raising issues of sustainability. The driving force for their active involvement needs to be investigated in terms of motivation. It was observed in Uganda for example that volunteer community health workers (CHWs) were actually participating with an expectation of future rewards (Kasteng et al., 2016). In contrast, a qualitative study from this region of Ethiopia suggested current dominance of intrinsic motivators (such as community recognition and appreciation) among the HEWs and their supporters (Tulloch et al., 2015).

The current study detected 544 individuals with a positive cough screen among >24,000 screened. The overall prevalence of laboratory-confirmed TB was 139 per 100,000 population, much lower than the national prevalence of 277 per 100 000 population (95%CI 208-347) (Kebede et al., 2014). The prevalence of smear positive pulmonary TB was also lower than in several previous studies in Ethiopia including the national prevalence survey (Tadesse et al., 2011, Berhe et al., 2013, Hamusse et al., 2017, Shargie et al., 2006b, Yimer et al., 2009, Kebede et al., 2014), but higher than a report from southwest Ethiopia (Deribew et al., 2012). Direct comparison is difficult because of differences in study methodology, population and time. More than 50% of all confirmed TB cases in the national survey had no cough but were identified through chest X ray (CXR) screening (Kebede et al., 2014), a method not included in this study; chest radiographs are not available at most health centers in Ethiopia and CXR is not routinely employed in the diagnosis of pulmonary TB. Ethiopia has overall shown a declining trend in tuberculosis in the last years (WHO, 2018).

The spoligotyping revealed that all the 13 *M. tuberculosis* isolates belong to Euro-American lineage (Lineage 4) and the dominant shared type was SIT149 (4, 31%). This could be due to the predominant nature of the lineage 4 and SIT 149 in the Ethiopian context as described earlier (Tulu and Ameni, 2018) and in the current study of the health facility-based study in Shashemene area. In the earlier study in the rural community in South East Ethiopia (Debebe et al., 2014), it was also showed that majority of the strains were form lineage 4.

In the current study, 34 previously undetected cases of active PTB were diagnosed in just four weeks using a community-based ACF strategy. In contrast, only one PTB patient was identified by the routine passive case finding procedure in the same period in the study population. ACF has the added benefit of reaching those with limited access, the economically disadvantaged, elderly people and those with poor health seeking behavior (Yassin et al., 2013, Datiko et al., 2015). The routine TB diagnostic method in the health facilities, including at the current study site, is smear microscopy which is known for its poor sensitivity (Merid et al., 2009). Xpert MTB/RIF is being rolled out at many health centers in Ethiopia. The study used a combination of smear microscopy, Xpert MTB/RIF and culture. Xpert MTB/RIF detected 94% of the TB cases whereas smear microscopy

detected only 38%. In the current study, culture yield was much lower than expected (38%). This may at least in part be due to loss of viability of *M. tuberculosis* following repeated freeze and thaw of sputum samples following power failures in the field during specimen storage and transportation to AHRI for culture facility.

TB prevalence rates are higher in men than in women globally (WHO, 2001) and this is true for Ethiopia as well (WHO, 2018). However, unlike in health facility based passive case finding, the proportion of women with TB increased consistently when community-based screening was conducted in southern Ethiopia (Yassin et al., 2013, Datiko and Lindtjorn, 2009, Datiko et al., 2017) due to probably improved access to women who would have otherwise remained undetected. In a case control study of communities where HEWs were employed in active case finding, the male: female ratio of TB cases changed from 1.3:1 to 1:1 following intervention (Yassin et al., 2013, Datiko and Lindtjorn, 2009). The male to female ratio of 1:1.1 among newly diagnosed cases in the current study seems to further confirm the value of community-based health intervention in accessing the hard to reach pockets among the rural population.

In multivariate analysis, cough of ≥4 weeks was an independent risk factor associated with a TB diagnosis among persons with a positive symptom screen while TB was less likely to occur among older persons (≥35 years of age) with a positive symptom screen. It is known that TB is more likely to occur in older individuals than in younger ones. However, older individuals have more frequent causes of chronic cough than younger ones (Morice et al., 2014) and the probability of the chronic cough being due to TB in older individuals is lower than in younger individual as it was observed in the current study. TB-HIV co-infection was not reported in our study and this could be related to the overall low prevalence of HIV infection in rural communities of Southern Ethiopia (EPHI, 2015).

Low case detection rate remains a global challenge with 36% of prevalent cases missing (WHO, 2018). Community-based TB activities are increasingly reported from several high burden countries. Ethiopia is strengthening surveillance and improving the diagnostic capacity (WHO, 2012) of the TB control program with a rollout of Xpert MTB/RIF testing (FMOH, 2016). In the experience reported here, the reach of the HEWs is extended deep

into their communities through engagement of HDAs. Symptomatic screening at community level coupled with rapid diagnosis using Xpert MTB/RIF allows health system access to underserved rural community pockets more effectively. HEWs in Ethiopia are paid female professionals who bridge care and are extensively engaged in community service packages that link health with integrated development; satisfying three main principles recently proposed by Palazuelos et al as essential values for trust in the health system and a path to equitable outcomes of health coverage (Palazuelos et al., 2018).

4.2. Limitations of the study

4.2.1. Prison study

The study is subject to some limitations. These include having HIV testing offered about 6 months after TB screening rather than concurrently. Given the turnover in prisons, not all of those screened for TB were present when HIV testing was offered (and vice-versa). The study relied on Xpert TB/RIF as the definitive diagnosis for TB rather than the gold standard of culture. Since the sensitivity of culture is higher than Xpert among those that are smear negative, the study findings may have underestimated the prevalence of PTB. However, since culture is not widely available in many high TB burden, resource limited countries including Ethiopia, use of Xpert is more feasible in many settings. Among the three TB cases that had a prior history of TB treatment, culture was performed in only one, the MDR case with RPM resistance on Xpert.

4.2.2. Health facility-based study

The study had certain limitations. First, as our study participants were only newly diagnosed TB cases, it was not possible to assess the magnitude of drug resistant TB in the previously treated TB cases and the strain types among these groups. This has limited us from assessing the overall burden of drug resistant TB in the study area. Secondly, study participants were all patients seeking treatment at health facilities. Findings from such a selected population may not indicate the true burden of the problem at community level. Third, the identification of clustered and new strains was performed using spoligotyping; other techniques such as whole genome sequencing or MIRU-VNTR may have a more discriminatory power.

Chapter V. Conclusions and recommendations

5.1. Prison study

The study found that active TB case finding which combined the use of a cough screen plus a commercially available molecular diagnostic test (Xpert MTB/RIF) had high utility in detecting incarcerated persons with active PTB disease at a large prison in Ethiopia. Despite a low HIV seroprevalence among those incarcerated, the overall prevalence of PTB exceeded 1.7% of the prison population in Hawassa, Ethiopia. A cough >4 weeks was the only risk factor for TB identified among those with a positive symptom (cough) screen. Active TB case finding using a symptom screen in combination with Xpert has the potential to interrupt transmission of *M. tuberculosis* in correctional facilities in high burden, low and middle-income countries. Further work is needed to assess the impact of active TB case finding (cough screen and Xpert) at other Ethiopian prisons in order to scale up this intervention throughout Ethiopia.

5.2. Health Facility-based Study

The study identified a heterogeneous pool of *M. tuberculosis* strains with several clusters including lineage 7 strains circulating in Southern Ethiopia. No MDR-TB case was reported in the study area; however, the high proportion of INH monoresistance could suggest the potential development of MDR-TB in the study area as INH monoresistance is the initial step towards anti-TB drug resistance and a common pathway to the development of MDR-TB. SIT 149 (T3-ETH) was the most dominant strain circulating in the study area including among drug resistant cases. The findings suggest the ongoing transmission of TB, including of drug resistant TB in the Southern part of Ethiopia and calls for surveillance and wider monitoring of DST and highlights the need for molecular testing laboratories to monitor transmission trends and improved control responses.

5. 3. Community-based Study

The study identified a very high proportion of undiagnosed TB cases using volunteer women community workers in the rural community of Hawassa zuria wereda and allowed to screen large communities (>24,000 persons) in a relatively short period of time with minimal costs.

The use of volunteer community workers together with Xpert MTB/RIF has the potential of increasing TB case detection, reducing the pool of undetected cases and in curbing the transmission of TB in rural settings of Ethiopia. Implementation and scale up of this strategy could help LMICs increase case detection in rural settings.

5.4. Summary

Overall this PhD project demonstrated the difference in the burden of TB and drug resistant TB in different settings: congregate (in a prison), at health facilities (passive case detection) and community based (house-to-house survey in a rural community). The three studies are summarized below.

1. TB disease burden is higher in prisons compared to the general population. The impact of TB in prisons extends beyond prison walls into surrounding communities. The study aimed to estimate the burden of TB in Hawassa prison and assess the value of active TB case finding in a prison setting. A total of 2068 prisoners were screened using active case finding strategy and out of these 372 (18%) had a positive cough screen. A point prevalence of TB was 1789 per 100,000 in the prison population and it is over 16 times higher than the prevalence found in the general Ethiopian population. The study highlighted the high prevalence of TB in Hawassa prison and the importance of active surveillance supported by highly sensitive and specific diagnostic tests like the molecular testing of Xpert MTB/RIF in prison settings.

2. Molecular epidemiologic data on TB including drug resistant TB could help the TB control program by providing better understanding of the transmission dynamics of TB in specific settings and to stimulate the designing and implementation of appropriate intervention measures in the prevention and control of the disease. The study characterized the DST patterns and genetic diversity of *M. tuberculosis* isolates circulating in nine health facilities in Southern Ethiopia. A total of 250 newly diagnosed patients with TB were enrolled in the study, of which 230 isolates were obtained from the sputum culture. A total of 65 spoligotype patterns identified, of which 29 (45%) were new; 81% - Euro-American lineage, 14% - East-African-Indian and 4% - Lineage 7 (Ethiopian lineage). A total of 29 strain clusters were identified and clustering of strains by geographic locations was observed. DST revealed that 14% of Mtb isolates tested were resistant to $\geq$ 1 first line anti-TB drugs and 11% to isoniazid. SIT 149 was the most prevalent spoligotype among drug

resistant isolates. WGS analysis identified different drug resistance mutations in Mtb isolates. These findings suggest the ongoing transmission of TB, including of drug resistant TB in Southern Ethiopia and calls for surveillance and wider monitoring of DST, the need for molecular testing laboratories to monitor transmission trends and improved control responses.

3. One of the most pressing challenges to eliminate TB is the high number of undetected cases. Rural settings are particularly challenging areas to detect and diagnose TB due to limited healthcare services, poor healthcare seeking behavior, and limited awareness and knowledge about TB. Understanding the burden of TB in poor rural areas has large implications for TB control and is needed to design optimal case finding strategies. A population-based TB screening was carried out utilizing volunteer health workers (Health Development Army) and paid community health workers (Health Extension Workers) in a rural area in Southern Ethiopia. A total of 24,517 adults were screened in a short period of time (~1 month) and detect 34 previously undiagnosed active TB cases, primarily through the use of Xpert MTB/RIF. Point TB prevalence was 139 per 100,000 population. The study demonstrates the feasibility of a large TB screening program using community health volunteers doing the initial symptom screen and referrals and paid community health workers for further testing and confirmation. The high prevalence of previously undiagnosed TB identified in the current study highlights the hidden burden of TB in rural settings and the need for additional active screening programs. In our setting, we show that an approach using community health workers can carry out an impressive large-scale screening program and this may be a useful approach to consider for other similar rural LMIC settings.

Overall, the results of the three study findings could significantly impact the TB control program of the country in improving the prevention and control of the disease and add knowledge to the science.

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Annexes

Questionnaires (English version)

Initial of suspect_____ Study code_____ Card no._____

Part I. Socio-demographic characteristics

No	Questions	Coding category/response	Skip to
1	Age in years	----------years	
2	Sex	0. Female 1. Male	
3	Residence	0. Urban 1. Rural	
4	Marital status	0. Single 1. Married 2. Divorced 3. Widowed 4. Separated	
5	Education	0. Not educated 1. Primary (1-8) 2. Secondary (9-10 or 12) 3. Collage (10+ or 12+) 4. Other……	
6	Occupation (Occupation before imprisonment for prisoners)	0. Civil servant 1. Farmer 2. Daily labourer 3. Student 4. House wife 5. Unemployed 6. Merchant 7. Others……	

Part II. Tuberculosis symptoms

1	Did you experience cough for two or more weeks?	0. No 1. Yes	
2	If yes to Q1, for how many weeks?	---------- weeks	
3	Is the cough productive of sputum?	0. No 1. Yes	
4	If yes to Q3, does it contain blood?	0. No 1. Yes	
5	Did you have fever?	0. No 1. Yes	
6	If yes to Q5, for how many weeks?	---------- weeks	
7	Did you have night sweats?	0. No 1. Yes	
8	If yes to Q7, for how many weeks?	---------- weeks	
9	Did you have loss of appetite?	0. No 1. Yes	
10	If yes for Q9, for how many weeks?	---------- weeks	
11	Did you loss weight?	0. No 1. Yes	
12	Did you have chest pain?	0. No 1. Yes	
13	If yes for Q12, for how many weeks?	---------- weeks	
14	Did you have shortness of breath?	0. No 1. Yes	
15	If yes for Q14, for how many weeks?	---------- weeks	

Part III. Predisposing factors for TB

1	Did you have past history of TB?	0. No 1. Yes	
2	Did you have closer contact with known TB patient?	0. No 1. Yes	
3	Is there TB patient in the family?	0. No 1. Yes	
4	Do you have diabetes mellitus?	0. No 1. Yes	
5	Do you smoke cigarette?	0. No 1. Yes	
6	If yes to Q5, for how long?	---------- years	
7	Do you chew "chat"?	0. No 1. Yes	
8	If yes for Q7, for how long?	---------- years	
9	Do you drink alcohol?	0. No 1. Yes	
10	If yes for Q9, how many bottles/cups per day/weeks?	----------day/week	
11	If yes for Q9, for how long?	---------- years	
12	Do you have bronchial asthma?	0. No 1. Yes	
13	With what material was the **wall** of the house made of?	0. Mud/mud brick 1. Cement	
14	With what material was the **floor** of the house made of?	0. Mud/mud brick 1. Cement	
15.	Number of family members in the house	----------	
16	Do you have window in your home?	0. No 1. Yes	
17	If yes for Q17, how often do you open the window?	0. Usually 1. Less time 2. Very less time	
18	HIV status (To be documented)	0. Negative 1. Positive	

Part IV. Predisposing factors for MDR TB

1	Did you have history of tuberculosis treatment?	0. No 1. Yes	
2	If yes to Q1, how is the treatment outcome?	0. Cure 1. Treatment complete 2. Treatment failure 3. Treatment default	
3	If yes to Q1, at which health facility was the treatment initiated?	0. Health Center 1. Hospital 2. Health post	
4	If yes to Q1, in which health facility was the treatment initiated?	0. Governmental 1. Private	
5	Did you have history of imprisonment?	0. No 1. Yes	
6	If yes to Q5, for how long?	---------- months/years	
7	Did you have history of previous hospitalization?	0. No 1. Yes	
8	If yes for Q7, for how long?	---------- years/months	
9	If yes for Q7, what was the reason of hospitalization?	……..	
10	Did you have closer contact with known MDR TB patient?	0. No 1. Yes 2. I don't remember	
11	Is there MDR TB patient in the family?	0. No 1. Yes	
12	Where did you live?	0. In own house 1. In rented house 2. In dormitory 3. Homeless 4. Other ……..	

V. Prison history and condition

1	Do you have support from family in terms of visit and bringing food?	0. I don't have 1. visit only 2. food only 3. visit and food	
2	If you have family visit, how many times per week do they bring food?	----------per week	
3	How long did you imprisoned in the current prison?	------months	
4	How many times did you get imprisonment in the current prison?	-------- times	
5	Have you been imprisoned in another prison?	0. no 1. yes , if no	Skip to Q8
6	If yes to Q5, how many times?	-------times	
7	If yes to Q5, how long?	--------months	
8	Have you been imprisoned with known TB patient in same cell?	0. no 1. yes 2. I don't know	
9	If Yes to Q.8, for how long?	--------months/years	
10	Have you imprisoned with chronically coughing person in same cell?	0. no 1. yes, if no	Skip to Q12
11	If yes, for how long?	---------- months/years	
12	How many inmates are imprisoned in your cell?	----------per cell	
13	Do you have window in your cell?	0. no 1. yes, if no	Skip to Q15
14	If yes to Q13, How often do you open the window?	0. usually 1. less time 2. very less time	
15	How frequently are you spending your time outside of your cell?	0. everyday 1. sometimes 2. none	
16	Do you share drinking and eating materials with other persons?	0. no 1. yes	

VI. Morbidity History and Status of prisoners

1	Currently, do you have any kind symptoms/complaints?	0. No 1. Yes	
2	If Yes for Q1, what type of symptoms/complaints do you have?	0. cough 1. chest pain 2. difficulty of breathing 3. fever 4. weight loss 5. night sweating 6. loss of appetite 7. malaise 8. fatigue 9. others(specify)	
3	For how long have you been coughing?	----------per week	
4	Did you visit and receive any treatment for your current complaint?	0. No, if no 1. yes	Skip to Q7
5	If yes to Q4, where?	0. health institution outside of the prison 1. prison's clinic difficulty of breathing 2. both 3. others----------	
6	How many times did you visit for these symptoms (those mentioned in Q2)?	----times	
7	If no to Q4, why?	----------	
8	Did you have these symptoms (those mentioned in Q2) before your imprisonment in this prison?	0. No, if no 1. yes	
9	Have you been diagnosed for TB?	0. No 1. yes	
10	If yes to Q9, When have you been diagnosed for TB?	0. Before imprisonment 1. During imprisonment 2. I don't know	
11	If yes to Q9, did you take treatment?	0. No 1. yes	
12	If yes to Q11, did you complete the full course of treatment?	0. No 1. yes	
13	If no to Q12, why?	----------	
14	Do you have identified or diagnosed health problem like Diabetic mellitus, Hypertension…etc?	0. No 1. yes 2. I don't know	
15	If yes to Q14, what is/are the problem?	----------	
16	If yes to Q14, are you taking any treatment?	0. No 1. yes	

17	If no to Q16, why?	----------	
18	Have you ever been hospitalized?	0. No, if no 1. yes	Skip to Q21
19	If yes to Q18, how long?	---------months	
20	If yes to Q18, What was the reason for hospitalization?	----------	
21	Did you have contact with known TB patient at home?	0. No 1. yes 2. I don't know	
22	Currently, are you taking anti-TB treatment?	0. No 1. Yes	
23	Did you know your sputum result before you take your anti-TB treatment?	0. No 1. Yes 2. I don't know	
24	If yes for Q no.23 what was it?	…….	
25	Collected sputum (to be filled by data collector): make mark if taken.	0. Spot 1. Morning 2. 2nd spot 3. No sputum (write reason why there is no sputum)	

VII. Medical Knowledge of TB

1**.** Do you know the causes of TB?

0. No 1. Yes

2.If Yes to Q1, what would be the cause?

.....

3. Do you think TB is transmitted from TB patient to health person?

0. No 1. Yes

4. If Yes to the Q3, What do you think the mode of transmission?

……

5.Is there any treatment for TB?/

0. No 1. Yes

6.If Yes to Q 5, Is a person receiving TB treatment can be cured? Is TB cured?

……

7.Woud there be any danger if a TB patient is not treated??

0. No 1. Yes

8. If Yes to Q7, what type of danger/problem could be caused?

0. To the patient……..?

1. To the people around……..?

9. Would there be any problem by interrupting TB treatment?

0. No 1. Yes

10.If Yes to Q9, what type of problem do could be caused?

……

11. Did you know that the TB treatment is available free of charge?

0. No 1. Yes 2. I don't know

12. How TB would be prevented?

……

13. Do you know that TB in prison has different pattern from TB in community? (Question only for prisnors)

0. No 1. Yes

Subject Information sheet for Health Institute study (English version)

Subject Information sheet for Adult (_> 18 years)

Study title: "Molecular Epidemiology and Drug Resistance of Tuberculosis in Southern Region of Ethiopia"

Background

Tuberculosis (TB) is an infectious disease that affects lungs and responsible for many illnesses and deaths worldwide. Ethiopia is one of the countries seriously affected by the disease. TB is transmitted by a bacterium called *Mycobacterium tuberculosis (M. tuberculosis).* Recently, TB transmitted by a bacterium resistant to anti tuberculosis drug is spreading in the world. This makes the situation more serious and difficult in controlling the disease. Laboratory based investigation aiming at identifying the causative agent of the disease and its characterization would help in providing valuable information in the prevention and control of the disease. Therefore, it is planned to study on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

Aim of the study

To provide data on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

Study procedure

The type of samples that will be taken for the study is sputum, which is a sample that will be provided for the routine diagnosis of tuberculosis. Therefore, there would not be an extra sputum sample taken for the study. You will be requested to participate in the study and will be enrolled in to it after having adequate information about the study and given your informed consent. Then, you will sign on the informed consent form and participate on the study. If your physician diagnosed you to have pulmonary tuberculosis, you will provide three sputum samples for laboratory diagnosis. Sputum samples will be collected by a laboratory personnel on a screw-cupped container designed for sputum collection. The

sputum samples will be used for diagnosing your disease condition as well as for the research purpose. In addition to this, if you are found to be pulmonary TB positive, your HIV test result will be collected from the result document and will be utilized for the analysis of the study result. There will also be an interview on personal and medical condition and about tuberculosis disease. The interview will be carried out by a nurse in the TB clinic of the health institute. The interview will be carried out in isolated place where your privacy will be kept.

Risk and complications

The study will not impose major risk (or with minimal risk) to you as the procedure only demands producing sputum. The sputum collection process follows the routine procedures for laboratory diagnosis of the disease.

Benefits

As a study participant, you will receive no direct benefit from the study, and as you voluntarily participate in this study; there will be no inducement. However, the outcome of the study will contribute to the epidemiology of pulmonary tuberculosis in Ethiopia. You will not be charged for the cost of laboratory tests involved it the identification and characterization of the causative agent of the disease or the other tests involved. The diagnosis and treatment of TB is free of charge in the country, however, if you are hospitalized, you will yourself have to pay for your hospitalization according to standard procedures in the health facilities.

Withdrawal from the study

All study participants will be informed and their consent sought for the study. Such consents can however, like all other consents, be annulled at any time by the patient with no consequences to the continued care of the individual.

Confidentiality

All personal records will be kept in locked cabinet and therefore confidentiality will be maintained. No personal identifiers will appear in any report from the study. All test results will be treated confidentially with use of coded labels on specimens.

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Name of sponsors: Armauer Hansen Research institute (AHRI) and Addis Ababa University, Medical Faculty School of Graduate Studies.

Subject Information sheet for Parent/Guardian (for 5-11 years)

Study title: "Molecular Epidemiology and Drug Resistance of Tuberculosis in Southern Region of Ethiopia"

Background

Tuberculosis (TB) is an infectious disease that affects lungs and responsible for many illnesses and deaths worldwide. Ethiopia is one of the countries seriously affected by the disease. TB is transmitted by a bacterium called *Mycobacterium tuberculosis (M. tuberculosis).* Recently, TB transmitted by a bacterium resistant to anti tuberculosis drug is spreading in the world. This makes the situation more serious and difficult in controlling the disease. Laboratory based investigation aiming at identifying the causative agent of the disease and its characterization would help in providing valuable information in the prevention and control of the disease. Therefore, it is planned to study on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

Aim of the study

To provide data on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

Study procedure

The type of samples that will be taken for the study is sputum, which is a sample that will be provided for the routine diagnosis of tuberculosis. Therefore, there would not be an extra sputum sample taken for the study. If you are a parent or a next-of-kin of the children, you will be requested for your consent for your child and your child will be enrolled in to the study after having adequate information about the study and given informed consent. Then, you will sign on the informed consent form (on behalf of your child) and your child will participate in the study. If the physician diagnosed your child to have pulmonary

tuberculosis, your child will provide three sputum samples for laboratory diagnosis. Sputum samples will be collected by a laboratory personnel by a screw-cupped container designed for sputum collection. The sputum samples will be used for diagnosing your child disease condition as well as for the research purpose. In addition to this, if your child is found to be pulmonary TB positive, his/her HIV test result will be collected from the result document and will be utilized for the analysis of the study result. There will also be an interview on personal and medical condition and about tuberculosis disease. The interview will be carried out by a nurse in the TB clinic of the health institution. The interview will be carried out in isolated place where your privacy will be kept.

Risk and complications

The study will not impose major risk (or with minimal risk) to your child as the procedure only demands producing sputum. The sputum collection process follows the routine procedures for laboratory diagnosis of the disease.

Benefits

As a study participant, your child will receive no direct benefit from the study, and as your child voluntarily participate in this study; there will be no inducement. However, the outcome of the study will contribute to the epidemiology of pulmonary tuberculosis in Ethiopia. Your child will not be charged for the cost of laboratory tests involved it the identification and characterization of the causative agent of the disease or the other tests involved. The diagnosis and treatment of TB is free of charge in the country, however, if your child hospitalized, you will yourself have to pay for the hospitalization according to standard procedures in the health facilities.

Withdrawal from the study

All study participants will be informed and their assent/consent sought for the study. Such consents can however, like all other consents, be annulled at any time by the patient with no consequences to the continued care of the individual.

Confidentiality

All personal records will be kept in locked cabinet and therefore confidentiality will be maintained. No personal identifiers will appear in any report from the study. All test results will be treated confidentially with use of coded labels on specimens.

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Name of sponsors: Armauer Hansen Research institute (AHRI) and Addis Ababa University, Medical Faculty School of Graduate Studies.

Subject Information Sheet for Children (12-17 years)

Study title: "Molecular Epidemiology and Drug Resistance of Tuberculosis in Southern Region of Ethiopia"

Background

Tuberculosis (TB) is an infectious disease that affects lungs and responsible for many illnesses and deaths worldwide. Ethiopia is one of the countries seriously affected by the disease. TB is transmitted by a bacterium called *Mycobacterium tuberculosis (M. tuberculosis).* Recently, TB transmitted by a bacterium resistant to anti tuberculosis drug is spreading in the world. This makes the situation more serious and difficult in controlling the disease. Laboratory based investigation aiming at identifying the causative agent of the disease and its characterization would help in providing valuable information in the prevention and control of the disease. Therefore, it is planned to study on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

Aim of the study

To provide data on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

Study procedure

The type of samples that will be taken for the study is sputum, which is a sample that will be provided for the routine diagnosis of tuberculosis. Therefore, there would not be an extra sputum sample taken for the study. You will be requested to participate in the study and will be enrolled in to it after having adequate information about the study and given your informed consent. Then, you will sign on the informed consent form and participate on the study. If your physician diagnosed you to have pulmonary tuberculosis, you will provide three sputum samples for laboratory diagnosis. Sputum samples will be collected by a laboratory personnel on a screw-cupped container designed for sputum collection. The

sputum samples will be used for diagnosing your disease condition as well as for the research purpose. In addition to this, if you are found to be pulmonary TB positive, your HIV test result will be collected from the result document and will be utilized for the analysis of the study result. There will also be an interview on personal and medical condition and about tuberculosis disease. The interview will be carried out by a nurse in the TB clinic of the health institution. The interview will be carried out in isolated place where your privacy will be kept.

Risk and complications

The study will not impose major risk (or with minimal risk) to you as the procedure only demands producing sputum. The sputum collection process follows the routine procedures for laboratory diagnosis of the disease.

Benefits

As a study participant, you will receive no direct benefit from the study, and as you voluntarily participate in this study; there will be no inducement. However, the outcome of the study will contribute to the epidemiology of pulmonary tuberculosis in Ethiopia. You will not be charged for the cost of laboratory tests involved it the identification and characterization of the causative agent of the disease or the other tests involved. The diagnosis and treatment of TB is free of charge in the country, however, if you are hospitalized, you will yourself have to pay for your hospitalization according to standard procedures in the health facilities.

Withdrawal from the study

All study participants will be informed and their assent/consent sought for the study. Such consents can however, like all other consents, be annulled at any time by the patient with no consequences to the continued care of the individual.

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Name of sponsors: Armauer Hansen Research institute (AHRI) and Addis Ababa University, Medical Faculty School of Graduate Studies.

Subject Information sheet for Community study (English version)

Subject Information sheet for Adult (_> 18 years)

Study title: "Molecular Epidemiology and Drug Resistance of Tuberculosis in Southern Region of Ethiopia"

Background

Tuberculosis (TB) is an infectious disease that affects lungs and responsible for many illnesses and deaths worldwide. Ethiopia is one of the countries seriously affected by the disease. TB is transmitted by a bacterium called *Mycobacterium tuberculosis (M. tuberculosis).* Recently, TB transmitted by a bacterium resistant to anti tuberculosis drug is spreading in the world. This makes the situation more serious and difficult in controlling the disease. Laboratory based investigation aiming at identifying the causative agent of the disease and its characterization would help in providing valuable information in the prevention and control of the disease. Therefore, it is planned to study on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

Aim of the study

To provide data on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

Study procedure

The type of samples that will be taken for the study is sputum, which is a sample that will be provided for the routine diagnosis of tuberculosis. Therefore, there would not be an extra sputum sample taken for the study. You will be requested to participate in the study and will be enrolled in to it after having adequate information about the study and given your informed consent. Then, you will sign on the informed consent form and participate on the study. If you are suspected for pulmonary tuberculosis, you will provide two sputum samples for laboratory diagnosis. And if it is confirmed to be pulmonary tuberculosis, you

will be requested for HIV counseling and testing. Sputum samples will be collected by a health extension worker on a screw-cupped container designed for sputum collection. The sputum samples will be used for diagnosing your disease condition as well as for the research purpose. There will also be an interview on personal and medical condition and about tuberculosis disease. The interview will be carried out by a health extension worker. The interview will be carried out in isolated place where your privacy will be kept.

Risk and complications

The study will not impose major risk (or with minimal risk) to you as the procedure only demands producing sputum. The sputum collection process follows the routine procedures for laboratory diagnosis of the disease. If you are diagnosed for pulmonary tuberculosis and decided to give blood for HIV testing, there would be a minor pain during finger pricking.

Benefits

As a study participant, you will receive no direct benefit from the study, and as you voluntarily participate in this study; there will be no inducement. However, the outcome of the study will contribute to the epidemiology of pulmonary tuberculosis in Ethiopia. You will not be charged for the cost of laboratory tests involved it the identification and characterization of the causative agent of the disease or the other tests involved. The diagnosis and treatment of TB is free of charge in the country, however, if you are hospitalized, you will yourself have to pay for your hospitalization according to standard procedures in the health facilities.

Withdrawal from the study

All study participants will be informed and their consent sought for the study. Such consents can however, like all other consents, be annulled at any time by the patient with no consequences to the continued care of the individual.

Confidentiality

All personal records will be kept in locked cabinet and therefore confidentiality will be maintained. No personal identifiers will appear in any report from the study. All test results will be treated confidentially with use of coded labels on specimens.

Study contacts

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Name of sponsors: Armauer Hansen Research institute (AHRI) and Addis Ababa University, Medical Faculty School of Graduate Studies.

Subject Information sheet for Prison study (English version)

Subject Information sheet for Adult (_> 18 years)

Study title: "Molecular Epidemiology and Drug Resistance of Tuberculosis in Southern Region of Ethiopia"

Background

Tuberculosis (TB) is an infectious disease that affects lungs and responsible for many illnesses and deaths worldwide. Ethiopia is one of the countries seriously affected by the disease. TB is transmitted by a bacterium called *Mycobacterium tuberculosis (M. tuberculosis).* Recently, TB transmitted by a bacterium resistant to anti tuberculosis drug is spreading in the world. This makes the situation more serious and difficult in controlling the disease. Laboratory based investigation aiming at identifying the causative agent of the disease and its characterization would help in providing valuable information in the prevention and control of the disease. Therefore, it is planned to study on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

Aim of the study

To provide data on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

Study procedure

The type of samples that will be taken for the study is sputum, which is a sample that will be provided for the routine diagnosis of tuberculosis. Therefore, there would not be an extra sputum sample taken for the study. You will be requested to participate in the study and will be enrolled in to it after having adequate information about the study and given your informed consent. Then, you will sign on the informed consent form and participate on the study. If you are suspected for pulmonary tuberculosis, you will provide three sputum samples for laboratory diagnosis. And if it is confirmed to be pulmonary tuberculosis, you

will be requested for HIV counseling and testing. Sputum samples will be collected by a nurse on a screw-cupped container designed for sputum collection. The sputum samples will be used for diagnosing your disease condition as well as for the research purpose. There will also be an interview on personal and medical condition and about tuberculosis disease. The interview will be carried out by a nurse in the clinic. The interview will be carried out in isolated place where your privacy will be kept.

Risk and complications

The study will not impose major risk (or with minimal risk) to you as the procedure only demands producing sputum. The sputum collection process follows the routine procedures for laboratory diagnosis of the disease. If you are diagnosed for pulmonary tuberculosis and decided to give blood for HIV testing, there would be a minor pain during finger pricking.

Benefits

As a study participant, you will receive no direct benefit from the study, and as you voluntarily participate in this study; there will be no inducement. However, the outcome of the study will contribute to the epidemiology of pulmonary tuberculosis in Ethiopia. You will not be charged for the cost of laboratory tests involved it the identification and characterization of the causative agent of the disease or the other tests involved. The diagnosis and treatment of TB is free of charge in the country, however, if you are hospitalized, you will yourself have to pay for your hospitalization according to standard procedures in the health facilities.

Withdrawal from the study

All study participants will be informed and their consent sought for the study. Such consents can however, like all other consents, be annulled at any time by the patient with no consequences to the continued care of the individual.

Confidentiality

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Name of sponsors: Armauer Hansen Research institute (AHRI) and Addis Ababa University, Medical Faculty School of Graduate Studies.

Subject Information sheet for Parent/Guardian (for 5-11 years)

Study title: "Molecular Epidemiology and Drug Resistance of Tuberculosis in Southern Region of Ethiopia"

Background

Tuberculosis (TB) is an infectious disease that affects lungs and responsible for many illnesses and deaths worldwide. Ethiopia is one of the countries seriously affected by the disease. TB is transmitted by a bacterium called *Mycobacterium tuberculosis (M. tuberculosis).* Recently, TB transmitted by a bacterium resistant to anti tuberculosis drug is spreading in the world. This makes the situation more serious and difficult in controlling the disease. Laboratory based investigation aiming at identifying the causative agent of the disease and its characterization would help in providing valuable information in the prevention and control of the disease. Therefore, it is planned to study on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

Aim of the study

To provide data on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

Sample uptake procedure

The type of samples that will be taken for the study is sputum, which is a sample that will be provided for the routine diagnosis of tuberculosis. Therefore, there would not be an extra sputum sample taken for the study. If you are a parent or a next-of-kin of the children, you will be requested for your consent for your child and your child will be enrolled in to the study after having adequate information about the study and given informed consent. Then, you will sign on the informed consent form (on behalf of your child) and your child will participate in the study. If your child is suspected for pulmonary tuberculosis, he/she will provide three sputum samples for laboratory diagnosis. And if it is confirmed to be

pulmonary tuberculosis, he/she will be requested for HIV counseling and testing. Sputum samples will be collected by a nurse on a screw-cupped container designed for sputum collection. The sputum samples will be used for diagnosing your child's disease condition as well as for the research purpose. There will also be an interview on personal and medical condition and about tuberculosis disease. The interview will be carried out by a nurse in the clinic. The interview will be carried out in isolated place where your privacy will be kept.

Risk and complications

The study will not impose major risk (or with minimal risk) to your child as the procedure only demands producing sputum. The sputum collection process follows the routine procedures for laboratory diagnosis of the disease. If your child is diagnosed for pulmonary tuberculosis and decided to give blood for HIV testing, there would be a minor pain during finger pricking.

Benefits

As a study participant, your child will receive no direct benefit from the study, and as your child voluntarily participate in this study; there will be no inducement. However, the outcome of the study will contribute to the epidemiology of pulmonary tuberculosis in Ethiopia. Your child will not be charged for the cost of laboratory tests involved it the identification and characterization of the causative agent of the disease or the other tests involved. The diagnosis and treatment of TB is free of charge in the country, however, if your child hospitalized, you will yourself have to pay for the hospitalization according to standard procedures in the health facilities.

Withdrawal from the study

All study participants will be informed and their assent/consent sought for the study. Such consents can however, like all other consents, be annulled at any time by the patient with no consequences to the continued care of the individual.

Confidentiality

All personal records will be kept in locked cabinet and therefore confidentiality will be maintained. No personal identifiers will appear in any report from the study. All test results will be treated confidentially with use of coded labels on specimens.

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Name of sponsors: Armauer Hansen Research institute (AHRI) and Addis Ababa University, Medical Faculty School of Graduate Studies.

Subject Information Sheet for Children (12-17 years)

Study title: "Molecular Epidemiology and Drug Resistance of Tuberculosis in Southern Region of Ethiopia"

Background

Tuberculosis (TB) is an infectious disease that affects lungs and responsible for many illnesses and deaths worldwide. Ethiopia is one of the countries seriously affected by the disease. TB is transmitted by a bacterium called *Mycobacterium tuberculosis (M. tuberculosis).* Recently, TB transmitted by a bacterium resistant to anti tuberculosis drug is spreading in the world. This makes the situation more serious and difficult in controlling the disease. Laboratory based investigation aiming at identifying the causative agent of the disease and its characterization would help in providing valuable information in the prevention and control of the disease. Therefore, it is planned to study on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

Aim of the study

To provide data on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

Study procedure

The type of samples that will be taken for the study is sputum, which is a sample that will be provided for the routine diagnosis of tuberculosis. Therefore, there would not be an extra sputum sample taken for the study. You will be requested to participate in the study and will be enrolled in to it after having adequate information about the study and given your informed consent. Then, you will sign on the informed consent form and participate on the study. If you are suspected for pulmonary tuberculosis, you will provide three sputum samples for laboratory diagnosis. And if it is confirmed to be pulmonary tuberculosis, you will be requested for HIV counseling and testing. Sputum samples will be collected by a

nurse on a screw-cupped container designed for sputum collection. The sputum samples will be used for diagnosing your disease condition as well as for the research purpose. There will also be an interview on personal and medical condition and about tuberculosis disease. The interview will be carried out by a nurse in the clinic. The interview will be carried out in isolated place where your privacy will be kept.

Risk and complications

The study will not impose major risk (or with minimal risk) to you as the procedure only demands producing sputum. The sputum collection process follows the routine procedures for laboratory diagnosis of the disease. If you are diagnosed for pulmonary tuberculosis and decided to give blood for HIV testing, there would be a minor pain during finger pricking.

Benefits

As a study participant, you will receive no direct benefit from the study, and as you voluntarily participate in this study; there will be no inducement. However, the outcome of the study will contribute to the epidemiology of pulmonary tuberculosis in Ethiopia. You will not be charged for the cost of laboratory tests involved it the identification and characterization of the causative agent of the disease or the other tests involved. The diagnosis and treatment of TB is free of charge in the country, however, if you are hospitalized, you will yourself have to pay for your hospitalization according to standard procedures in the health facilities.

Withdrawal from the study

All study participants will be informed and their assent/consent sought for the study. Such consents can however, like all other consents, be annulled at any time by the patient with no consequences to the continued care of the individual.

Confidentiality

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AHRI/ALERT Ethic Review Committee secretariat contact address -0118-962183

Name of sponsors: Armauer Hansen Research institute (AHRI) and Addis Ababa University, Medical Faculty School of Graduate Studies.

Consent form for Health Institute study (English version)

Consent form for Adult (_> 18 years)

Addis Ababa University in collaboration with Armauer Hansen Research Institute (AHRI), Oromia and the Southern Nations Nationalities Peoples Region (SNNPR) Health Bureaus, has planned to undertake a study on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

I am requested to participate in this study. It is very well explained to me and I have understood if I am sick with this disease and the physician recommends, sputum samples for laboratory diagnosis will be given. Elaborate information is given to me about that I have got the right to or not to participate in this study as well as discontinue from the study if I am not interested in the participation at any time and this doesn't have any impact on the medical follow up I should obtain. Moreover an explanation is given to me for things which need to be clarified to me. These include: to give three sputum samples for the study, to be interviewed on personal and medical condition and about tuberculosis disease. Besides, to utilize my clinical data including HIV test result for the study. I am also told that no personal identifiers will be disclosed and it will be kept confidential. With this, I therefore have voluntarily agreed to participate on this study.

Participant's Name_____ **Signature**_____**Date**_____

Nurses's Name _____ Signature_____ **Date**_____

Witnesses' Name_____ Signature_____ **Date**_____

Parents/Gurdians Consent form (for 5-11 years)

Addis Ababa University in collaboration with Armauer Hansen Research Institute (AHRI), Oromia and the Southern Nations Nationalities Peoples Region (SNNPR) Health Bureaus, has planned to undertake a study on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

I am requested that my child may participate in this study. It is very well explained to me and I have understood if the child diagnosed for this disease and the physician recommends, sputum samples for laboratory diagnosis will be given. Elaborate information is given to me about that I have got the right to or not to make my child participate in this study. My child however could as well discontinue from the study if I or my child are not interested in the participation at any time and this doesn't have any impact on the medical follow up procedures my child should obtain. Moreover an explanation is given to me for things which need to be clarified to me on behalf of my child. These include: my child will give three sputum samples, will be interviewed on personal and medical condition and about tuberculosis disease, and my child's clinical data including the HIV test result will be utilized for the study. Besides, I am told that no personal identifiers will be disclosed and will be kept confidential. With this, I therefore have voluntarily agreed to make my child participate on this study.

Parent's/Gurdian's Name_____ **Signature----------Date----------**

Nurses's Name _____ Signature_____ **Date----------**

Witnesses' Name_____Signature_____ **Date----------**

Assent form for children (12-17 years)

Addis Ababa University in collaboration with Armauer Hansen Research Institute (AHRI), Oromia and the Southern Nations Nationalities Peoples Region (SNNPR) Health Bureaus, has planned to undertake a study on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

I am requested to participate in this study. It is very well explained to me and I have understood if I am diagnosed for pulmonary tuberculosis and the physician recommends, sputum samples for laboratory diagnosis will be given. Elaborate information is given to me about that I have got the right to or not to participate in this study as well as discontinue from the study if I am not interested in the participation at any time and this doesn't have any impact on the medical follow up I should obtain. Moreover an explanation is given to me for things which need to be clarified to me. These include: to give three sputum samples for the study, to be interviewed on personal and medical condition and about tuberculosis disease. Besides, to utilize my clinical data including HIV test result for the study. I am also told that no personal identifier will be disclosed and it will be kept confidential. With this, I therefore have voluntarily agreed to participate on this study.

Participant's Name_____ Signature----------Date---------

Nurses's Name _____ Signature_____ **Date-------**

Witnesses' Name_____Signature_____ **Date--------**

Consent form for Community study

Consent form for Adults (_>18 years)

Addis Ababa University in collaboration with Armauer Hansen Research Institute (AHRI), Oromia and the Southern Nations Nationalities Peoples Region (SNNPR) Health Bureaus, has planned to undertake a study on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

I am requested to participate in this study. It is very well explained to me and I have understood if I am suspected for pulmonary tuberculosis, two sputum samples will be given for laboratory diagnosis. And if it is confirmed to be pulmonary tuberculosis, I will undergo HIV counseling and testing. Elaborate information is given to me about that I have got the right to or not to participate in this study as well as discontinue from the study if I am not interested in the participation at any time and this doesn't have any impact on the medical follow up I should obtain. Moreover an explanation is given to me for things which need to be clarified to me. These include: to give two sputum samples for the study, to be interviewed on personal and medical condition and about tuberculosis disease. Besides, to utilize my clinical data including HIV test result for the study. I am also told that no personal identifiers will be disclosed and it will be kept confidential. With this, I therefore have voluntarily agreed to participate on this study.

Participant Name_____**Signature**_____
Date_____

Nurses's Name _____ Signature_____ **Date**_____

Witnesses' Name_____ Signature_____ **Date**_____

Consent form for Prison study

Consent form for Adults (_>18 years)

Addis Ababa University in collaboration with Armauer Hansen Research Institute (AHRI), Oromia and the Southern Nations Nationalities Peoples Region (SNNPR) Health Bureaus, has planned to undertake a study on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

I am requested to participate in this study. It is very well explained to me and I have understood if I am suspected for pulmonary tuberculosis, three sputum samples will be given for laboratory diagnosis. And if it is confirmed to be pulmonary tuberculosis, I will undergo HIV counseling and testing. Elaborate information is given to me about that I have got the right to or not to participate in this study as well as discontinue from the study if I am not interested in the participation at any time and this doesn't have any impact on the medical follow up I should obtain. Moreover an explanation is given to me for things which need to be clarified to me. These include: to give three sputum samples for the study, to be interviewed on personal and medical condition and about tuberculosis disease. Besides, to utilize my clinical data including HIV test result for the study. I am also told that no personal identifiers will be disclosed and it will be kept confidential. With this, I therefore have voluntarily agreed to participate on this study.

Participant Name_____Signature_____

Date_____

Nurses's Name _____ Signature_____ **Date_____**

Witnesses' Name_____ Signature_____ **Date_____**

Parents/Gurdians consent form (5-11 years)

Addis Ababa University in collaboration with Armauer Hansen Research Institute (AHRI), Oromia and the Southern Nations Nationalities Peoples Region (SNNPR) Health Bureaus, has planned to undertake a study on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs.

I am requested that my child may participate in this study. It is very well explained to me and I have understood if the child is suspected for pulmonary tuberculosis, three sputum samples will be given for laboratory diagnosis. And if it is confirmed to be pulmonary tuberculosis, the child will undergo HIV counseling and testing. Elaborate information is given to me about that I have got the right to or not to make my child participate in this study. My child however could as well discontinue from the study if I or my child are not interested in the participation at any time and this doesn't have any impact on the medical follow up procedures my child should obtain. Moreover an explanation is given to me for things which need to be clarified to me on behalf of my child. These include: my child will give three sputum samples, will be interviewed on personal and medical condition and about tuberculosis disease, and my child's clinical data including the HIV test result will be utilized for the study. Besides, I am told that no personal identifiers will be disclosed and will be kept confidential. With this, I therefore have voluntarily agreed to make my child participate on this study.

Parents/Gurdians Name_____ **Signature**----------
Date_____

Nurses's Name _____ Signature_____
Date_____

Witnesses' Name_____Signature_____
Date_____

Assent form for children (12-17 years)

Addis Ababa University in collaboration with Armauer Hansen Research Institute (AHRI), Oromia and the Southern Nations Nationalities Peoples Region (SNNPR) Health Bureaus, has planned to undertake a study on the prevalence and distribution of pulmonary tuberculosis with particular emphasis on the disease that is resistant to anti tuberculosis drugs. I am requested to participate in this study. It is very well explained to me and I have understood if I am suspected for pulmonary tuberculosis, three sputum samples will be given for laboratory diagnosis. And if it is confirmed to be pulmonary tuberculosis, I will undergo HIV counseling and testing. Elaborate information is given to me about that I have got the right to or not to participate in this study as well as discontinue from the study if I am not interested in the participation at any time and this doesn't have any impact on the medical follow up I should obtain. Moreover an explanation is given to me for things which need to be clarified to me. These include: to give three sputum samples for the study, to be interviewed on personal and medical condition and about tuberculosis disease. Besides, to utilize my clinical data including HIV test result for the study. I am also told that no personal identifiers will be disclosed and it will be kept confidential. With this, I therefore have voluntarily agreed to participate on this study.

Participant Name_____Signature_____
Date_____

Nurses's Name _____ Signature_____ **Date_____**

Witnesses' Name_____ Signature_____ **Date_____**

Odefaanoo qoranoo buufata fayyaa irra jiraanif (afaan Oromoo version)

Guca odeefannoo hirmaattotaa (ga'eessa waggaa18 olif)

Mata dure qorannoo: Tatamsa'ina dhukkuba daranyoo sombaa molekulara fi walbariinsa qorachaanii Godina kibba Itiyoopiyaatti

Durduubee

Dhukkubni daranyoo sombaa dhukkuba dadarbaa fi miidhama sombaa fiduu fi du'a garagaraa addunyaa irratti fideedha. Itiyoophiyaanis biyyota dhukkuba kanaan miidhaman kessaa biyya ishe tokkoodha. Dhukkubni daranyoo sombaa baakteeriya Mayikobakteriyem tuberkuulosisi jedhamuun nama gara namaatti darbuun dha. Dhiyeenyatti, immoo dhukkubni kun baakteriyaa qorichaa isaati wal-bareen kan addunyaa irra dadarbaa jiruudha.haalli kunis to'aanno fi ittisa dhukkubichaaf godhamu dadhabsisaa fi rakkisaa gochaa jira.qoorannoon laboratorii irratti hundaa'ee baakteriyaa dhibee kana fiduu addaan baasuu fi amaleessun qoraannoo dhibee kana ittisuu fi to'achuuf godhamuuf bu'a qabeessa ta'a jedhamee fudhatama. Kanaafuu kaayyeefamee tamsa'inaa fi hirama daranyoo sombaa keessatuu dhibeeqorichaa isaan wal-baree irraati fuulleachuun barbaachisaadha.

Kayyoo qorannichi kayyefameef

Tatamsa'ina fi hirmama dhukkuba daranyoo sombaa kessatuu dhibee qorichaan walbare irraatti galmee gahaa ta'e dhiiyyeesu oola.

Haala hiddaatto itti fudhaatamu

Gosni hiddaatto qoraannoo kana fudhamuu gorora,yoo ta'u, kunis kan qoranno daranyoo sombaa yeroo kaanifis ooluudha. Kanafuu goroora dabalataa fudhannu hin qabnu. Eenyuu iyyu qoranno kanatti hirmaachuu keessanin dura ibsa gahaan isinif kennamee, gucha hirmaattotas isnif kennamen booda mallateesitanii hirmaachuu keessan ibsiitu. Yoo haakimiin keessan ilaalee dhukkuba daranyoo sombaa kana qabaachuu keessan isiiniif himee booda, akka goroora kessaan si'a/ naqaa/ sadii /3/ akka laboratooritti kennitan isin gaafanna. Goroorrichis meesha dhimma kanaa f qopha'ee qofaa kan chufa qabuun funannaa. Goroorri kunis haala dhibee keessani fi qaronnoof kan oolu ta'a.

Gaaffi fi deebi

Gaaffii dhunfaa fi haala fayyumma waa'ee dhibee daranyoo somba ilaalchisee isiniif taasifama.Gaaffi fi deebiin kunis nama leenji'een, kan abba qarannoo kanaa kaa'een adeemsifama. Yeroo gaaffi kana isin gaaffannus iddo duuwwaa lafa namni isin hin argineeti baakka itti iciitin keessan isinif eegamuti ta'a.

Soda fi rakkoo

Qorannoon kun hanga dada'aeemetti rakkoo xiqqoodhaa,haala ittin isin hancufa ykn gorora kessan kennitanin deema. haalli adeemsa gurra gororaa haala fudhanna laboratoorii itiin dhukubicha ilaaluuf tasifamuun adeema.

Bu'aa/ fayidaale

Hirmaata qoranno kanaa ta'uu kessanin wanti isinif kallatiin godhamu jiraachhu baatus fedha keessanin waan hitrmaataniifdhiibaan ta'us hin jiru. Haata'utii bu'aan qoranno kanaa ragaa tamsa'ina dhibee kanaa itiyophiya keessa jiru oola. Qoranoo labortorii keessatti isisniif godhamuf gatiin isin baaftan homtuu hin jiru. Ilaalamuun fi qoramuun dhibee daraynoo sombaa itiyopiyaa keesaatti bilisaa akka ta'e beekamaadha. Hata'uutii yoo akka tasaa akka siree qabattan isinitti himamee isinumtii ofii keessanii akkaa seera mana yaala saanitti akka ofyaalataan ni gaafatamtuu.

Qorannicha dhisanii ba'uu

Hirmaatootni hundumtuu haala ibsameefin fi waligaltee issanitin qoranichaatti hirmaatu. Walii galteen kun akkuma waligaltee kan biroo dhiibaa hirmaataa utuu hingahin yeroo fedhetti dheesii ba'uu ni danda'a.

Ofitti amanumaa

Ragaan nama kamiiyyu iddo cufaa fi furtuun cufameeti olkaa'ma kanafu wanti hundinuu iccitiidhan kan eeggamu dha. Odeefannoon dhuunfaa kamiyyuu qoranno kana irratti hin maxxanfaman. Qorannoon hundinuu bifa dhokataa (kodiidhan) waan ka'amanif wati hunduu dhokataa(iccitiidhaan) ka'amu.

Teesso qorratottaa

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Barreessa koree itiiksii AHRI/ALERT, teessoon lakk. Bil 0118-962183

Maqaa sponserootaa: Giddu-gala qorannoo Armawar Hansaan (AHRI) and yuniversitii Finfinnee mummee fayyaagaree qoranno ebbifamtota.

Guca odeefannoo hirmaattotaa (maatii/ guddistoota waggaa 5-12)

Mata dure qorannoo: Tatamsa'ina dhukkuba daranyoo sombaa molekulara fi walbariinsa qorachaanii Godina kibba Itiyoopiyaatti

Durduubee

Dhukkubni daranyoo sombaa dhukkuba dadarbaa fi miidhama sombaa fiduu fi du'a garagaraa addunyaa irratti fideedha. Itiyoophiyaanis biyyota dhukkuba kanaan miidhaman kessaa biyya ishe tokkoodha. Dhukkubni daranyoo sombaa baakteeriya Mayikobakteriyem tuberkuulosisi jedhamuun nama gara namaatti darbuun dha. Dhiyeenyatti, immoo dhukkubni kun baakteriyaa qorichaa isaati wal-bareen kan addunyaa irra dadarbaa jiruudha.haalli kunis to'aanno fi ittisa dhukkubichaaf godhamu dadhabsisaa fi rakkisaa gochaa jira.qoorannoon laboratorii irratti hundaa'ee baakteriyaa dhibee kana fiduu addaan baasuu fi amaleessun qoraannoo dhibee kana ittisuu fi to'achuuf godhamuuf bu'a qabeessa ta'a jedhamee fudhatama. Kanaafuu kaayyeefamee tamsa'inaa fi hirama daranyoo sombaa keessatuu dhibeeqorichaa isaan wal-baree irraati fuulleachuun barbaachisaadha.

Kayyoo qorannichi kayyefameef

Tatamsa'ina fi hirmama dhukkuba daranyoo sombaa kessatuu dhibee qorichaan walbare irraatti galmee gahaa ta'e dhiiyyeesu oola.

Haala hiddaatto itti fudhaanna

Gosni hiddaatto qoraannoo kana fudhamuu gorora,yoo ta'u, kunis kan qoranno daranyoo sombaa yeroo kaanifis ooluudha. Kanafuu goroora dabalataa fudhannu hin qabnu yoo isin waarra mucaa kanaa yoo kaan fira dhiyoo taatan waa'een qoranno kanaa isinif himamee mucaan keessaan qorannoo kanaa akka hrmaatu ni gafaatamtuu. Booda irra isn iddoo/bakka mucaa kanaa mallateesitani , yoo haakimiin ilaalee dhibee kanaaf shaakkame hidaatoon ijjoolle /mucaa kessan irraa akka fudhamu ni tasifama. Goroorrichis meesha dhimma kanaa f qopha'ee qofaa kan chufa qabuun funannaa. Goroorri kunis haala dhibee keessani fi qaronnoof kan oolu ta'a.

Gaaffi fi deebi

Gaaffii dhunfaa fi haala fayyumma waa'ee dhibee daranyoo somba ilaalchisee isiniif taasifama.Gaaffi fi deebiin kunis nama leenji'een, kan abba qarannoo kanaa kaa'een

adeemsifama. Yeroo gaaffi kana isin gaaffannus iddo duuwwaa lafa namni isin hin argineeti baakka itti iciitin keessan isinif eegamuti ta'a.

Soda fi rakkoo

Qorannoon kun hanga dada'aeemetti rakkoo xiqqoodhaa,haala ittin isin hancufa ykn gorora kessan kennitanin deema. haalli adeemsa gurra gororaa haala fudhanna laboratoorii itiin dhukubicha ilaaluuf tasifamuun adeema.

Bu'aa/ fayidaale

Hirmaata qoranno kanaa ta'uu kessanin wanti isinif kallatiin godhamu jiraachhu baatus fedha keessanin waan hitrmaataniif dhiibaan ta'us hin jiru. Haata'utii bu'aan qoranno kanaa ragaa tamsa'ina dhibee kanaa itiyophiya keessa jiru oola. Qoranoo labortorii keessatti isisniif godhamuf gatiin isin baaftan homtuu hin jiru. Ilaalamuun fi qoramuun dhibee daraynoo sombaa itiyopiyaa keesaatti bilisaa akka ta'e beekamaadha. Hata'uutii yoo akka tasaa akka siree qabattan isinitti himamee isinumtii ofii keessanii akkaa seera mana yaala saanitti akka ofyaalataan ni gaafatamtuu.

Qorannicha dhianii ba'uu

Hirmaatootni hundumtuu haala ibsameefin fi waligaltee issanitin qoranichaatti hirmaatu. Walii galteen kun akkuma waligaltee kan biroo dhiibaa hirmaataa utuu hingahin yeroo fedhetti dheesii ba'uu ni danda'a.

Ofitti amanumaa

Ragaan nama kamiiyyu iddo cufaa fi furtuun cufameeti olkaa'ma kanafu wanti hundinuu iccitiidhan kan eeggamu dha. Odeefannoon dhuunfaa kamiyyuu qoranno kana irratti hin maxxanfaman. Qorannoon hundinuu bifa dhokataa (kodiidhan) waan ka'amanif wati hunduu dhokataa(iccitiidhaan) ka'amu.

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Guca odeefannoo hirmaattotaa (ijjoollee waggaa 12-17)

Mata dure qorannoo: Tatamsa'ina dhukkuba daranyoo sombaa molekulara fi walbariinsa qorachaanii Godina kibba Itiyoopiyaatti

Durduubee

Dhukkubni daranyoo sombaa dhukkuba dadarbaa fi miidhama sombaa fiduu fi du'a garagaraa addunyaa irratti fideedha. Itiyoophiyaanis biyyota dhukkuba kanaan miidhaman kessaa biyya ishe tokkoodha. Dhukkubni daranyoo sombaa baakteeriya Mayikobakteriyem tuberkuulosisi jedhamuun nama gara namaatti darbuun dha. Dhiyeenyatti, immoo dhukkubni kun baakteriyaa qorichaa isaati wal-bareen kan addunyaa irra dadarbaa jiruudha.haalli kunis to'aanno fi ittisa dhukkubichaaf godhamu dadhabsisaa fi rakkisaa gochaa jira.qoorannoon laboratorii irratti hundaa'ee baakteriyaa dhibee kana fiduu addaan baasuu fi amaleessun qoraannoo dhibee kana ittisuu fi to'achuuf godhamuuf bu'a qabeessa ta'a jedhamee fudhatama. Kanaafuu kaayyeefamee tamsa'inaa fi hirama daranyoo sombaa keessatuu dhibeeqorichaa isaan wal-baree irraati fuulleachuun barbaachisaadha.

Kayyoo qorannichi kayyefameef

Tatamsa'ina fi hirmama dhukkuba daranyoo sombaa kessatuu dhibee qorichaan walbare irraatti galmee gahaa ta'e dhiiyyeesu oola.

Haala hiddaatto itti fudhaanna

Gosni hiddaatto qoraannoo kana fudhamuu gorora,yoo ta'u, kunis kan qoranno daranyoo sombaa yeroo kaanifis ooluudha. Kanafuu goroora dabalataa fudhannu hin qabnu. Eenyuu iyyu qoranno kanatti hirmaachuu keessanin dura ibsa gahaan isinif kennamee, gucha hirmaattotas isnif kennamen booda mallateesitanii hirmaachuu keessan ibsiitu. Yoo haakimmiin keessan ilaalee dhukkuba daranyoo sombaa kana qabaachuu keessan isiiniif himee booda, akka goroora kessaan si'a/ naqaa/ sadii /3/ akka laboratopritti kennitan isin gaafanna. Goroorrichis meesha dhimma kanaa f qopha'ee qofaa kan chufa qabuun funannaa. Goroorri kunis haala dhibee keessani fi qaronnoof kan oolu ta'a.

Gaaffi fi deebi

Gaaffii dhunfaa fi haala fayyumma waa'ee dhibee daranyoo somba ilaalchisee isiniif taasifama.Gaaffi fi deebiin kunis nama leenji'een, kan abba qarannoo kanaa kaa'een

adeemsifama. Yeroo gaaffi kana isin gaaffannus iddo duuwwaa lafa namni isin hin argineeti baakka itti iciitin keessan isinif eegamuti ta'a.

Soda fi rakkoo

Qorannoon kun hanga dada'aeemetti rakkoo xiqqoodhaa,haala ittin isin hancufa ykn gorora kessan kennitanin deema. haalli adeemsa gurra gororaa haala fudhanna laboratoorii itiin dhukubicha ilaaluuf tasifamuun adeema.

Bu'aa/ fayidaale

Hirmaata qoranno kanaa ta'uu kessanin wanti isinif kallatiin godhamu jiraachhu baatus fedha keessanin waan hitrmaataniif dhiibaan ta'us hin jiru. Haata'utii bu'aan qoranno kanaa ragaa tamsa'ina dhibee kanaa itiyophiya keessa jiru oola. Qoranoo labortorii keessatti isisniif godhamuf gatiin isin baaftan homtuu hin jiru. Ilaalamuun fi qoramuun dhibee daraynoo sombaa itiyopiyaa keesaatti bilisaa akka ta'e beekamaadha. Hata'uutii yoo akka tasaa akka siree qabattan isinitti himamee isinumtii ofii keessanii akkaa seera mana yaala saanitti akka ofyaalataan ni gaafatamtuu.

Qorannicha dhianii ba'uu

Hirmaatootni hundumtuu haala ibsameefin fi waligaltee issanitin qoranichaatti hirmaatu. Walii galteen kun akkuma waligaltee kan biroo dhiibaa hirmaataa utuu hingahin yeroo fedhetti dheesii ba'uu ni danda'a.

Ofitti amanumaa

Ragaan nama kamiiyyu iddo cufaa fi furtuun cufameeti olkaa'ma kanafu wanti hundinuu iccitiidhan kan eeggamu dha. Odeefannoon dhuunfaa kamiyyuu qoranno kana irratti hin maxxanfaman. Qorannoon hundinuu bifa dhokataa (kodiidhan) waan ka'amanif wati hunduu dhokataa(iccitiidhaan) ka'amu.

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Maqaa sponserootaa: Giddu-gala qorannoo Armawar Hansaan (AHRI) and yuniversitii Finfinnee mummee fayyaagaree qoranno ebbifamtota.

Guca Odeeffannoo Qqorannoo Hirmaattota Hawasaa (Info Comm. Afan oromoo version)

Gucha odeefannoo hirmaattotaa (ga'eessa waggaa18 olif)

Mata dure qorannoo: Tatamsa'ina dhukkuba daranyoo sombaa molekulara fi walbariinsa qorachaanii Godina kibba Itiyoopiyaatti

Durduubee

Dhukkubni daranyoo sombaa dhukkuba dadarbaa fi miidhama sombaa fi du'a garagaraa addunyaa irratti geessisuudha. Itiyoophiyaanis biyyota dhukkuba kanaan miidhaman kessaa biyya ishe tokkoodha. Dhukkubni daranyoo sombaa baakteeriya Mayikobakteriyem tuberkuulosisi jedhamuun nama gara namaatti darbuun dha. Dhiyeenyatti, immoo dhukkubni kun baakteriyaa qorichaa isaati wal-bareen kan addunyaa irra dadarbaa jiruudha.haalli kunis to'aanno fi ittisa dhukkubichaaf godhamu dadhabsisaa fi rakkisaa gochaa jira.qoorannoon laboratorii irratti hundaa'ee baakteriyaa dhibee kana fiduu addaan baasuu fi amaleessun qoraannoo dhibee kana ittisuu fi to'achuuf godhamuuf bu'a qabeessa ta'a jedhamee fudhatama. Kanaafuu kaayyeefamee tamsa'inaa fi hirama daranyoo sombaa keessatuu dhibeeqorichaa isaan wal-baree irraati fuullefachuun barbaachisaadha.

Kayyoo qorannichi kayyefameef

Tatamsa'ina fi hirmama dhukkuba daranyoo sombaa, kessatuu dhibee qorichaan walbare irraatti galmee gahaa ta'e dhiiyyeesuf oola.

Haala hiddaatto itti fudhaanna

Gosni hiddaatto qoraannoo kana fudhamuu gorora,yoo ta'u, kunis kan qoranno daranyoo sombaa yeroo kaanifis ooluudha. Kanafuu goroora dabalataa fudhannu hin qabnu. Eenyuu iyyu qoranno kanatti hirmaachuu keessanin dura ibsa gahaan isinif kennamee, gucha hirmaattotas isnif kennamen booda mallateesitanii hirmaachuu keessan ibsitu. Yoo exetenishiin fayyaa,fayyaa keessan ilaalee dhukkuba daranyoo sombaa kana qabaachuu keessan isiiniif himee booda, akka goroora kessaan si'a/ naqaa/ lamaa /2/ akka laboratooritti kennitan isin gaafanna. Goroorrichis meesha dhimma kanaaf qopha'ee qofaa kan chufa qabuun fudhama . Goroorri kunis haala dhibee keessani fi qaronnoof kan oolu ta'a. **Gaaffi fi deebi**

Gaaffii dhunfaa fi haala fayyumma waa'ee dhibee daranyoo somba ilaalchisee isiniif taasifama.Gaaffi fi deebiin kunis nama leenji'een, kan abba qarannoo kanaa kaa'een adeemsifama. Yeroo gaaffi kana isin gaaffannus iddo duuwwaa lafa namni isin hin argineeti baakka itti iciitin keessan isinif eegamuti ta'a.

Soda fi rakkoo

Qorannoon kun hanga dada'aeemetti rakkoo xiqqoodhaan,haala ittin isin hancufa ykn gorora kessan kennitanin deema. haalli adeemsa guurra gororaa haala fudhanna laboratoorii itiin dhukubicha ilaaluuf tasifamuun adeema. Yerroo dhiga qoraanoo HIV tahu dhigaa tiqqoo bahu dandaha kuni immoo waa tokko illee bada gara hamaatti kan sii fudhaatu miti.

Bu'aa/ fayidaale

Hirmaata qoranno kanaa ta'uu kessanin wanti isinif kallatiin godhamu jiraachhu baatus fedha keessanin waan hitrmaataniif dhiibaan ta'us hin jiru. Haata'utii bu'aan qoranno kanaa ragaa tamsa'ina dhibee kanaa Itiyophiya keessa jiru oola. Qoranoo labortorii keessatti isiniif godhamuf gatiin isin baaftan homtuu hin jiru. Ilaalamuun fi qoramuun dhibee daraynoo sombaa Itiyopiyaa keesaatti bilisaa akka ta'e beekamaadha. Hata'uutii yoo akka tasaa akka siree qabattan isinitti himamee isinumtii ofii keessanii akkaa seera mana yaala saanitti akka ofyaaltan ni gaafatamtuu.

Qorannicha dhisanii ba'uu

Hirmaatootni hundumtuu haala ibsameefin fi waligaltee issanitin qoranichaatti hirmaatu. Walii galteen kun akkuma waligaltee kan biroo dhiibaa hirmaataairraatti utuu hingahin yeroo fedhetti dheesii ba'uu ni danda'a.

Ofitti amanumaa

Ragaan nama kamiiyyu iddo cufaa fi furtuun cufameeti olkaa'ma, kanafu wanti hundinuu iccitiidhan kan eeggamu dha. Odeefannoon dhuunfaa kamiyyuu qoranno kana irratti hin maxxanfaman. Qorannoon hundinuu bifa dhokataa (kodiidhan) waan ka'amanif wati hunduu dhokataa(iccitiidhaan) ka'amu.

Teesso qorratottaa

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Maqaa sponserootaa: Giddu-gala qorannoo Armaawar Hansaan (AHRI) and Yuunivarsitii Finfinnee mummee fayyaagaree qoranno ebbifamtota.

Odefaanoo qoranoo mana amala sirreessaa jiraniif (Afaan oromoo version)

Gucha odeefannoo hirmaattotaa (ga'eessa waggaa18 olif)

Mata dure qorannoo: Tatamsa'ina dhukkuba daranyoo sombaa molekulara fi walbariinsa qorachaanii Godina kibba Itiyoopiyaatti

Durduubee

Dhukkubni daranyoo sombaa dhukkuba dadarbaa fi miidhama sombaa fiduu fi du'a garagaraa addunyaa irratti fideedha. Itiyoophiyaanis biyyota dhukkuba kanaan miidhaman kessaa biyya ishe tokkoodha. Dhukkubni daranyoo sombaa baakteeriya Mayikobakteriyem tuberkuulosisi jedhamuun nama gara namaatti darbuun dha. Dhiyeenyatti, immoo dhukkubni kun baakteriyaa qorichaa isaati wal-bareen kan addunyaa irra dadarbaa jiruudha.haalli kunis to'aanno fi ittisa dhukkubichaaf godhamu dadhabsisaa fi rakkisaa gochaa jira.qoorannoon laboratorii irratti hundaa'ee baakteriyaa dhibee kana fiduu addaan baasuu fi amaleessun qoraannoo dhibee kana ittisuu fi to'achuuf godhamuuf bu'a qabeessa ta'a jedhamee fudhatama. Kanaafuu kaayyeefamee tamsa'inaa fi hirama daranyoo sombaa keessatuu dhibeeqorichaa isaan wal-baree irraati fuulleachuun barbaachisaadha.

Kayyoo qorannichi kayyefameef

Tatamsa'ina fi hirmama dhukkuba daranyoo sombaa kessatuu dhibee qorichaan walbare irraatti galmee gahaa ta'e dhiiyyeesu oola.

Haala hiddaatto itti fudhaanna

Gosni hiddaatto qoraannoo kana fudhamuu gorora,yoo ta'u, kunis kan qoranno daranyoo sombaa yeroo kaanifis ooluudha. Kanafuu goroora dabalataa fudhannu hin qabnu. Eenyuu iyyu qoranno kanatti hirmaachuu keessanin dura ibsa gahaan isinif kennamee, gucha hirmaattotas isnif kennamen booda mallateesitanii hirmaachuu keessan ibsiitu. Yoo Naarisiin keessan ilaalee dhukkuba daranyoo sombaa kana qabaachuu keessan isiiniif himee booda, akka goroora kessaan si'a/ naqaa/ sadii /3/ akka laboratooritti kennitan isin gaafanna. Goroorrichis meesha dhimma kanaa f qopha'ee qofaa kan chufa qabuun funannaa. Goroorri kunis haala dhibee keessani fi qaronnoof kan oolu ta'a.

Gaaffi fi deebi

Gaaffii dhunfaa fi haala fayyumma waa'ee dhibee daranyoo somba ilaalchisee isiniif taasifama.Gaaffi fi deebiin kunis nama leenji'een, kan abba qarannoo kanaa kaa'een adeemsifama. Yeroo gaaffi kana isin gaaffannus iddo duuwwaa lafa namni isin hin argineeti baakka itti iciitin keessan isinif eegamuti ta'a.

Soda fi rakkoo

Qorannoon kun hanga dada'aeemetti rakkoo xiqqoodhaa,haala ittin isin hancufa ykn gorora kessan kennitanin deema. haalli adeemsa gurra gororaa haala fudhanna laboratoorii itiin dhukubicha ilaaluuf tasifamuun adeema. Yerroo dhiga qoraanoo HIV tahu dhigaa tiqqoo bahu dandaha kuni immoo waa tokko illee bada gara hammaatti kan sii fudhaatu miti.

Bu'aa/ fayidaale

Hirmaata qoranno kanaa ta'uu kessanin wanti isinif kallatiin godhamu jiraachhu baatus fedha keessanin waan hitrmaataniifdhiibaan ta'us hin jiru. Haata'utii bu'aan qoranno kanaa ragaa tamsa'ina dhibee kanaa itiyophiya keessa jiru oola. Qoranoo labortorii keessatti isisniif godhamuf gatiin isin baaftan homtuu hin jiru. Ilaalamuun fi qoramuun dhibee daraynoo sombaa itiyopiyaa keesaatti bilisaa akka ta'e beekamaadha. Hata'uutii yoo akka tasaa akka siree qabattan isinitti himamee isinumtii ofii keessanii akkaa seera mana yaala saanitti akka ofyaalataan ni gaafatamtuu.

Qorannicha dhisanii ba'uu

Hirmaatootni hundumtuu haala ibsameefin fi waligaltee issanitin qoranichaatti hirmaatu. Walii galteen kun akkuma waligaltee kan biroo dhiibaa hirmaataa utuu hingahin yeroo fedhetti dheesii ba'uu ni danda'a.

Ofitti amanumaa

Ragaan nama kamiiyyu iddo cufaa fi furtuun cufameeti olkaa'ma kanafu wanti hundinuu iccitiidhan kan eeggamu dha. Odeefannoon dhuunfaa kamiyyuu qoranno kana irratti hin maxxanfaman. Qorannoon hundinuu bifa dhokataa (kodiidhan) waan ka'amanif wati hunduu dhokataa(iccitiidhaan) ka'amu.

Teesso qorratottaa

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Maqaa sponserootaa: Giddu-gala qorannoo Armawar Hansaan (AHRI) and yuniversitii Finfinnee mummee fayyaagaree qoranno ebbifamtota.

Guca odeefannoo hirmaattotaa (maatii/guddistoota waggaa 5-12)

Mata dure qorannoo: Tatamsa'ina dhukkuba daranyoo sombaa molekulara fi walbariinsa qorachaanii Godina kibba Itiyoopiyaatti

Durduubee

Dhukkubni daranyoo sombaa dhukkuba dadarbaa fi miidhama sombaa fiduu fi du'a garagaraa addunyaa irratti fideedha. Itiyoophiyaanis biyyota dhukkuba kanaan miidhaman kessaa biyya ishe tokkoodha. Dhukkubni daranyoo sombaa baakteeriya Mayikobakteriyem tuberkuulosisi jedhamuun nama gara namaatti darbuun dha. Dhiyeenyatti, immoo dhukkubni kun baakteriyaa qorichaa isaati wal-bareen kan addunyaa irra dadarbaa jiruudha.haalli kunis to'aanno fi ittisa dhukkubichaaf godhamu dadhabsisaa fi rakkisaa gochaa jira.qoorannoon laboratorii irratti hundaa'ee baakteriyaa dhibee kana fiduu addaan baasuu fi amaleessun qoraannoo dhibee kana ittisuu fi to'achuuf godhamuuf bu'a qabeessa ta'a jedhamee fudhatama. Kanaafuu kaayyeefamee tamsa'inaa fi hirama daranyoo sombaa keessatuu dhibeeqorichaa isaan wal-baree irraati fuulleachuun barbaachisaadha.

Kayyoo qorannichi kayyefameef

Tatamsa'ina fi hirmama dhukkuba daranyoo sombaa kessatuu dhibee qorichaan walbare irraatti galmee gahaa ta'e dhiiyyeesu oola.

Haala hiddaatto itti fudhaanna

Gosni hiddaatto qoraannoo kana fudhamuu gorora,yoo ta'u, kunis kan qoranno daranyoo sombaa yeroo kaanifis ooluudha. Kanafuu goroora dabalataa fudhannu hin qabnu yoo isin waarra mucaa kanaa yoo kaan fira dhiyoo taatan waa'een qoranno kanaa isinif himamee mucaan keessaan qorannoo kanaa akka hrmaatu ni gafaatamtuu. Booda irra isn iddoo/bakka mucaa kanaa mallateesitani , yoo naarisiin ilaalee dhibee kanaaf shaakkame hidaatoon ijjoolle /mucaa kessan irraa akka fudhamu ni tasifama. Goroorrichis meesha dhimma kanaa f qopha'ee qofaa kan chufa qabuun funannaa. Goroorri kunis haala dhibee keessani fi qaronnoof kan oolu ta'a.

Gaaffi fi deebi

Gaaffii dhunfaa fi haala fayyumma waa'ee dhibee daranyoo somba ilaalchisee isiniif taasifama.Gaaffi fi deebiin kunis nama leenji'een, kan abba qarannoo kanaa kaa'een

adeemsifama. Yeroo gaaffi kana isin gaaffannus iddo duuwwaa lafa namni isin hin argineeti baakka itti iciitin keessan isinif eegamuti ta'a.

Soda fi rakkoo

Qorannoon kun hanga dada'aeemetti rakkoo xiqqoodhaa,haala ittin isin hancufa ykn gorora kessan kennitanin deema. haalli adeemsa gurra gororaa haala fudhanna laboratoorii itiin dhukubicha ilaaluuf tasifamuun adeema. Yerroo dhiga qoraanoo HIV tahu dhigaa tiqqoo bahu dandaha kuni immoo waa tokko illee bada gara hammaatti kan sii fudhaatu miti.

Bu'aa/ fayidaale

Hirmaata qoranno kanaa ta'uu kessanin wanti isinif kallatiin godhamu jiraachhu baatus fedha keessanin waan hitrmaataniif dhiibaan ta'us hin jiru. Haata'utii bu'aan qoranno kanaa ragaa tamsa'ina dhibee kanaa itiyophiya keessa jiru oola. Qoranoo labortorii keessatti isisniif godhamuf gatiin isin baaftan homtuu hin jiru. Ilaalamuun fi qoramuun dhibee daraynoo sombaa itiyopiyaa keesaatti bilisaa akka ta'e beekamaadha. Hata'uutii yoo akka tasaa akka siree qabattan isinitti himamee isinumtii ofii keessanii akkaa seera mana yaala saanitti akka ofyaalataan ni gaafatamtuu.

Qorannicha dhianii ba'uu

Hirmaatootni hundumtuu haala ibsameefin fi waligaltee issanitin qoranichaatti hirmaatu. Walii galteen kun akkuma waligaltee kan biroo dhiibaa hirmaataa utuu hingahin yeroo fedhetti dheesii ba'uu ni danda'a.

Ofitti amanumaa

Ragaan nama kamiiyyu iddo cufaa fi furtuun cufameeti olkaa'ma kanafu wanti hundinuu iccitiidhan kan eeggamu dha. Odeefannoon dhuunfaa kamiyyuu qoranno kana irratti hin maxxanfaman. Qorannoon hundinuu bifa dhokataa (kodiidhan) waan ka'amanif wati hunduu dhokataa(iccitiidhaan) ka'amu.

Teesso qorratottaa

Dursaa qoranno obbo Yared Merid

Yuniversitii Finfinne , muummee fayya

Giddu-gala qorannoo Armawar Hansaan (AHRI)

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E-mail: aseffaa@gmail.com

Lakk.bil: +251 911 24 74 25

Barreessa koree itiiksii AHRI/ALERT, teessoon lakk. Bil 0118-962183

Maqaa sponserootaa: Instiitutti qorannoo Armawar Hansaan (AHRI) and yuniversitii Finfinnee mummee fayyaagaree qoranno ebbifamtota.

Gucha odeefannoo hirmaattotaa (ijjoollee waggaa 12-17)

Mata dure qorannoo: Tatamsa'ina dhukkuba daranyoo sombaa molekulara fi walbariinsa qorachaanii Godina kibba Itiyoopiyaatti

Durduubee

Dhukkubni daranyoo sombaa dhukkuba dadarbaa fi miidhama sombaa fiduu fi du'a garagaraa addunyaa irratti fideedha. Itiyoophiyaanis biyyota dhukkuba kanaan iidhaman kessaa biyya ishe tokkoodha. Dhukkubni daranyoo sombaa baakteeriya Mayikobakteriyem tuberkuulosisi jedhamuun nama gara namaatti darbuun dha. Dhiyeenyatti, immoo dhukkubni kun baakteriyaa qorichaa isaati wal-bareen kan addunyaa irra dadarbaa jiruudha.haalli kunis to'aanno fi ittisa dhukkubichaaf godhamu dadhabsisaa fi rakkisaa gochaa jira.qoorannoon laboratorii irratti hundaa'ee baakteriyaa dhibee kana fiduu addaan baasuu fi amaleessun qoraannoo dhibee kana ittisuu fi to'achuuf godhamuuf bu'a qabeessa ta'a jedhamee fudhatama. Kanaafuu kaayyeefamee tamsa'inaa fi hirama daranyoo sombaa keessatuu dhibeeqorichaa isaan wal-baree irraati fuulleachuun barbaachisaadha.

Kayyoo qorannichi kayyefameef

Tatamsa'ina fi hirmama dhukkuba daranyoo sombaa kessatuu dhibee qorichaan walbare irraatti galmee gahaa ta'e dhiiyyeesu oola.

Haala hiddaatto itti fudhaanna

Gosni hiddaatto qoraannoo kana fudhamuu gorora,yoo ta'u, kunis kan qoranno daranyoo sombaa yeroo kaanifis ooluudha. Kanafuu goroora dabalataa fudhannu hin qabnu. Eenyuu iyyu qoranno kanatti hirmaachuu keessanin dura ibsa gahaan isinif kennamee, gucha hirmaattotas isnif kennamen booda mallateesitanii hirmaachuu keessan ibsiitu. Yoo naarsii keessan ilaalee dhukkuba daranyoo sombaa kana qabaachuu keessan isiiniif himee booda, akka goroora kessaan si'a/ naqaa/ sadii /3/ akka laboratopritti kennitan isin gaafanna. Goroorrichis meesha dhimma kanaa f qopha'ee qofaa kan chufa qabuun funannaa. Goroorri kunis haala dhibee keessani fi qaronnoof kan oolu ta'a.

Gaaffi fi deebi

Gaaffii dhunfaa fi haala fayyumma waa'ee dhibee daranyoo somba ilaalchisee isiniif taasifama.Gaaffi fi deebiin kunis nama leenji'een, kan abba qarannoo kanaa kaa'een

adeemsifama. Yeroo gaaffi kana isin gaaffannus iddo duuwwaa lafa namni isin hin argineeti baakka itti iciitin keessan isinif eegamuti ta'a.

Soda fi rakkoo

Qorannoon kun hanga dada'aeemetti rakkoo xiqqoodhaa,haala ittin isin hancufa ykn gorora kessan kennitanin deema. haalli adeemsa gurra gororaa haala fudhanna laboratoorii itiin dhukubicha ilaaluuf tasifamuun adeema. Yerroo dhiga qoraanoo HIV tahu dhigaa tiqqoo bahu dandaha kuni immoo waa tokko illee bada gara hammaatti kan sii fudhaatu miti.

Bu'aa/ fayidaale

Hirmaata qoranno kanaa ta'uu kessanin wanti isinif kallatiin godhamu jiraachhu baatus fedha keessanin waan hitrmaataniif dhiibaan ta'us hin jiru. Haata'utii bu'aan qoranno kanaa ragaa tamsa'ina dhibee kanaa itiyophiya keessa jiru oola. Qoranoo labortorii keessatti isisniif godhamuf gatiin isin baaftan homtuu hin jiru. Ilaalamuun fi qoramuun dhibee daraynoo sombaa itiyopiyaa keesaatti bilisaa akka ta'e beekamaadha. Hata'uutii yoo akka tasaa akka siree qabattan isinitti himamee isinumtii ofii keessanii akkaa seera mana yaala saanitti akka ofyaalataan ni gaafatamtuu.

Qorannicha dhianii ba'uu

Hirmaatootni hundumtuu haala ibsameefin fi waligaltee issanitin qoranichaatti hirmaatu. Walii galteen kun akkuma waligaltee kan biroo dhiibaa hirmaataa utuu hingahin yeroo fedhetti dheesii ba'uu ni danda'a.

Ofitti amanumaa

Ragaan nama kamiiyyu iddo cufaa fi furtuun cufameeti olkaa'ma kanafu wanti hundinuu iccitiidhan kan eeggamu dha. Odeefannoon dhuunfaa kamiyyuu qoranno kana irratti hin maxxanfaman. Qorannoon hundinuu bifa dhokataa (kodiidhan) waan ka'amanif wati hunduu dhokataa(iccitiidhaan) ka'amu.

Teesso qorratottaa

Dursaa qoranno obbo Yared Merid

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Barreessa koree itiiksii AHRI/ALERT, teessoon lakk. Bil 0118-962183

Maqaa sponserootaa: Giddu-gala qorannoo Armawar Hansaan (AHRI) and yuniversitii Finfinnee mummee fayyaagaree qoranno ebbifamtota.

Consent form for Health Institute (Afaan Oromoo version)

Guca waliigaltee hirmaattotaa (ga'eessa waggaa 18 oli)

Yunivarsitiin Finfinnee , Giddu-galeessi Qorannoo Armaawar Hansaan fi Waajjirooleen Eegumsa Fayyaa Oromiyaa fi Uummattota sabaa fi sab-lammota Kibbaa waliin ta'udhaan dhibee daranyoo sombaa irratti kessattu dhibee qorichaan walbare irraatii tamsaa'ina fi hirmaannaa isaa irratti qorannoo geggessuu barbaadu.

Anis akkan qoranno kana irraatti hirmaadhu gaafatamera. Dhimmi kun naaf ibsamee anis naaf galee yoo dhibee kanaan shakkame akkan gorora kennu nan gaafatama. Ibsi gahan naaf kennamee yeroon fedhetti hirmaachuu dhisuu akkan mirga qabufi utuu haala yaala koti hin midhiin dhiise bahu akkan danda'u nati himameera. Hanga gaha ta'een ibsi barbaachisaan naaf kenamera. Kunis si'a sadi akkan gorara kennu, akkan gaaffi dhunfaa fi waa'ee dhibee dhukkuba daranyoo sombaa koo akkan gaafatamuu fi dabalataanis galmee waa'ee fayyaa koo kan akka dhukkuba HIV adefanoof akka itti gargaaraman beekera. . Galmeen koo kamiyyuu akka iccitii qabamu natti himameera. Kanaafuu ani fedhii kootin qorannoo kanairratti hirmaachuudhaaf waligaleera.

Maqaa hirmataa/ttuu _____Mallattoo _____ guyaa_____

Maqaa Ogeessa Fayyaa _____ Mallattoo_____ Guyaa_____

Maqa ragaa bahaa_____ Mallattoo

_____Guyaa_____

Guca walii-galtee hirmaattotta (warra/guddistoota ijoollee waggaa 5-11)

Yunivarsitiin Finfinnee , Giddu-galeessi Qorannoo Armaawar Hansaan fi Waajjirooleen Eegumsa Fayyaa Oromiyaa fi Uumattota sabaa fi sab-lammoota Kibbaa waliin ta'udhaan dhibee daranyoo sombaa irratti kessattu dhibee qorichaan walbare irraatii tamsaa'ina fi hirmaannaa isaa irratti qorannoo geggessuu barbaadu.

Mucaan koo akkan qoranno kana irraatti hirmaatu/ttu gaafatamera. Muccan koo dhibee dhukkuba daranyoo sombaaf ogeessa fayyatiin yoo shakkame gorora akka kennu/nitu sirritti waan naaf ibsameef hubadheera. Dhukkuba daranyoo sombaan qabamuun isaa/ishee yoo mirkanaa'e qorannoon dhukkuba HIV akka godhamuuf odeeffanoon isaas qoranoo kannaf akka oolu natti himameera. Qorannoo kana irratti mucaan koo hirmmachuu fi hirmmachu dhiisuu isaa/ishee mirga murteessuu akkan qabu naaf himameera. Muucaan koo yeroo barbaadametti sababa tokko malee addaan kutuu akka danda'uuf kunis taajila fayyaa aratu/ttu irratti dhiibaa akka hinqabnes naaf ibsameera. Gorora al sadii mucaan koo akka nennus/nnitus bareera. , Gaaffii dhunfaa fi waa'ee dhibee kanaa gaafatumu dabalatanis galmee odeffanoo HIV mucaakoo akka itti fayadaman eeyameera. Oodeefanoon galmee mucaa koo irra jirus iciitiin akka eegamu natti himameera.. Kanaafu mucaan koo qorannoo kana irratti hirmaatu/ttu waligaleera.

Maqaa hirmataa/ttuu _____Mallattoo _____ guyaa_____

Maqaa Ogeessa Fayyaa _____ Mallattoo_____ Guyaa_____

Maqa ragaa bahaa_____ Mallattoo

_____Guyaa_____

Guca walii-galtee hirmaatota (ijjoollee waggaa 12-17)

Yunivarsitiin Finfinnee, Giddu-galeessi Qorannoo Armaawar Hansaan fi Waajjirooleen Eegumsa Fayyaa Oromiyaa fi Uumattota sabaa fi sab-lammoota Kibbaa waliin ta'udhaan dhibee daranyoo sombaa irratti kessattu dhibee qorichaan walbare irraatii tamsaa'ina fi hirmaannaa isaa irratti qorannoo geggessuu barbaadu.

Anis akkan qoranno kana irraatti hirmaadhu gaafatamera. Dhimmi kun naaf ibsamee anis naaf galee yoo dhibee kanaan shakkame akkan gorora kennu nan gaafatama. Ibsi gahan naaf kennamee yeroon fedhetti hirmaachuu dhisuu akkan mirga qabufi utuu haala yaala koti hin midhiin dhiise bahu akkan danda'u nati himameera. Hanga gaha ta'een ibsi barbaachisaan naaf kennameera. Kunis si'a sadi akkan gorara kennu, akkan gaaffi dhunfaa fi waa'ee dhibee dhukkuba daranyoo sombaa koo akkan gaafatamuu fi dabalataanis galmee waa'ee fayyaa koo kan akka dhukkuba HIV adefanoof akka itti gargaaraman beekera. Galmeen koo kamiyyuu akka iccitii qabamu natti himameera. Kanaafuu ani fedhii kootin qorannoo kanairratti hirmaachuudhaaf waligaleera.

Maqaa hirmataa/ttuu _____Mallattoo _____ guyaa_____

Maqaa Ogeessa Fayyaa _____ Mallattoo_____ Guyaa_____

Maqa ragaa bahaa_____ Mallattoo

_____Guyaa_____

Consent form for Community study (Afann oromoo version)

Guca waligaltee fedhiihirmaattotaa (ga'eessa waggaa 18 oli)

Yunivarsitiin Finfinnee , Giddu-galeessi Qorannoo Armaawar Hansaan fi Waajjirooleen Eegumsa Fayyaa Oromiyaa fi Uumattota sabaa fi sab-lammota Kibbaa waliin ta'uun dhibee daranyoo sombaa irratti kessattu dhibee qorichaan walbare irraatii tamsaa'ina fi heduminna isaa irratti qorannoo geggessuu barbaadu.

Anis akkan qoranno kana irraatti hirmaadhu gaafatamera. Dhimmi kun naaf ibsamee anis naaf galee yoo dhibee kanaan dhukkubsachaan jira ta'eef gorora qoranoo labooratoorif akkn kennu ogeessa fayyaatin murtaa'e akkan gorora kennu nan gaafatama. Ibsi gahan naaf kennamee yeroon fedhetti hirmaachuu dhisuu akkan mirga qabufi utuu haala yaala koti hin midhiin hirmannaa koo addan kutuu akkan danda'u nati himameera. Hanga gaha ta'een ibsi barbaachisaan naaf kenamera. Kunis si'a sadi akkan gorara kennu, akkan gaaffi dhunfaa fi waa'ee dhibee dhukkuba daranyoo sombaa koo akkan gaafatamuu fi dabalataanis galmee waa'ee fayyaa koo kan akka dhukkuba HIV adefanoof akka itti gargaaraman beekera. . Galmeen koo kamiyyuu akka iccitii qabamu natti himameera. Kanaafuu ani fedhii kootin qorannoo kanairratti hirmaachuudhaaf waligaleera

Maqaa hirmataa _____Mallattoo _____ Guyaa_____

Maqaa Ogeessa Fayyaa _____ Mallattoo_____ Guyaa_____

Maqa ragaa bahaa_____ Mallattoo _____Guyaa_____

Guca walii galtee hirmaattotaa (warra/ guddistooota ijoolee waggaa 5-11)

Yunivarsitiin Finfinnee , Giddu-galeessi Qorannoo Armaawar Hansaan fi Waajjirooleen Eegumsa Fayyaa Oromiyaa fi Uumattota sabaa fi sab-lammota Kibbaa waliin ta'uun dhibee daranyoo sombaa irratti kessattu dhibee qorichaan walbare irraatii tamsaa'ina fi hirmaannaa isaa irratti qorannoo geggessuu barbaadu.

Anis akkan qoranno kana irraatti hirmaadhu gaafatamera. Dhimmi kun naaf ibsamee anis naaf galee yoo dhibee kanaan shakkame akkan gorora al lama kennu nan gaafatama. Dhkkuba daranyoo sombaatiin qabamuunkoo yoo mirkanaa'e qorannoo dhukkuba HIV akkan naaf taassisamuu fi gorsis akka naaf kennamu natti himameera.

Ibsi gahan naaf kennamee yeroon fedhetti hirmaachuu dhisuu akkan mirga qabufi utuu haala yaala koti hin midhiin hirmaannaa koo addan kutuu akkan danda'u nati himameera. Hanga gaha ta'een ibsi barbaachisaan naaf kenamera. Kunis si'a sadi akkan gorara kennu, akkan gaaffi dhunfaa fi waa'ee dhibee dhukkuba daranyoo sombaa koo akkan gaafatamuu fi dabalataanis galmee waa'ee fayyaa koo kan akka dhukkuba HIV adefanoof akka itti gargaaraman beekera. . Galmeen koo kamiyyuu akka iccitii qabamu natti himameera. Kanaafuu ani fedhii kootin qorannoo kanairratti hirmaachuudhaaf waligaleer

Maqaa hirmataa/ttuu _____Mallattoo_____
guyaa_____

Maqaa Ogeessa Fayyaa _____ Mallattoo_____
Guyaa_____

Maqa ragaa bahaa_____ Mallattoo
_____Guyaa_____

Guca walii galtee hirmaattotaa (ijjoollee waggaa 12-17)

Yunivarsitiin Finfinnee , Giddu-galeessi Qorannoo Armaawar Hansaan fi Waajjirooleen Eegumsa Fayyaa Oromiyaa fi Uumattota sabaa fi sab-lammota Kibbaa waliin ta'uun dhibee daranyoo sombaa irratti kessattu dhibee qorichaan walbare irraatii tamsaa'ina fi hirmaannaa isaa irratti qorannoo geggessuu barbaadu

Anis akkan qoranno kana irraatti hirmaadhu gaafatamera. Dhimmi kun naaf ibsamee anis naaf galee yoo dhibee kanaan shakkame akkan gorora kennu nan gaafatama. Ibsi gahan naaf kennamee yeroon fedhetti hirmaachuu dhisuu akkan mirga qabufi utuu haala yaala koti hin midhiin dhiise bahu akkan danda'u nati himameera. Hanga gaha ta'een ibsi barbaachisaan naaf kennameera. Kunis si'a sadi akkan gorara kennu, akkan gaaffi dhunfaa fi waa'ee dhibee dhukkuba daranyoo sombaa koo akkan gaafatamuu fi dabalataanis galmee waa'ee fayyaa koo kan akka dhukkuba HIV adefanoof akka itti gargaaraman beekera. . Galmeen koo kamiyyuu akka iccitii qabamu natti himameera. Kanaafuu ani fedhii kootin qorannoo kanairratti hirmaachuudhaaf waligaleera

Maqaa hirmataa/ttuu _____Mallattoo_____
Guyaa_____

Maqaa Ogeessa Fayyaa _____ Mallattoo_____
Guyaa_____

Maqa ragaa bahaa_____ Mallattoo_____Guyaa_____

Consent form for Prison study (Afaan Oromoo version)

Guca waligaltee hirmaattotaa (ga'eessa waggaa 18 oli)

Yunivarsitiin Finfinnee , Giddu-galeessi Qorannoo Armaawar Hansaan fi Waajjirooleen Eegumsa Fayyaa Oromiyaa fi Uumattota sabaa fi sab-lammota Kibbaa waliin ta'uun dhibee daranyoo sombaa irratti kessattu dhibee qorichaan walbare irraatii tamsaa'ina fi hirmaannaa isaa irratti qorannoo geggessuu barbaadu.

Anis akkan qoranno kana irraatti hirmaadhu gaafatamera. Dhimmi kun naaf ibsamee anis naaf galee yoo dhibee kanaan shakkame akkan gorora kennu nan gaafatama. Ibsi gahan naaf kennamee yeroon fedhetti hirmaachuu dhisuu akkan mirga qabufi utuu haala yaala koti hin midhiin dhiise bahu akkan danda'u nati himameera. Hanga gaha ta'een ibsi barbaachisaan naaf kenamera. Kunis si'a sadi akkan gorara kennu, akkan gaaffi dhunfaa fi waa'ee dhibee dhukkuba daranyoo sombaa koo akkan gaafatamuu fi dabalataanis galmee waa'ee fayyaa koo kan akka dhukkuba HIV adefanoof akka itti gargaaraman beekera. . Galmeen koo kamiyyuu akka iccitii qabamu natti himameera. Kanaafuu ani fedhii kootin qorannoo kanairratti hirmaachuudhaaf waligaleera.

Maqaa hirmataa/ttuu _____Mallattoo _____ guyaa_____

Maqaa Ogeessa Fayyaa _____ Mallattoo_____ Guyaa_____

Maqa ragaa bahaa_____ Mallattoo

_____Guyaa_____

Guca waliigaltee hirmattota (warraa/gudistoota ijoollee waggaa 5-11)

Yunivarsitiin Finfinnee , Giddu-galeessi Qorannoo Armaawar Hansaan fi Waajjirooleen Eegumsa Fayyaa Oromiyaa fi Uumattota sabaa fi sab-lammota Kibbaa waliin ta'uun dhibee daranyoo sombaa irratti kessattu dhibee qorichaan walbare irraatii tamsaa'ina fi hirmaannaa isaa irratti qorannoo geggessuu barbaadu.

Anis akkan qoranno kana irraatti hirmaadhu gaafatamera. Dhimmi kun naaf ibsamee anis naaf galee yoo dhibee kanaan shakkame akkan gorora kennu nan gaafatama. Ibsi gahan naaf kennamee yeroon fedhetti hirmaachuu dhisuu akkan mirga qabufi utuu haala yaala koti hin midhiin dhiise bahu akkan danda'u nati himameera. Hanga gaha ta'een ibsi barbaachisaan naaf kenamera. Kunis si'a sadi akkan gorara kennu, akkan gaaffi dhunfaa fi waa'ee dhibee dhukkuba daranyoo sombaa koo akkan gaafatamuu fi dabalataanis galmee waa'ee fayyaa koo kan akka dhukkuba HIV adefanoof akka itti gargaaraman beekera. . Galmeen koo kamiyyuu akka iccitii qabamu natti himameera. Kanaafuu ani fedhii kootin qorannoo kanairratti hirmaachuudhaaf waligaleera.

Maqaa hirmataa/ttuu _____Mallattoo _____ guyaa_____

Maqaa Ogeessa Fayyaa _____ Mallattoo_____ Guyaa_____

Maqa ragaa bahaa_____ Mallattoo

_____Guyaa_____

Guca waliigaltee hirmaattota (ijjoollee waggaa 12-17)

Yunivarsitiin Finfinnee, Giddu-galeessi Qorannoo Armaawar Hansaan fi Waajjirooleen Eegumsa Fayyaa Oromiyaa fi Uumattota sabaa fi sab-lammoota Kibbaa waliin ta'udhaan dhibee daranyoo sombaa irratti kessattu dhibee qorichaan walbare irraatii tamsaa'ina fi hirmaannaa isaa irratti qorannoo geggessuu barbaadu.

Anis akkan qoranno kana irraatti hirmaadhu gaafatamera. Dhimmi kun naaf ibsamee anis naaf galee yoo dhibee kanaan shakkame akkan gorora kennu nan gaafatama. Ibsi gahan naaf kennamee yeroon fedhetti hirmaachuu dhisuu akkan mirga qabufi utuu haala yaala koti hin midhiin dhiise bahu akkan danda'u nati himameera. Hanga gaha ta'een ibsi barbaachisaan naaf kennameera. Kunis si'a sadi akkan gorara kennu, akkan gaaffi dhunfaa fi waa'ee dhibee dhukkuba daranyoo sombaa koo akkan gaafatamuu fi dabalataanis galmee waa'ee fayyaa koo kan akka dhukkuba HIV adefanoof akka itti gargaaraman beekera. . Galmeen koo kamiyyuu akka iccitii qabamu natti himameera. Kanaafuu ani fedhii kootin qorannoo kanairratti hirmaachuudhaaf waligaleera

Maqaa hirmataa/ttuu _____Mallattoo _____ Guyaa_____

Maqaa Ogeessa Fayyaa _____ Mallattoo_____ Guyaa_____

Maqa ragaa bahaa_____ Mallattoo

_____Guyaa_____

Subject Information sheet for Health Institute study (Amharic version)

<u>የጥናቱ ተሳትፊ መረጃ ቅጽ (>18 አመት))</u>

መግቢያ

ቲቢ (የሳንባ ቲቢ) የሰውነታችንን የሳንባ ክፍል የሚያጠቃ በሽታ ሲሆን ይህ በሽታ በመላው አለም ህመም እና ሞትን ከሚያስከትሉ ዋና ዋና የጤና ችግሮች አንዱ ነው፡፡ ሀገራችን ኢትዮጵያ በቲቢ በሽታ በከፍተኛ ደረጃ ከተጠቁት ሀገራት አንዷ ናት፡፡ አብዛኛዎቹ የቲቢ በሽታ ህመምተኞች የሚጠቁት ማይኮባክቴሪየም ቱበርኩሎሲስ በሚባል የባክቴሪያ ዝሪያ አይነት ነው፡፡ የሚተላለፈውም በትንፋሽ ሲሆን አብዛኛውን ጊዜ በበሽታው የተጠቁ ግለሰብ በሚስል እና በሚያስነጥስ ጊዜ ነው፡፡

ከቅርብ ጊዜ ወዲህ መድሀኒቱን የተለማመደ የቲቢ ዝርያ በመስፋፋት ላይ ይገኛል፡፡ ይህም የችግሩን መጠን ከፍ ከማድረጉም በላይ በሽታውን ለመከላከል እና ለመቆጣጠር የሚደረገውን ጥረት አዳጋች ያደርገዋል፡፡ በላቦራቶሪ ምርመራ የተደገፈ የህመም መንስኤው ላይ የሚደረግ ጥናት ጠቃሚ መረጃዎችን በማመንጨት በሽታውን ለመከላከል እና ለመቆጣጠር ከፍተኛ እገዛ ያደርጋል፡፡ በመሆኑም ይህ ጥናት የቲቢ በሽታን ጫናውንና ስርጭቱን ለማጥናት የሚካሄድ ጥናት ሲሆን በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ ላይ ትኩረት ሰጥቶ ይካሄዳል፡፡

የጥናቱ አላማ

የቲቢ በሽታ (በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ) ስርጭት እና ጫና ላይ መረጃ ማቅረብ ነው፡፡

የጥናቱ ክንውን ሰነ-ስርአት

ለጥናቱ የሚወስደው የናሙና አይነት አክታ ነው፡፡ ይህም የአክታ ናሙና ደግሞ ለመደበኛ የቲቢ የላቦራቶሪ ምርመራ የሚሰጥ በመሆኑ በጥናቱ ምክንያት የተለየ የሚወሰድ ናሙና የለም፡፡ በመሆኑም እርሶ በጥናቱ ውስጥ እንዲሳተፉ ፈቃደኝነትዎ ይጠየቃል፡፡ ስለጥናቱ በቂ መረጃ አግኝተው ፈቃደኝነትዎ ሲገልጹ የፈቃደኝነት ቅፁን ሞልተው ይፈርማሉ፡፡ በጥናቱም ተሳታፊ ይሆናሉ፡፡ የሳንባ ቲቢ በሽታ እንዳለብዎ በሃኪም ከተገመተ ሶስት የአክታ ናሙና ለምርመራ እንዲሰጡ ይጠየቃሉ፡፡ አክታውን የሚሰበስበው የላቦራቶሪ ባለሙያ ሲሆን የሚሰበሰበው ለዚህ ስራ ተብሎ በተዘጋጀ እቃ (አነስተኛ ጣሳ) ነው፡፡ የአክታ ናሙናው ለእርሶ የህክምና ምርመራና የታቀደውን ጥናት ለማካሄድ ይውላል፡፡ በተጨማሪም የ ቲቢ በሽታ እንዳለቦት ከተረጋገጠ የኤችአይቪ ምርመራ ዉጤቶ ከ ምርመራ መዝገብ ላይ ተወስዶ ለጥናቱ አገልግሎት ይውላል፡፡ ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆችም ይደረግሎታል፡፡ ቃለ መጠይቁ የሚካሄደው በነርስ ሲሆን የሚከናወነውም ምቾቶትን በጠበቀ ገለል ባለ ስፍራ ነው፡፡

ሰጋት እና ተከታይ ውሰብሰብ የጤና ችግሮች

ከጥናቱ ጋር በተያያዘ በእርስዎ ላይ የሚደርስ ከባድም ሆነ መጠነኛ ጉዳት የለም፡፡ ምክንያቱም ጥናቱ ከእርስዎ የሚጠይቀው የአክታ ናሙና ብቻ እንዲሰጡ ነው፡፡ ይህ ደግሞ መደበኛ የቲቢ ላቦራቶሪ ምርመራ ሲያደርጉ የሚጠየቁትና የሚሰጡት ናሙና ነው፡፡

የሚገኙ ጥቅሞች

እርስዎ በዚህ ጥናት ውስጥ ተሳታፊ በመሆንዎ እና በጥናት ውስጥ ለመሳተፍ በነ ፈቃድ በማሳየትዎ ከጥናቱ በቀጥታ የሚያገኙት ጥቅም አይኖርም፣ ከጥናቱ ጋር በተያያዘ የሚከፈል ማበረታቻ አይኖርም፡፡ ሆኖም ግን ከጥናቱ የሚገኘው ውጤት የቲቢ በሽታ ስርጭትን በማወቅ ረገድ ለሀገሪቷ ከፍተኛ አስተዋጽኦ አለው፡፡ ለበሽታው መንስኤ የሆኑትን የባክቴሪያ ዝርያዎች ለማወቅ ወይም ከዚህ ጋር ተያያዥ ለሆነው ምርመራ ወጪ ምንም አይነት ክፍያ እንዲፈጽሙ አይጠየቁም፡፡ የቲቢ በሽታ ምርመራ እና ህክምና በሀገሪቱ በነጻ ነው የሚሰጠው፡፡ ስለዚህ ለምርመራም ሆነ ለህክምናዎ ክፍያ አይጠየቁም፡፡ ነገር ግን በቲቢ በሽታ ምክንያት አልጋ ይዘው እንዲታከሙ ከተደረገ ለዚህ አገልግሎት የጤና ድርጅቱ የሚጠይቀውን መክፈል ይጠበቅቦታል፡፡

ከጥናቱ ስለመውጣት

የጥናቱ ተሳታፊዎች የጥናቱን ምንነት እንዲያውቁት ከተደረገ በኋላ ፈቃደኝነታቸውን እንዲገልጹ ይጠየቃሉ፡፡ ሆኖም ግን በዚህ ጥናት ውስጥ ለመሳተፍ የሰጡትን ፈቃደኝነት በማንኛውም ግዜ ሊሰርዙት ይችላሉ፡፡ የጥናቱ ተሳታፊ ራሱን ከጥናቱ በማግለሉ በቀጣይነት በሚያገኘው የጤና እንክብካቤ ላይ ምንም አይነት ተጽእኖ አይኖረውም፡፡

ሚስጥራዊነት

ማንኛውም ማንነቶን የሚገልጽ መረጃ ቁልፍ ባለው መሳቢያ/ሎከር/ ዉስጥ ስለሚቀመጥ ሚስጥራዊነቱ የተጠበቀ ነው፡፡ በዚህ ጥናት ላይ በሚዘጋጅ በማንኛውም ሪፖርት ላይ ግለሰባዊ መረጃዎች አይካተቱም፡፡ ሁሉም የምርመራ ውጤቶች በናሙናዎቹ ላይ በሚጻፍ ድብቅ ስያሜዎች ላይ በመመስረት በሚስጥራዊነት ይጠበቃሉ፡፡

የጥናቱ የግኙኝነት አድራሻዎች

ተ.ቁ	ስም	አድራሻ
1.	አቶ ያሬድ መርእድ	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት አ.አ አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0916823701 ኢሜይል yaredmerid@yahoo.com
2.	ዶ/ር ይምጡበዝናሽ ወ/አማኑኤል	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት ስልክ ቁጥር 0911225832 ኢሜይል yimtuwa@gmail.com
3.	ዶ/ር አብርሀም አሰፋ	አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0911247425 ኢሜይል aseffaa@gmail.com
የ አለርት/አርሙር ሀንሰን የምርምር ኢንስቲቱዩት የምርምር ስነምግባር ኮሚቴ አድራሻ		ስልክ ቁጥር 0118-962183

የጥናቱ ተሳትፊ መረጃ ቅጽ (ለወላጅ/አሳዳጊ-5-11 አመት)

መግቢያ

ቲቢ (የሳንባ ቲቢ) የሰውነታችንን የሳንባ ክፍል የሚያጠቃ በሽታ ሲሆን ይህ በሽታ በመላው አለም ህመም እና ሞትን ከሚያስከትሉ ዋና ዋና የጤና ችግሮች አንዱ ነው፡፡ ሀገራችን ኢትዮጵያ በቲቢ በሽታ በከፍተኛ ደረጃ ከተጠቁት ሀገራት አንዷ ናት፡፡ አብዛኛዎቹ የቲቢ በሽታ ህመምተኞች የሚጠቁት ማይኮባክቴሪየም ቱበርኩሎሲስ በሚባል የባክቴሪያ ዝሪያ አይነት ነው፡፡ የሚተላለፈውም በትንፋሽ ሲሆን አብዛኛውን ጊዜ በበሽታው የተጠቁ ግለሰብ በሚስል እና በሚያስነጥስ ጊዜ ነው፡፡

ከቅርብ ጊዜ ወዲህ መድሀኒቱን የተለማመደ የቲቢ ዝርያ በመስፋፋት ላይ ይገኛል፡፡ ይህም የችግሩን መጠን ከፍ ከማድረጉም በላይ በሽታውን ለመከላከል እና ለመቆጣጠር የሚደረገውን ጥረት አዳጋች ያደርገዋል፡፡ በላቦራቶሪ ምርመራ የተደገፈ የህመም መንስኤው ላይ የሚደረግ ጥናት ጠቃሚ መረጃዎችን በማመንጨት በሽታውን ለመከላከል እና ለመቆጣጠር ከፍተኛ እገዛ ያደርጋል፡፡ በመሆኑም ይህ ጥናት የቲቢ በሽታን ጫናውንና ስርጭቱን ለማጥናት የሚካሄድ ጥናት ሲሆን በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ ላይ ትኩረት ሰጥቶ ይካሄዳል፡፡

የጥናቱ አላማ

የቲቢ በሽታ (በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ) ስርጭት እና ጫና ላይ መረጃ ማቅረብ ነው፡፡

የጥናቱ ክንውን ሰነ-ስርአት

ለጥናቱ የሚወስደው የናሙና አይነት አክታ ነው፡፡ ይህም የአክታ ናሙና ደግሞ ለመደበኛ የቲቢ የላቦራቶሪ ምርመራ የሚሰጥ በመሆኑ በጥናቱ ምክንያት የተለየ የሚወሰድ ናሙና የለም፡፡ በመሆኑም እርስዎ የልጆች ወላጅ ወይም ቅርብ የስጋ ዘመድ ከሆኑ ልጅዎ በጥናቱ ውስጥ እንዲሳተፍ ፈቃደኝነትዎ ይጠየቃል፡፡ እርሶም ሆኑ ልጅዎ ስለጥናቱ በቂ መረጃ አግኝታችሁ ፈቃደኝነታችሁን ስትገልፁ የፈቃደኝነት ቅፁን ሞልተው ይፈርማሉ፡፡ ልጆም በጥናቱም ተሳታፊ ይሆናል፡፡ ልጅዎ የሳንባ ቲቢ በሽታ እንዳለበት በሃኪም ከተገመተ ሁለት የአክታ ናሙና ለምርመራ እንዲሰጥ ይጠየቃል፡፡ አክታው የሚሰበሰበው ለዚህ ስራ ተብሎ በተዘጋጀ እቃ (አነስተኛ ጣሳ) ነው፡፡ የአክታ ናሙናው ለልጅዎ የህክምና ምርመራና የታቀደውን ጥናት ለማካሄድ ይውላል፡፡ በተጨማሪም ልጅዎ የ ቲቢ በሽታ እንዳለበት ከተረጋገጠ የኤችአይቪ ምርመራ ዉጤቱ ከ ምርመራ መዝገብ ላይ ተወስዶ ለጥናቱ አገልግሎት ይውላል፡፡ ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆችም ይደረግለታል፡፡ ቃለ መጠይቁ የሚካሄደው በነርስ ሲሆን የሚከናወነውም ምቾቶትን በጠበቀ ገለል ባለ ስፍራ ነው፡፡

ሰጋት እና ተከታይ ውሰብሰብ የጤና ችግሮች

ከጥናቱ ጋር በተያያዘ በእርስዎ ላይ የሚደርስ ከባድም ሆነ መጠነኛ ጉዳት የለም፡፡ ምክንያቱም ጥናቱ ከእርስዎ የሚጠይቀው የአክታ ናሙና ብቻ እንዲሰጡ ነው፡፡ ይህ ደግሞ መደበኛ የቲቢ ላቦራቶሪ ምርመራ ሲያደርጉ የሚጠየቁትና የሚሰጡት ናሙና ነው፡፡

የሚገኙ ጥቅሞች

እርስዎ በዚህ ጥናት ውስጥ ተሳታፊ በመሆንዎ እና በጥናት ውስጥ ለመሳተፍ በነ ፈቃድ በማሳየትዎ ከጥናቱ በቀጥታ የሚያገኙት ጥቅም አይኖርም፣ ከጥናቱ ጋር በተያያዘ የሚከፈል ማበረታቻ አይኖርም፡፡ ሆኖም ግን ከጥናቱ የሚገኘው ውጤት የቲቢ በሽታ ስርጭትን በማወቅ ረገድ ለሀገሪቷ ከፍተኛ አስተዋጽኦ አለው፡፡ ለበሽታው መንስኤ የሆኑትን የባክቴሪያ ዝርያዎች ለማወቅ ወይም ከዚህ ጋር ተያያዥ ለሆነው ምርመራ ወጪ ምንም አይነት ክፍያ እንዲፈጽሙ አይጠየቁም፡፡ የቲቢ በሽታ ምርመራ እና ህክምና በሀገሪቱ በነጻ ነው የሚሰጠው፡፡ ስለዚህ ለምርመራም ሆነ ለህክምናዎ ክፍያ አይጠየቁም፡፡ ነገር ግን በቲቢ በሽታ ምክንያት አልጋ ይዘው እንዲታከሙ ከተደረገ ለዚህ አገልግሎት የጤና ድርጅቱ የሚጠይቀውን መክፈል ይጠበቅቦታል፡፡

ከጥናቱ ስለመውጣት

የጥናቱ ተሳታፊዎች የጥናቱን ምንነት እንዲያውቁት ከተደረገ በኋላ ፈቃደኝነታቸውን እንዲገልጹ ይጠየቃሉ፡፡ ሆኖም ግን በዚህ ጥናት ውስጥ ለመሳተፍ የሰጡትን ፈቃደኝነት በማንኛውም ግዜ ሊሰርዙት ይችላሉ፡፡ የጥናቱ ተሳታፊ ራሱን ከጥናቱ በማግለሉ በቀጣይነት በሚያገኘው የጤና እንክብካቤ ላይ ምንም አይነት ተጽእኖ አይኖረውም፡፡

ሚስጥራዊነት

ማንኛውም የልጅዎን ማንነት የሚገልጽ መረጃ ቁልፍ ባለው መሳቢያ/ሎከር/ ዉስጥ ስለሚቀመጥ ሚስጥራዊነቱ የተጠበቀ ነው፡፡ በዚህ ጥናት ላይ በሚዘጋጅ በማንኛውም ሪፖርት ላይ ግለሰባዊ መረጃዎች አይካተቱም፡፡ ሁሉም የምርመራ ውጤቶች በናሙናዎቹ ላይ በሚጻፍ ድብቅ ስያሜዎች ላይ በመመስረት በሚስጥራዊነት ይጠበቃሉ፡፡

የጥናቱ የግኙኝነት አድራሻዎች

ተ.ቁ	ስም	አድራሻ
1.	አቶ ያሬድ መርእድ	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት አ.አ አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0916823701 ኢሜይል yaredmerid@yahoo.com
2.	ዶ/ር ይምጡበዝናሽ ወ/አማኑኤል	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት ስልክ ቁጥር 0911225832 ኢሜይል yimtuwa@gmail.com
3.	ዶ/ር አብርሀም አሰፋ	አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0911247425 ኢሜይል aseffaa@gmail.com
የ አለርት/አርሙር ሀንሰን የምርምር ኢንስቲቱዩት የምርምር ስነምግባር ኮሚቴ አድራሻ		ስልክ ቁጥር 0118-962183

የጥናቱ ተሳትፊ መረጃ ቅጽ (ለልጅ 11-17 አመት)

መግቢያ

ቲቢ (የሳንባ ቲቢ) የሰውነታችንን የሳንባ ክፍል የሚያጠቃ በሽታ ሲሆን ይህ በሽታ በመላው አለም ህመም እና ሞትን ከሚያስከትሉ ዋና ዋና የጤና ችግሮች አንዱ ነው፡፡ ሀገራችን ኢትዮጵያ በቲቢ በሽታ በከፍተኛ ደረጃ ከተጠቁት ሀገራት አንዷ ናት፡፡ አብዛኛዎቹ የቲቢ በሽታ ህመምተኞች የሚጠቁት ማይኮባክቴሪየም ቱበርኩሎሲስ በሚባል የባክቴሪያ ዝሪያ አይነት ነው፡፡ የሚተላለፈውም በትንፋሽ ሲሆን አብዛኛውን ጊዜ በበሽታው የተጠቁ ግለሰብ በሚስል እና በሚያስነጥስ ጊዜ ነው፡፡

ከቅርብ ጊዜ ወዲህ መድሀኒቱን የተለማመደ የቲቢ ዝርያ በመስፋፋት ላይ ይገኛል፡፡ ይህም የችግሩን መጠን ከፍ ከማድረጉም በላይ በሽታውን ለመከላከል እና ለመቆጣጠር የሚደረገውን ጥረት አዳጋች ያደርገዋል፡፡ በላቦራቶሪ ምርመራ የተደገፈ የህመም መንስኤው ላይ የሚደረግ ጥናት ጠቃሚ መረጃዎችን በማመንጨት በሽታውን ለመከላከል እና ለመቆጣጠር ከፍተኛ እገዛ ያደርጋል፡፡ በመሆኑም ይህ ጥናት የቲቢ በሽታን ጫናውንና ስርጭቱን ለማጥናት የሚካሄድ ጥናት ሲሆን በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ ላይ ትኩረት ሰጥቶ ይካሄዳል፡፡

የጥናቱ አላማ

የቲቢ በሽታ (በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ) ስርጭት እና ጫና ላይ መረጃ ማቅረብ ነው፡፡

የጥናቱ ክንውን ሰነ-ስርአት

ለጥናቱ የሚወስደው የናሙና አይነት አክታ ነው፡፡ ይህም የአክታ ናሙና ደግሞ ለመደበኛ የቲቢ የላቦራቶሪ ምርመራ የሚሰጥ በመሆኑ በጥናቱ ምክንያት የተለየ የሚወሰድ ናሙና የለም፡፡ በመሆኑም እርስዎ የልጆች ወላጅ ወይም ቅርብ የስጋ ዘመድ ከሆኑ ልጅዎ በጥናቱ ውስጥ እንዲሳተፍ ፈቃደኝነትዎ ይጠየቃል፡፡ እርሶም ሆኑ ልጅዎ ስለጥናቱ በቂ መረጃ አግኝታችሁ ፈቃደኝነታችሁን ስትገልፁ የፈቃደኝነት ቅፁን ሞልተው ይፈርማሉ፡፡ ልጆም በጥናቱም ተሳታፊ ይሆናል፡፡ ልጅዎ የሳንባ ቲቢ በሽታ እንዳለበት በሃኪም ከተገመተ ሁለት የአክታ ናሙና ለምርመራ እንዲሰጥ ይጠየቃል፡፡ አክታው የሚሰበሰበው ለዚህ ስራ ተብሎ በተዘጋጀ እቃ (አነስተኛ ጣሳ) ነው፡፡ የአክታ ናሙናው ለአንተ/ለአንቺ የህክምና ምርመራና የታቀደውን ጥናት ለማካሄድ ይውላል፡፡ በተጨማሪም የ ቲቢ በሽታ እንዳለብህ/እንዳለብሽ ከተረጋገጠ የኤችአይቪ ምርመራ ዉጤቱ ከ ምርመራ መዝገብ ላይ ተወስዶ ለጥናቱ አገልግሎት ይውላል፡፡ ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆችም ይደረግልሃል/ሻል፡፡ ቃለ መጠይቁ የሚካሄደው በነርስ ሲሆን የሚከናወነውም ምቾቶትን በጠበቀ ገለል ባለ ስፍራ ነው፡፡

ሰጋት እና ተከታይ ውሰብሰብ የጤና ችግሮች

ከጥናቱ ጋር በተያያዘ በእርስዎ ላይ የሚደርስ ከባድም ሆነ መጠነኛ ጉዳት የለም፡፡ ምክንያቱም ጥናቱ ከእርስዎ የሚጠይቀው የአክታ ናሙና ብቻ እንዲሰጡ ነው፡፡ ይህ ደግሞ መደበኛ የቲቢ ላቦራቶሪ ምርመራ ሲያደርጉ የሚጠየቁትና የሚሰጡት ናሙና ነው፡፡

የሚገኙ ጥቅሞች

እርስዎ በዚህ ጥናት ውስጥ ተሳታፊ በመሆንዎ እና በጥናት ውስጥ ለመሳተፍ በነ ፈቃድ በማሳየትዎ ከጥናቱ በቀጥታ የሚያገኙት ጥቅም አይኖርም፣ ከጥናቱ ጋር በተያያዘ የሚከፈል ማበረታቻ አይኖርም፡፡ ሆኖም ግን ከጥናቱ የሚገኘው ውጤት የቲቢ በሽታ ስርጭትን በማወቅ ረገድ ለሀገሪቷ ከፍተኛ አስተዋጽኦ አለው፡፡ ለበሽታው መንስኤ የሆኑትን የባክቴሪያ ዝርያዎች ለማወቅ ወይም ከዚህ ጋር ተያያዥ ለሆነው ምርመራ ወጪ ምንም አይነት ክፍያ እንዲፈጽሙ አይጠየቁም፡፡ የቲቢ በሽታ ምርመራ እና ህክምና በሀገሪቱ በነጻ ነው የሚሰጠው፡፡ ስለዚህ ለምርመራም ሆነ ለህክምናዎ ክፍያ አይጠየቁም፡፡ ነገር ግን በቲቢ በሽታ ምክንያት አልጋ ይዘው እንዲታከሙ ከተደረገ ለዚህ አገልግሎት የጤና ድርጅቱ የሚጠይቀውን መክፈል ይጠበቅቦታል፡፡

ከጥናቱ ስለመውጣት

የጥናቱ ተሳታፊዎች የጥናቱን ምንነት እንዲያውቁት ከተደረገ በኋላ ፈቃደኝነታቸውን እንዲገልጹ ይጠየቃሉ፡፡ ሆኖም ግን በዚህ ጥናት ውስጥ ለመሳተፍ የሰጡትን ፈቃደኝነት በማንኛውም ግዜ ሊሰርዙት ይችላሉ፡፡ የጥናቱ ተሳታፊ ራሱን ከጥናቱ በማግለሉ በቀጣይነት በሚያገኘው የጤና እንክብካቤ ላይ ምንም አይነት ተጽእኖ አይኖረውም፡፡

ሚስጥራዊነት

ማንኛውም ማንነትህን/ማንነትሽን የሚገልጽ መረጃ ቁልፍ ባለው መሳቢያ/ሎከር/ ዉስጥ ስለሚቀመጥ ሚስጥራዊነቱ የተጠበቀ ነው፡፡ በዚህ ጥናት ላይ በሚዘጋጅ በማንኛውም ሪፖርት ላይ ግለሰባዊ መረጃዎች አይካተቱም፡፡ ሁሉም የምርመራ ውጤቶች በናሙናዎቹ ላይ በሚጻፍ ድብቅ ስያሜዎች ላይ በመመስረት በሚስጥራዊነት ይጠበቃሉ፡፡

የጥናቱ የግኙኝነት አድራሻዎች

ተ.ቁ	ስም	አድራሻ
1.	አቶ ያሬድ መርእድ	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት አ.አ አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0916823701 ኢሜይል yaredmerid@yahoo.com
2.	ዶ/ር ይምጡበዝናሽ ወ/አማኑኤል	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት ስልክ ቁጥር 0911225832 ኢሜይል yimtuwa@gmail.com
3.	ዶ/ር አብርሀም አሰፋ	አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0911247425 ኢሜይል aseffaa@gmail.com
የ አለርት/አርሙር ሀንሰን የምርምር ኢንስቲቱዩት የምርምር ስነምግባር ኮሚቴ አድራሻ		ስልክ ቁጥር 0118-962183

Subject Information sheet for Community study (Amharic version)

<u>የጥናቱ ተሳትፊ መረጃ ቅጽ (ለአዋቂ (_>18 አመት))</u>

መግቢያ

ቲቢ (የሳንባ ቲቢ) የሰውነታችንን የሳንባ ክፍል የሚያጠቃ በሽታ ሲሆን ይህ በሽታ በመላው አለም ህመም እና ሞትን ከሚያስከትሉ ዋና ዋና የጤና ችግሮች አንዱ ነው፡፡ ሀገራችን ኢትዮጵያ በቲቢ በሽታ በከፍተኛ ደረጃ ከተጠቁት ሀገራት አንዷ ናት፡፡ አብዛኛዎቹ የቲቢ በሽታ ህመምተኞች የሚጠቁት ማይኮባክቴሪየም ቱበርኩሎሲስ በሚባል የባክቴሪያ ዝሪያ አይነት ነው፡፡ የሚተላለፈውም በትንፋሽ ሲሆን አብዛኛውን ጊዜ በበሽታው የተጠቁ ግለሰብ በሚስል እና በሚያስነጥስ ጊዜ ነው፡፡

ከቅርብ ጊዜ ወዲህ መድሀኒቱን የተለማመደ የቲቢ ዝርያ በመስፋፋት ላይ ይገኛል፡፡ ይህም የችግሩን መጠን ከፍ ከማድረጉም በላይ በሽታውን ለመከላከል እና ለመቆጣጠር የሚደረገውን ጥረት አዳጋች ያደርገዋል፡፡ በላቦራቶሪ ምርመራ የተደገፈ የህመም መንስኤው ላይ የሚደረግ ጥናት ጠቃሚ መረጃዎችን በማመንጨት በሽታውን ለመከላከል እና ለመቆጣጠር ከፍተኛ እገዛ ያደርጋል፡፡ በመሆኑም ይህ ጥናት የቲቢ በሽታን ጫናውንና ስርጭቱን ለማጥናት የሚካሄድ ጥናት ሲሆን በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ ላይ ትኩረት ሰጥቶ ይካሄዳል፡፡

የጥናቱ አላማ

የቲቢ በሽታ (በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ) ስርጭት እና ጫና ላይ መረጃ ማቅረብ ነው፡፡

የጥናቱ ክንውን ሰነ-ሰርአት

ለጥናቱ የሚወስደው የናሙና አይነት አክታ ነው፡፡ ይህም የአክታ ናሙና ደግሞ ለመደበኛ የቲቢ የላቦራቶሪ ምርመራ የሚሰጥ በመሆኑ በጥናቱ ምክንያት የተለየ የሚወሰድ ናሙና የለም፡፡ በመሆኑም እርሶ በጥናቱ ውስጥ እንዲሳተፉ ፈቃደኝነትዎ ይጠየቃል፡፡ ስለጥናቱ በቂ መረጃ አግኝተው ፈቃደኝነትዎ ሲገልጹ የፈቃደኝነት ቅፁን ሞልተው ይፈርማሉ፡፡ በጥናቱም ተሳታፊ ይሆናሉ፡፡ የሳንባ ቲቢ በሽታ እንዳለብዎ በሃኪም ከተገመተ ሁለት የአክታ ናሙና ለምርመራ እንዲሰጡ ይጠየቃሉ፡፡ የምርመራው ዉጤት የ ቲቢ በሽታ እንዳለቦት ካረጋገጠ የ ኤች አይ ቪ ምርመራ እንዲያደርጉ ይጠየቃሉ፡፡ ዉጤቱም ለጥናቱ አገልግሎት ይውላል፡፡ አክታውን የምትሰበስበው የጤና ኤክስቴንሽ ባለሙያዋ ስትሆን የሚሰበሰበው ለዚህ ስራ ተብሎ በተዘጋጀ እቃ (አነስተኛ ጣሳ) ነው፡፡ የአክታ ናሙናው ለእርሶ የህክምና ምርመራና የታቀደውን ጥናት ለማካሄድ ይውላል፡፡ ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆችም ይደረግሎታል፡፡ ቃለ

መጠይቁ የሚካሄደው በጤና ኤክስቴንሽ ባለሙያዋ ሲሆን የሚከናወነውም ምቾቶትን በጠበቀ ገለል ባለ ስፍራ ነው፡፡

ሲጋት እና ተከታይ ውሰብሰብ የጤና ችግሮች

ከጥናቱ ጋር በተያያዘ በእርስዎ ላይ የሚደርስ ከባድም ሆነ መጠነኛ ጉዳት የለም፡፡ ምክንያቱም ጥናቱ ከእርስዎ የሚጠይቀው የአከታ ናሙና ብቻ እንዲሰጡ ነው፡፡ ይህ ደግሞ መደበኛ የቲቢ ላቦራቶሪ ምርመራ ሲያደርጉ የሚጠየቁትና የሚሰጡት ናሙና ነው፡፡

የሚገኙ ጥቅሞች

እርስዎ በዚህ ጥናት ውስጥ ተሳታፊ በመሆንዎ እና በጥናት ውስጥ ለመሳተፍ በነ ፈቃድ በማሳየትዎ ከጥናቱ በቀጥታ የሚያገኙት ጥቅም አይኖርም፣ ከጥናቱ ጋር በተያያዘ የሚከፈል ማበረታቻ አይኖርም፡፡ ሆኖም ግን ከጥናቱ የሚገኘው ውጤት የቲቢ በሽታ ስርጭትን በማወቅ ረገድ ለሀገሪቷ ከፍተኛ አስተዋጽኦ አለው፡፡ ለበሽታው መንስኤ የሆኑትን የባክቴሪያ ዝርያዎች ለማወቅ ወይም ከዚህ ጋር ተያያዥ ለሆነው ምርመራ ወጪ ምንም አይነት ክፍያ እንዲፈጽሙ አይጠየቁም፡፡ የቲቢ በሽታ ምርመራ እና ህክምና በሀገሪቱ በነጻ ነው የሚሰጠው፡፡ ስለዚህ ለምርመራም ሆነ ለህክምናዎ ክፍያ አይጠየቁም፡፡ ነገር ግን በቲቢ በሽታ ምክንያት አልጋ ይዘው እንዲታከሙ ከተደረገ ለዚህ አገልግሎት የጤና ድርጅቱ የሚጠይቀውን መክፈል ይጠበቅቦታል፡፡

ከጥናቱ ስለመውጣት

የጥናቱ ተሳታፊዎች የጥናቱን ምንነት እንዲያውቁት ከተደረገ በኋላ ፈቃደኝነታቸውን እንዲገልጹ ይጠየቃሉ፡፡ ሆኖም ግን በዚህ ጥናት ውስጥ ለመሳተፍ የሰጡትን ፈቃደኝነት በማንኛውም ግዜ ሊሰርዙት ይችላሉ፡፡ የጥናቱ ተሳታፊ ራሱን ከጥናቱ በማግለሉ በቀጣይነት በሚያገኘው የጤና እንክብካቤ ላይ ምንም አይነት ተጽእኖ አይኖረውም፡፡

ሚስጥራዊነት

ማንኛውም ማንነቶን የሚገልጽ መረጃ ቁልፍ ባለው መሳቢያ/ሎከር/ ዉስጥ ስለሚቀመጥ ሚስጥራዊነቱ የተጠበቀ ነው፡፡ በዚህ ጥናት ላይ በሚዘጋጅ በማንኛውም ሪፖርት ላይ ግለሰባዊ መረጃዎች አይካተቱም፡፡ ሁሉም የምርመራ ውጤቶች በናሙናዎቹ ላይ በሚጻፍ ድብቅ ስያሜዎች ላይ በመመስረት በሚስጥራዊነት ይጠበቃሉ፡፡

የጥናቱ የግኙኝነት አድራሻዎች

ተ.ቁ	ስም	አድራሻ
1.	አቶ ያሬድ መርእድ	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት አ.አ አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0916823701 ኢሜይል yaredmerid@yahoo.com
2.	ዶ/ር ይምጡበዝናሽ ወ/አማኑኤል	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት ስልክ ቁጥር 0911225832 ኢሜይል yimtuwa@gmail.com
3.	ዶ/ር አብርሀም አሰፋ	አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0911247425 ኢሜይል aseffaa@gmail.com
የ አለርት/አርሙር ሀንሰን የምርምር ኢንስቲቱዩት የምርምር ስነምግባር ኮሚቴ አድራሻ		ስልክ ቁጥር 0118-962183

<u>የጥናቱ ተሳትፈ መረጃ ቅጽ (ለወላጅ/አሳዳጊ- 5-11 አመት)</u>

መግቢያ

ቲቢ (የሳንባ ቲቢ) የሰውነታችንን የሳንባ ክፍል የሚያጠቃ በሽታ ሲሆን ይህ በሽታ በመላው አለም ህመም እና ሞትን ከሚያስከትሉ ዋና ዋና የጤና ችግሮች አንዱ ነው፡፡ ሀገራችን ኢትዮጵያ በቲቢ በሽታ በከፍተኛ ደረጃ ከተጠቁት ሀገራት አንዷ ናት፡፡ አብዛኛዎቹ የቲቢ በሽታ ህመምተኞች የሚጠቁት ማይኮባክቴሪየም ቱበርኩሎሲስ በሚባል የባክቴሪያ ዝሪያ አይነት ነው፡፡ የሚተላለፈውም በትንፋሽ ሲሆን አብዛኛውን ጊዜ በበሽታው የተጠቁ ግለሰብ በሚስል እና በሚያስነጥስ ጊዜ ነው፡፡

ከቅርብ ጊዜ ወዲህ መድሀኒቱን የተለማመደ የቲቢ ዝርያ በመስፋፋት ላይ ይገኛል፡፡ ይህም የችግሩን መጠን ከፍ ከማድረጉም በላይ በሽታውን ለመከላከል እና ለመቆጣጠር የሚደረገውን ጥረት አዳጋች ያደርገዋል፡፡ በላቦራቶሪ ምርመራ የተደገፈ የህመም መንስኤው ላይ የሚደረግ ጥናት ጠቃሚ መረጃዎችን በማመንጨት በሽታውን ለመከላከል እና ለመቆጣጠር ከፍተኛ እገዛ ያደርጋል፡፡ በመሆኑም ይህ ጥናት የቲቢ በሽታን ጫናውንና ስርጭቱን ለማጥናት የሚካሄድ ጥናት ሲሆን በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ ላይ ትኩረት ሰጥቶ ይካሄዳል፡፡

የጥናቱ አላማ

የቲቢ በሽታ (በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ) ስርጭት እና ጫና ላይ መረጃ ማቅረብ ነው፡፡

የጥናቱ ክንውን ሰነ-ስርአት

ለጥናቱ የሚወስደው የናሙና አይነት አክታ ነው፡፡ ይህም የአክታ ናሙና ደግሞ ለመደበኛ የቲቢ የላቦራቶሪ ምርመራ የሚሰጥ በመሆኑ በጥናቱ ምክንያት የተለየ የሚወሰድ ናሙና የለም፡፡ በመሆኑም እርስዎ የልጆች ወላጅ ወይም ቅርብ የስጋ ዘመድ ከሆኑ ልጅዎ በጥናቱ ውስጥ እንዲሳተፍ ፈቃደኝነትዎ ይጠየቃል፡፡ እርሶም ሆኑ ልጅዎ ስለጥናቱ በቂ መረጃ አግኝታችሁ ፈቃደኝነታችሁን ስትገልፁ የፈቃደኝነት ቅፁን ሞልተው ይፈርማሉ፡፡ ልጆም በጥናቱም ተሳታፊ ይሆናል፡፡ ልጅዎ የሳንባ ቲቢ በሽታ እንዳለበት በሃኪም ከተገመተ ሁለት የአክታ ናሙና ለምርመራ እንዲሰጥ ይጠየቃል፡፡ የምርመራው ዉጤት ልጅዎ የሳንባ ቲቢ በሽታ እንዳለበት ካረጋገጠ፤ ልጅዎ የ ኤች አይ ቪ ምርመራ እንዲያደርግ ይጠየቃሉ፡፡ ዉጤቱም ለጥናቱ አገልግሎት ይውላል፡፡ አክታውን የምትሰበስበው የጤና ኤክስቴንሽ ባለሙያዋ ስትሆን የሚሰበሰበው ለዚህ ስራ ተብሎ በተዘጋጀ እቃ (አነስተኛ ጣሳ) ነው፡፡ የአክታ ናሙናው ለልጅዎ የህክምና ምርመራና የታቀደውን ጥናት ለማካሄድ ይውላል፡፡ ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆችም ይደረግለታል፡፡ ቃለ መጠይቁ የሚካሄደው በነርስ ሲሆን የሚከናወነውም ምቾቶትን በጠበቀ ገለል ባለ ስፍራ ነው፡፡

ሲጋት እና ተከታይ ውስብስብ የጤና ችግሮች

ከጥናቱ ጋር በተያያዘ በእርስዎ ላይ የሚደርስ ከባድም ሆነ መጠነኛ ጉዳት የለም፡፡ ምክንያቱም ጥናቱ ከእርስዎ የሚጠይቀው የአክታ ናሙና ብቻ እንዲሰጡ ነው፡፡ ይህ ደግሞ መደበኛ የቲቢ ላቦራቶሪ ምርመራ ሲያደርጉ የሚጠየቁትና የሚሰጡት ናሙና ነው፡፡

የሚገኙ ጥቅሞች

እርስዎ በዚህ ጥናት ውስጥ ተሳታፊ በመሆንዎ እና በጥናት ውስጥ ለመሳተፍ በነ ፈቃድ በማሳየትዎ ከጥናቱ በቀጥታ የሚያገኙት ጥቅም አይኖርም፣ ከጥናቱ ጋር በተያያዘ የሚከፈል ማበረታቻ አይኖርም፡፡ ሆኖም ግን ከጥናቱ የሚገኘው ውጤት የቲቢ በሽታ ስርጭትን በማወቅ ረገድ ለሀገሪቷ ከፍተኛ አስተዋጽኦ አለው፡፡ ለበሽታው መንስኤ የሆኑትን የባክቴሪያ ዝርያዎች ለማወቅ ወይም ከዚህ ጋር ተያያዥ ለሆነው ምርመራ ወጪ ምንም አይነት ክፍያ እንዲፈጽሙ አይጠየቁም፡፡ የቲቢ በሽታ ምርመራ እና ህክምና በሀገሪቱ በነጻ ነው የሚሰጠው፡፡ ስለዚህ ለምርመራም ሆነ ለህክምናዎ ክፍያ አይጠየቁም፡፡ ነገር ግን በቲቢ በሽታ ምክንያት አልጋ ይዘው እንዲታከሙ ከተደረገ ለዚህ አገልግሎት የጤና ድርጅቱ የሚጠይቀውን መክፈል ይጠበቅቦታል፡፡

ከጥናቱ ስለመውጣት

የጥናቱ ተሳታፊዎች የጥናቱን ምንነት እንዲያውቁት ከተደረገ በኋላ ፈቃደኝነታቸውን እንዲገልጹ ይጠየቃሉ፡፡ ሆኖም ግን በዚህ ጥናት ውስጥ ለመሳተፍ የሰጡትን ፈቃደኝነት በማንኛውም ግዜ ሊሰርዙት ይችላሉ፡፡ የጥናቱ ተሳታፊ ራሱን ከጥናቱ በማግለሉ በቀጣይነት በሚያገኘው የጤና እንክብካቤ ላይ ምንም አይነት ተጽእኖ አይኖረውም፡፡

ሚስጥራዊነት

ማንኛውም የልጅዎን ማንነት የሚገልጽ መረጃ ቁልፍ ባለው መሳቢያ/ሎከር/ ዉስጥ ስለሚቀመጥ ሚስጥራዊነቱ የተጠበቀ ነው፡፡ በዚህ ጥናት ላይ በሚዘጋጅ በማንኛውም ሪፖርት ላይ ግለሰባዊ መረጃዎች አይካተቱም፡፡ ሁሉም የምርመራ ውጤቶች በናሙናዎቹ ላይ በሚጻፍ ድብቅ ስያሜዎች ላይ በመመስረት በሚስጥራዊነት ይጠበቃሉ፡፡

የጥናቱ የግኙነት አድራሻዎች

ተ.ቁ	ስም	አድራሻ
1.	አቶ ያሬድ መርእድ	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት አ.አ አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0916823701 ኢሜይል yaredmerid@yahoo.com
2.	ዶ/ር ይምጡበዝናሽ ወ/አማኑኤል	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት ስልክ ቁጥር 0911225832 ኢሜይል yimtuwa@gmail.com
3.	ዶ/ር አብርሀም አሰፋ	አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0911247425 ኢሜይል aseffaa@gmail.com
የ አለርት/አርሙር ሀንሰን የምርምር ኢንስቲቱዩት የምርምር ስነምግባር ኮሚቴ አድራሻ		ስልክ ቁጥር 0118-962183

<u>የጥናቱ ተሳትፊ መረጃ ቅጽ (ለህፃናት- 11-17 አመት)</u>

መግቢያ

ቲቢ (የሳንባ ቲቢ) የሰውነታችንን የሳንባ ክፍል የሚያጠቃ በሽታ ሲሆን ይህ በሽታ በመላው አለም ህመም እና ሞትን ከሚያስከትሉ ዋና ዋና የጤና ችግሮች አንዱ ነው፡፡ ሀገራችን ኢትዮጵያ በቲቢ በሽታ በከፍተኛ ደረጃ ከተጠቁት ሀገራት አንዷ ናት፡፡ አብዛኛዎቹ የቲቢ በሽታ ህመምተኞች የሚጠቁት ማይኮባክቴሪየም ቱበርኩሎሲስ በሚባል የባክቴሪያ ዝሪያ አይነት ነው፡፡ የሚተላለፈውም በትንፋሽ ሲሆን አብዛኛውን ጊዜ በበሽታው የተጠቁ ግለሰብ በሚስል እና በሚያስነጥስ ጊዜ ነው፡፡

ከቅርብ ጊዜ ወዲህ መድሀኒቱን የተለማመደ የቲቢ ዝርያ በመስፋፋት ላይ ይገኛል፡፡ ይህም የችግሩን መጠን ከፍ ከማድረጉም በላይ በሽታውን ለመከላከል እና ለመቆጣጠር የሚደረገውን ጥረት አዳጋች ያደርገዋል፡፡ በላቦራቶሪ ምርመራ የተደገፈ የህመም መንስኤው ላይ የሚደረግ ጥናት ጠቃሚ መረጃዎችን በማመንጨት በሽታውን ለመከላከል እና ለመቆጣጠር ከፍተኛ እገዛ ያደርጋል፡፡ በመሆኑም ይህ ጥናት የቲቢ በሽታን ጫናውንና ስርጭቱን ለማጥናት የሚካሄድ ጥናት ሲሆን በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ ላይ ትኩረት ሰጥቶ ይካሄዳል፡፡

የጥናቱ አላማ

የቲቢ በሽታ (በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ) ስርጭት እና ጫና ላይ መረጃ ማቅረብ ነው፡፡

የጥናቱ ክንውን ሰነ-ሰርአት

ለጥናቱ የሚወስደው የናሙና አይነት አክታ ነው፡፡ ይህም የአክታ ናሙና ደግሞ ለመደበኛ የቲቢ የላቦራቶሪ ምርመራ የሚሰጥ በመሆኑ በጥናቱ ምክንያት የተለየ የሚወሰድ ናሙና የለም፡፡ በመሆኑም በጥናቱ ዉስጥ እንድትሳተፍ/ፊ ፈቃደኝነትህ/ሽ ይጠየቃል፡፡ ስለጥናቱ በቂ መረጃ አግኝተህ/ሽ ፈካደኝነትህ/ሽን ስትገልጽ/ጪ የፈቃደኝነት ቅፁን ሞልተህ/ሽ ትፈርምበታለህ/ትፈርሚበታለሽ/፡፡ በጥናቱም ተሳታፊ ትሆናለህ/ትሆኛለሽ፡፡ የሳንባ ቲቢ በሽታ እንዳለብህ/እንዳለብሽ በሃኪም ከተገመተ ሁለት የአክታ ናሙና ለምርመራ እንድትሰጥ/እንድትሰጪ ትጠየቃለህ/ትጠየቂያለሽ/፡፡ የምርመራው ዉጤት የ ቲቢ በሽታ እንዳለብህ/እንዳለብሽ ካረጋገጠ የ ኤች አይ ቪ ምርመራ እንድታደርግ/እንድታደርጊ ትጠየቃለህ/ትጠየቂያለሽ፡፡ ዉጤቱም ለጥናቱ አገልግሎት ይውላል፡፡ አክታውን የምትሰበስበው የጤና ኤክስቴንሽ ባለሙያዋ ስትሆን የሚሰበሰበው ለዚህ ስራ ተብሎ በተዘጋጀ እቃ (አነስተኛ ጣሳ) ነው፡፡ የአክታ ናሙናው ለአንተ/ለአንቺ የህክምና ምርመራና የታቀደውን ጥናት ለማካሄድ ይውላል፡፡ ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆችም ይደረግልሃል/ይደረግልሻል፡፡ቃለ ቃለ መጠይቁ

የሚካሄደው በጤና ኤክስቴንሽ ባለሙያዋ ሲሆን የሚከናወነውም ምቾቶትን በጠበቀ ገለል ባለ ስፍራ ነው፡፡

ሰጋት እና ተከታይ ውሰብሰብ የጤና ችግሮች

ከጥናቱ ጋር በተያያዘ በእርስዎ ላይ የሚደርስ ከባድም ሆነ መጠነኛ ጉዳት የለም፡፡ ምክንያቱም ጥናቱ ከእርስዎ የሚጠይቀው የአክታ ናሙና ብቻ እንዲሰጡ ነው፡፡ ይህ ደግሞ መደበኛ የቲቢ ላቦራቶሪ ምርመራ ሲያደርጉ የሚጠየቁትና የሚሰጡት ናሙና ነው፡፡

የሚገኙ ጥቅሞች

እርስዎ በዚህ ጥናት ውስጥ ተሳታፊ በመሆንዎ እና በጥናት ውስጥ ለመሳተፍ በነ ፈቃድ በማሳየትዎ ከጥናቱ በቀጥታ የሚያገኙት ጥቅም አይኖርም፣ ከጥናቱ ጋር በተያያዘ የሚከፈል ማበረታቻ አይኖርም፡፡ ሆኖም ግን ከጥናቱ የሚገኘው ውጤት የቲቢ በሽታ ስርጭትን በማወቅ ረገድ ለሀገሪቷ ከፍተኛ አስተዋጽኦ አለው፡፡ ለበሽታው መንስኤ የሆኑትን የባክቴሪያ ዝርያዎች ለማወቅ ወይም ከዚህ ጋር ተያያዥ ለሆነው ምርመራ ወጪ ምንም አይነት ክፍያ እንዲፈጽሙ አይጠየቁም፡፡ የቲቢ በሽታ ምርመራ እና ህክምና በሀገሪቱ በነጻ ነው የሚሰጠው፡፡ ስለዚህ ለምርመራም ሆነ ለህክምናዎ ክፍያ አይጠየቁም፡፡ ነገር ግን በቲቢ በሽታ ምክንያት አልጋ ይዘው እንዲታከሙ ከተደረገ ለዚህ አገልግሎት የጤና ድርጅቱ የሚጠይቀውን መክፈል ይጠበቅቦታል፡፡

ከጥናቱ ስለመውጣት

የጥናቱ ተሳታፊዎች የጥናቱን ምንነት እንዲያውቁት ከተደረገ በኋላ ፈቃደኝነታቸውን እንዲገልጹ ይጠየቃሉ፡፡ ሆኖም ግን በዚህ ጥናት ውስጥ ለመሳተፍ የሰጡትን ፈቃደኝነት በማንኛውም ግዜ ሊሰርዙት ይችላሉ፡፡ የጥናቱ ተሳታፊ ራሱን ከጥናቱ በማግለሉ በቀጣይነት በሚያገኘው የጤና እንክብካቤ ላይ ምንም አይነት ተጽእኖ አይኖረውም፡፡

ሚስጥራዊነት

ማንኛውም ማንነትህን/ማንነትሽን የሚገልጽ መረጃ ቁልፍ ባለው መሳቢያ/ሎከር/ ዉስጥ ስለሚቀመጥ ሚስጥራዊነቱ የተጠበቀ ነው፡፡ በዚህ ጥናት ላይ በሚዘጋጅ በማንኛውም ሪፖርት ላይ ግለሰባዊ መረጃዎች አይካተቱም፡፡ ሁሉም የምርመራ ውጤቶች በናሙናዎቹ ላይ በሚጻፍ ድብቅ ስያሜዎች ላይ በመመስረት በሚስጥራዊነት ይጠበቃሉ፡፡

የጥናቱ የግኙኝነት አድራሻዎች

ተ.ቁ	ስም	አድራሻ
1.	አቶ ያሬድ መርእድ	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት አ.አ አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0916823701 ኢሜይል yaredmerid@yahoo.com
2.	ዶ/ር ይምጡበዝናሽ ወ/አማኑኤል	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት ስልክ ቁጥር 0911225832 ኢሜይል yimtuwa@gmail.com
3.	ዶ/ር አብርሀም አሰፋ	አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0911247425 ኢሜይል aseffaa@gmail.com
የ አለርት/አርሙር ሀንሰን የምርምር ኢንስቲቱዩት የምርምር ስነምግባር ኮሚቴ አድራሻ		ስልክ ቁጥር 0118-962183

Subject Information sheet for Prison study (Amharic version)

<u>የጥናቱ ተሳትፊ መረጃ ቅጽ (ለአዋቂ (_>18 አመት))</u>

መግቢያ

ቲቢ (የሳንባ ቲቢ) የሰውነታችንን የሳንባ ክፍል የሚያጠቃ በሽታ ሲሆን ይህ በሽታ በመላው አለም ህመም እና ሞትን ከሚያስከትሉ ዋና ዋና የጤና ችግሮች አንዱ ነው፡፡ ሀገራችን ኢትዮጵያ በቲቢ በሽታ በከፍተኛ ደረጃ ከተጠቁት ሀገራት አንዷ ናት፡፡ አብዛኛዎቹ የቲቢ በሽታ ህመምተኞች የሚጠቁት ማይኮባክቴሪየም ቱበርኩሎሲስ በሚባል የባክቴሪያ ዝሪያ አይነት ነው፡፡ የሚተላለፈውም በትንፋሽ ሲሆን አብዛኛውን ጊዜ በበሽታው የተጠቁ ግለሰብ በሚስል እና በሚያስነጥስ ጊዜ ነው፡፡

ከቅርብ ጊዜ ወዲህ መድሀኒቱን የተለማመደ የቲቢ ዝርያ በመስፋፋት ላይ ይገኛል፡፡ ይህም የችግሩን መጠን ከፍ ከማድረጉም በላይ በሽታውን ለመከላከል እና ለመቆጣጠር የሚደረገውን ጥረት አዳጋች ያደርገዋል፡፡ በላቦራቶሪ ምርመራ የተደገፈ የህመም መንስኤው ላይ የሚደረግ ጥናት ጠቃሚ መረጃዎችን በማመንጨት በሽታውን ለመከላከል እና ለመቆጣጠር ከፍተኛ እገዛ ያደርጋል፡፡ በመሆኑም ይህ ጥናት የቲቢ በሽታን ጫናውንና ስርጭቱን ለማጥናት የሚካሄድ ጥናት ሲሆን በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ ላይ ትኩረት ሰጥቶ ይካሄዳል፡፡

የጥናቱ አላማ

የቲቢ በሽታ (በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ) ስርጭት እና ጫና ላይ መረጃ ማቅረብ ነው፡፡

የጥናቱ ክንውን ሰነ-ሰርአት

ለጥናቱ የሚወስደው የናሙና አይነት አክታ ነው፡፡ ይህም የአክታ ናሙና ደግሞ ለመደበኛ የቲቢ የላቦራቶሪ ምርመራ የሚሰጥ በመሆኑ በጥናቱ ምክንያት የተለየ የሚወሰድ ናሙና የለም፡፡ በመሆኑም እርሶ በጥናቱ ውስጥ እንዲሳተፉ ፈቃደኝነትዎ ይጠየቃል፡፡ ስለጥናቱ በቂ መረጃ አግኝተው ፈቃደኝነትዎ ሲገልጹ የፈቃደኝነት ቅፁን ሞልተው ይፈርማሉ፡፡ በጥናቱም ተሳታፊ ይሆናሉ፡፡ የሳንባ ቲቢ በሽታ እንዳለብዎ በሃኪም ከተገመተ ሁለት የአክታ ናሙና ለምርመራ እንዲሰጡ ይጠየቃሉ፡፡ የምርመራው ዉጤት የ ቲቢ በሽታ እንዳለቦት ካረጋገጠ የ ኤች አይ ቪ ምርመራ እንዲያደርጉ ይጠየቃሉ፡፡ ዉጤቱም ለጥናቱ አገልግሎት ይውላል፡፡ አክታውን የሚሰበስበው የላቦራቶሪ ባለሙያ ሲሆን የሚሰበሰበው ለዚህ ስራ ተብሎ በተዘጋጀ እቃ (አነስተኛ ጣሳ) ነው፡፡ የአክታ ናሙናው ለእርሶ የህክምና ምርመራና የታቀደውን ጥናት ለማካሄድ ይውላል፡፡ ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆችም ይደረግሎታል፡፡ቃለ መጠይቁ የሚካሄደው በነርስ ሲሆን የሚከናወነውም ምቾቶትን በጠበቀ ገለል ባለ ስፍራ ነው፡፡

ሲጋት እና ተከታይ ውስብስብ የጤና ችግሮች

ከጥናቱ ጋር በተያያዘ በእርስዎ ላይ የሚደርስ ከባድም ሆነ መጠነኛ ጉዳት የለም፡፡ ምክንያቱም ጥናቱ ከእርስዎ የሚጠይቀው የአክታ ናሙና ብቻ እንዲሰጡ ነው፡፡ ይህ ደግሞ መደበኛ የቲቢ ላቦራቶሪ ምርመራ ሲያደርጉ የሚጠየቁትና የሚሰጡት ናሙና ነው፡፡

የሚገኙ ጥቅሞች

እርስዎ በዚህ ጥናት ውስጥ ተሳታፊ በመሆንዎ እና በጥናት ውስጥ ለመሳተፍ በነ ፈቃድ በማሳየትዎ ከጥናቱ በቀጥታ የሚያገኙት ጥቅም አይኖርም፣ ከጥናቱ ጋር በተያያዘ የሚከፈል ማበረታቻ አይኖርም፡፡ ሆኖም ግን ከጥናቱ የሚገኘው ውጤት የቲቢ በሽታ ስርጭትን በማወቅ ረገድ ለሀገሪቷ ከፍተኛ አስተዋጽኦ አለው፡፡ ለበሽታው መንስኤ የሆኑትን የባክቴሪያ ዝርያዎች ለማወቅ ወይም ከዚህ ጋር ተያያዥ ለሆነው ምርመራ ወጪ ምንም አይነት ክፍያ እንዲፈጽሙ አይጠየቁም፡፡ የቲቢ በሽታ ምርመራ እና ህክምና በሀገሪቱ በነጻ ነው የሚሰጠው፡፡ ስለዚህ ለምርመራም ሆነ ለህክምናዎ ክፍያ አይጠየቁም፡፡ ነገር ግን በቲቢ በሽታ ምክንያት አልጋ ይዘው እንዲታከሙ ከተደረገ ለዚህ አገልግሎት የጤና ድርጅቱ የሚጠይቀውን መክፈል ይጠበቅቦታል፡፡

ከጥናቱ ስለመውጣት

የጥናቱ ተሳታፊዎች የጥናቱን ምንነት እንዲያውቁት ከተደረገ በኋላ ፈቃደኝነታቸውን እንዲገልጹ ይጠየቃሉ፡፡ ሆኖም ግን በዚህ ጥናት ውስጥ ለመሳተፍ የሰጡትን ፈቃደኝነት በማንኛውም ግዜ ሊሰርዙት ይችላሉ፡፡ የጥናቱ ተሳታፊ ራሱን ከጥናቱ በማግለሉ በቀጣይነት በሚያገኘው የጤና እንክብካቤ ላይ ምንም አይነት ተጽእኖ አይኖረውም፡፡

ሚስጥራዊነት

ማንኛውም ማንነቶን የሚገልጽ መረጃ ቁልፍ ባለው መሳቢያ/ሎከር/ ዉስጥ ስለሚቀመጥ ሚስጥራዊነቱ የተጠበቀ ነው፡፡ በዚህ ጥናት ላይ በሚዘጋጅ በማንኛውም ሪፖርት ላይ ግለሰባዊ መረጃዎች አይካተቱም፡፡ ሁሉም የምርመራ ውጤቶች በናሙናዎቹ ላይ በሚጻፍ ድብቅ ስያሜዎች ላይ በመመስረት በሚስጥራዊነት ይጠበቃሉ፡፡

የጥናቱ የግኙኝነት አድራሻዎች

ተ.ቁ	ስም	አድራሻ
1.	አቶ ያሬድ መርእድ	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት አ.አ አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0916823701 ኢሜይል yaredmerid@yahoo.com
2.	ዶ/ር ይምጡበዝናሽ ወ/አማኑኤል	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት ስልክ ቁጥር 0911225832 ኢሜይል yimtuwa@gmail.com
3.	ዶ/ር አብርሀም አሰፋ	አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0911247425 ኢሜይል aseffaa@gmail.com
የ አለርት/አርሙር ሀንሰን የምርምር ኢንስቲቱዩት የምርምር ስነምግባር ኮሚቴ አድራሻ		ስልክ ቁጥር 0118-962183

<u>የጥናቱ ተሳትፈ መረጃ ቅጽ (ለወላጅ/አሳዳጊ –5–11 አመት)</u>

መግቢያ

ቲቢ (የሳንባ ቲቢ) የሰውነታችንን የሳንባ ክፍል የሚያጠቃ በሽታ ሲሆን ይህ በሽታ በመላው አለም ህመም እና ሞትን ከሚያስከትሉ ዋና ዋና የጤና ችግሮች አንዱ ነው፡፡ ሀገራችን ኢትዮጵያ በቲቢ በሽታ በከፍተኛ ደረጃ ከተጠቁት ሀገራት አንዷ ናት፡፡ አብዛኛዎቹ የቲቢ በሽታ ህመምተኞች የሚጠቁት ማይኮባክቴሪየም ቱበርኩሎሲስ በሚባል የባክቴሪያ ዝሪያ አይነት ነው፡፡ የሚተላለፈውም በትንፋሽ ሲሆን አብዛኛውን ጊዜ በበሽታው የተጠቁ ግለሰብ በሚስል እና በሚያስነጥስ ጊዜ ነው፡፡

ከቅርብ ጊዜ ወዲህ መድሀኒቱን የተለማመደ የቲቢ ዝርያ በመስፋፋት ላይ ይገኛል፡፡ ይህም የችግሩን መጠን ከፍ ከማድረጉም በላይ በሽታውን ለመከላከል እና ለመቆጣጠር የሚደረገውን ጥረት አዳጋች ያደርገዋል፡፡ በላቦራቶሪ ምርመራ የተደገፈ የህመም መንስኤው ላይ የሚደረግ ጥናት ጠቃሚ መረጃዎችን በማመንጨት በሽታውን ለመከላከል እና ለመቆጣጠር ከፍተኛ እገዛ ያደርጋል፡፡ በመሆኑም ይህ ጥናት የቲቢ በሽታን ጫናውንና ስርጭቱን ለማጥናት የሚካሄድ ጥናት ሲሆን በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ ላይ ትኩረት ሰጥቶ ይካሄዳል፡፡

የጥናቱ አላማ

የቲቢ በሽታ (በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ) ስርጭት እና ጫና ላይ መረጃ ማቅረብ ነው፡፡

የጥናቱ ክንውን ሰነ–ስርአት

ለጥናቱ የሚወስደው የናሙና አይነት አክታ ነው፡፡ ይህም የአክታ ናሙና ደግሞ ለመደበኛ የቲቢ የላቦራቶሪ ምርመራ የሚሰጥ በመሆኑ በጥናቱ ምክንያት የተለየ የሚወሰድ ናሙና የለም፡፡ በመሆኑም እርስዎ የልጆች ወላጅ ወይም ቅርብ የስጋ ዘመድ ከሆኑ ልጅዎ በጥናቱ ውስጥ እንዲሳተፍ ፈቃደኝነትዎ ይጠየቃል፡፡ እርሶም ሆኑ ልጅዎ ስለጥናቱ በቂ መረጃ አግኝታችሁ ፈቃደኝነታችሁን ስትገልፁ የፈቃደኝነት ቅፁን ሞልተው ይፈርማሉ፡፡ ልጆም በጥናቱም ተሳታፊ ይሆናል፡፡ ልጅዎ የሳንባ ቲቢ በሽታ እንዳለበት በሃኪም ከተገመተ ሁለት የአክታ ናሙና ለምርመራ እንዲሰጥ ይጠየቃል፡፡ የምርመራው ዉጤት ልጅዎ የሳንባ ቲቢ በሽታ እንዳለበት ካረጋገጠ፤ ልጅዎ የ ኤች አይ ቪ ምርመራ እንዲያደርግ ይጠየቃሉ፡፡ ዉጤቱም ለጥናቱ አገልግሎት ይውላል፡፡ አክታውን የሚሰበስበው የላቦራቶሪ ባለሙያ ሲሆን የሚሰበሰበው ለዚህ ስራ ተብሎ በተዘጋጀ እቃ (አነስተኛ ጣሳ) ነው፡፡ የአክታ ናሙናው ለልጅዎ የህክምና ምርመራና የታቀደውን ጥናት ለማካሄድ ይውላል፡፡ ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆችም ይደረግለታል፡፡ ቃለ መጠይቁ የሚካሄደው በነርስ ሲሆን የሚከናወነውም ምቾቶትን በጠበቀ ገለል ባለ ስፍራ ነው፡፡

ሲጋት እና ተከታይ ውስብስብ የጤና ችግሮች

ከጥናቱ ጋር በተያያዘ በእርስዎ ላይ የሚደርስ ከባድም ሆነ መጠነኛ ጉዳት የለም፡፡ ምክንያቱም ጥናቱ ከእርስዎ የሚጠይቀው የአክታ ናሙና ብቻ እንዲሰጡ ነው፡፡ ይህ ደግሞ መደበኛ የቲቢ ላቦራቶሪ ምርመራ ሲያደርጉ የሚጠየቁትና የሚሰጡት ናሙና ነው፡፡

የሚገኙ ጥቅሞች

እርስዎ በዚህ ጥናት ውስጥ ተሳታፊ በመሆንዎ እና በጥናት ውስጥ ለመሳተፍ በነ ፈቃድ በማሳየትዎ ከጥናቱ በቀጥታ የሚያገኙት ጥቅም አይኖርም፣ ከጥናቱ ጋር በተያያዘ የሚከፈል ማበረታቻ አይኖርም፡፡ ሆኖም ግን ከጥናቱ የሚገኘው ውጤት የቲቢ በሽታ ስርጭትን በማወቅ ረገድ ለሀገሪቷ ከፍተኛ አስተዋጽኦ አለው፡፡ ለበሽታው መንስኤ የሆኑትን የባክቴሪያ ዝርያዎች ለማወቅ ወይም ከዚህ ጋር ተያያዥ ለሆነው ምርመራ ወጪ ምንም አይነት ክፍያ እንዲፈጽሙ አይጠየቁም፡፡ የቲቢ በሽታ ምርመራ እና ህክምና በሀገሪቱ በነጻ ነው የሚሰጠው፡፡ ስለዚህ ለምርመራም ሆነ ለህክምናዎ ክፍያ አይጠየቁም፡፡ ነገር ግን በቲቢ በሽታ ምክንያት አልጋ ይዘው እንዲታከሙ ከተደረገ ለዚህ አገልግሎት የጤና ድርጅቱ የሚጠይቀውን መክፈል ይጠበቅቦታል፡፡

ከጥናቱ ስለመውጣት

የጥናቱ ተሳታፊዎች የጥናቱን ምንነት እንዲያውቁት ከተደረገ በኋላ ፈቃደኝነታቸውን እንዲገልጹ ይጠየቃሉ፡፡ ሆኖም ግን በዚህ ጥናት ውስጥ ለመሳተፍ የሰጡትን ፈቃደኝነት በማንኛውም ግዜ ሊሰርዙት ይችላሉ፡፡ የጥናቱ ተሳታፊ ራሱን ከጥናቱ በማግለሉ በቀጣይነት በሚያገኘው የጤና እንክብካቤ ላይ ምንም አይነት ተጽእኖ አይኖረውም፡፡

ሚስጥራዊነት

ማንኛውም የልጅዎን ማንነት የሚገልጽ መረጃ ቁልፍ ባለው መሳቢያ/ሎከር/ ዉስጥ ስለሚቀመጥ ሚስጥራዊነቱ የተጠበቀ ነው፡፡ በዚህ ጥናት ላይ በሚዘጋጅ በማንኛውም ሪፖርት ላይ ግለሰባዊ መረጃዎች አይካተቱም፡፡ ሁሉም የምርመራ ውጤቶች በናሙናዎቹ ላይ በሚጻፍ ድብቅ ስያሜዎች ላይ በመመስረት በሚስጥራዊነት ይጠበቃሉ፡፡

የጥናቱ የግኙኝነት አድራሻዎች

ተ.ቁ	ስም	አድራሻ
1.	አቶ ያሬድ መርእድ	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት አ.አ አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0916823701 ኢሜይል yaredmerid@yahoo.com
2.	ዶ/ር ይምጡበዝናሽ ወ/አማኑኤል	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት ስልክ ቁጥር 0911225832 ኢሜይል yimtuwa@gmail.com
3.	ዶ/ር አብርሀም አሰፋ	አርሙር ሀንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0911247425 ኢሜይል aseffaa@gmail.com
የ አለርት/አርሙር ሀንሰን የምርምር ኢንስቲቱዩት የምርምር ስነምግባር ኮሚቴ አድራሻ		ስልክ ቁጥር 0118-962183

የጥናቱ ተሳትፊ መረጃ ቅጽ (ለህፃናት- 11-17 አመት)

መግቢያ

ቲቢ (የሳንባ ቲቢ) የሰውነታችንን የሳንባ ክፍል የሚያጠቃ በሽታ ሲሆን ይህ በሽታ በመላው አለም ህመም እና ሞትን ከሚያስከትሉ ዋና ዋና የጤና ችግሮች አንዱ ነው፡፡ ሀገራችን ኢትዮጵያ በቲቢ በሽታ በከፍተኛ ደረጃ ከተጠቁት ሀገራት አንዷ ናት፡፡ አብዛኛዎቹ የቲቢ በሽታ ህመምተኞች የሚጠቁት ማይኮባክቴሪየም ቱበርኩሎሲስ በሚባል የባክቴሪያ ዝሪያ አይነት ነው፡፡ የሚተላለፈውም በትንፋሽ ሲሆን አብዛኛውን ጊዜ በበሽታው የተጠቁ ግለሰብ በሚስል እና በሚያስነጥስ ጊዜ ነው፡፡

ከቅርብ ጊዜ ወዲህ መድሀኒቱን የተለማመደ የቲቢ ዝርያ በመስፋፋት ላይ ይገኛል፡፡ ይህም የችግሩን መጠን ከፍ ከማድረጉም በላይ በሽታውን ለመከላከል እና ለመቆጣጠር የሚደረገውን ጥረት አዳጋች ያደርገዋል፡፡ በላቦራቶሪ ምርመራ የተደገፈ የህመም መንስኤው ላይ የሚደረግ ጥናት ጠቃሚ መረጃዎችን በማመንጨት በሽታውን ለመከላከል እና ለመቆጣጠር ከፍተኛ እገዛ ያደርጋል፡፡ በመሆኑም ይህ ጥናት የቲቢ በሽታን ጫናውንና ስርጭቱን ለማጥናት የሚካሄድ ጥናት ሲሆን በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ ላይ ትኩረት ሰጥቶ ይካሄዳል፡፡

የጥናቱ አላማ

የቲቢ በሽታ (በተለይም መድሀኒት በተለማመደ የቲቢ በሽታ) ስርጭት እና ጫና ላይ መረጃ ማቅረብ ነው፡፡

የጥናቱ ክንውን ሰነ-ስርአት

ለጥናቱ የሚወስደው የናሙና አይነት አከታ ነው፡፡ ይህም የአከታ ናሙና ደግሞ ለመደበኛ የቲቢ የላቦራቶሪ ምርመራ የሚሰጥ በመሆኑ በጥናቱ ምክንያት የተለየ የሚወሰድ ናሙና የለም፡፡ በመሆኑም በጥናቱ ዉስጥ እንድትሳተፍ/ፊ ፈቃደኝነትህ/ሽ ይጠየቃል፡፡ ስለጥናቱ በቂ መረጃ አግኝተህ/ሽ ፈካደኝነትህ/ሽን ስትገልጽ/ጪ የፈቃደኝነት ቅፁን ሞልተህ/ሽ ትፈርምበታለህ/ትፈርሚበታለሽ/፡፡ በጥናቱም ተሳታፊ ትሆናለህ/ትሆኛለሽ፡፡ የሳንባ ቲቢ በሽታ እንዳለብህ/እንዳለብሽ በሃኪም ከተገመተ ሶስት የአከታ ናሙና ለምርመራ እንድትሰጥ/አንድትሰጪ ትጠየቃለህ/ትጠየቂያለሽ/፡፡ የምርመራው ዉጤት የ ቲቢ በሽታ እንዳለብህ/እንዳለብሽ ካረጋገጠ የ ኤች አይ ቪ ምርመራ እንድታደርግ/እንድታደርጊ ትጠየቃለህ/ትጠየቂያለሽ፡፡ ዉጤቱም ለጥናቱ አገልግሎት ይውላል፡፡ አከታውን የሚሰበስበው የላቦራቶሪ ባለሙያ ሲሆን የሚሰበሰበው ለዚህ ስራ ተብሎ በተዘጋጀ እቃ (አነስተኛ ጣሳ) ነው፡፡ የአከታ ናሙናው ለአንተ/ለአንቺ የህክምና ምርመራና የታቀደውን ጥናት ለማካሄድ ይውላል፡፡ ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆችም ይደረግልሃል/ይደረግልሻል፡፡ቃለ መጠይቁ የሚካሄደው በነርስ ሲሆን የሚከናወነውም ምቾቶትን በጠበቀ ገለል ባለ ስፍራ ነው፡፡

ሰጋት እና ተከታይ ውሰብሰብ የጤና ችግሮች

ከጥናቱ ጋር በተያያዘ በእርስዎ ላይ የሚደርስ ከባድም ሆነ መጠነኛ ጉዳት የለም፡፡ ምክንያቱም ጥናቱ ከእርስዎ የሚጠይቀው የአክታ ናሙና ብቻ እንዲሰጡ ነው፡፡ ይህ ደግሞ መደበኛ የቲቢ ላቦራቶሪ ምርመራ ሲያደርጉ የሚጠየቁትና የሚሰጡት ናሙና ነው፡፡

የሚገኙ ጥቅሞች

እርስዎ በዚህ ጥናት ውስጥ ተሳታፊ በመሆንዎ እና በጥናት ውስጥ ለመሳተፍ በነ ፈቃድ በማሳየትዎ ከጥናቱ በቀጥታ የሚያገኙት ጥቅም አይኖርም፣ ከጥናቱ ጋር በተያያዘ የሚከፈል ማበረታቻ አይኖርም፡፡ ሆኖም ግን ከጥናቱ የሚገኘው ውጤት የቲቢ በሽታ ስርጭትን በማወቅ ረገድ ለሀገሪቷ ከፍተኛ አስተዋጽኦ አለው፡፡ ለበሽታው መንስኤ የሆኑትን የባክቴሪያ ዝርያዎች ለማወቅ ወይም ከዚህ ጋር ተያያዥ ለሆነው ምርመራ ወጪ ምንም አይነት ክፍያ እንዲፈጽሙ አይጠየቁም፡፡ የቲቢ በሽታ ምርመራ እና ህክምና በሀገሪቱ በነጻ ነው የሚሰጠው፡፡ ስለዚህ ለምርመራም ሆነ ለህክምናዎ ክፍያ አይጠየቁም፡፡ ነገር ግን በቲቢ በሽታ ምክንያት አልጋ ይዘው እንዲታከሙ ከተደረገ ለዚህ አገልግሎት የጤና ድርጅቱ የሚጠይቀውን መክፈል ይጠበቅቦታል፡፡

ከጥናቱ ስለመውጣት

የጥናቱ ተሳታፊዎች የጥናቱን ምንነት እንዲያውቁት ከተደረገ በኋላ ፈቃደኝነታቸውን እንዲገልጹ ይጠየቃሉ፡፡ ሆኖም ግን በዚህ ጥናት ውስጥ ለመሳተፍ የሰጡትን ፈቃደኝነት በማንኛውም ግዜ ሊሰርዙት ይችላሉ፡፡ የጥናቱ ተሳታፊ ራሱን ከጥናቱ በማግለሉ በቀጣይነት በሚያገኘው የጤና እንክብካቤ ላይ ምንም አይነት ተጽእኖ አይኖረውም፡፡

ሚስጥራዊነት

ማንኛውም ማንነትህን/ማንነትሽን የሚገልጽ መረጃ ቁልፍ ባለው መሳቢያ/ሎከር/ ዉስጥ ስለሚቀመጥ ሚስጥራዊነቱ የተጠበቀ ነው፡፡ በዚህ ጥናት ላይ በሚዘጋጅ በማንኛውም ሪፖርት ላይ ግለሰባዊ መረጃዎች አይካተቱም፡፡ ሁሉም የምርመራ ውጤቶች በናሙናዎቹ ላይ በሚጻፍ ድብቅ ስያሜዎች ላይ በመመስረት በሚስጥራዊነት ይጠበቃሉ፡፡

የጥናቱ የግኙኝነት አድራሻዎች

ተ.ቁ	ስም	አድራሻ
1.	አቶ ያሬድ መርእድ	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት አ.አ አርሙር ሃንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0916823701 ኢሜይል yaredmerid@yahoo.com
2.	ዶ/ር ይምጡበዝናሽ ወ/አማኑኤል	አዲስ አበባ ዩኒቨርሲቲ የህክምና ት/ቤት ስልክ ቁጥር 0911225832 ኢሜይል yimtuwa@gmail.com
3.	ዶ/ር አብርሀም አሰፋ	አርሙር ሃንሰን የምርምር ኢንስቲትዩት አ.አ ስልክ ቁጥር 0911247425 ኢሜይል aseffaa@gmail.com
የ አለርት/አርሙር ሃንሰን የምርምር ኢንስቲቱዩት የምርምር ስነምግባር ኮሚቴ አድራሻ		ስልክ ቁጥር 0118-962183

Consent form for Health Institute study (Amharic version)

<u>በማወቅ የሚሰጥ የፈቃደኝነት ቅጽ (ለአዋቂ የጥናት ተሳታፊ)</u>

አዲስ አበባ ዩኒቨርሲቲ ከአርሙር ሀንሰን የምርምር ተቋም፣ ከኦሮሚያ እና ደቡብ ጤና ቢሮዎች ጋር በመተባበር በቲቢ በሽታ ስርጭት አና መድሃኒቱን በተላመደ የቲቢ በሽታ ላይ ጥናት ለማድረግ አቅዷል፡፡

በዚህ ጥናት ውስጥ እንድሳተፍ ጥያቄ ቀርቦልኛል፡፡ በበሽታው ተይዤ የታመምኩ ከሆነ እና በሀኪሜ ከታዘዘ አክታ እንደምሰጥ በሚገባ ከተብራራልኝ በኋላ ተረድቼአለሁ፡፡ በዚህ ጥናት የመሳተፍም ሆነ ያለመሳተፍ መብት እንዳለኝ ዝርዝር መረጃ ተሰጥቶኛል፡፡ ከዚህም ሌላ በጥናቱ ውስጥ በተሳታፊነት ለመቀጠል ፍላጎት ከሌለኝ በማንኛውም ጊዜ ጥናቱን ለማቋረጥ እንደምችል እና ጥናቱን ለማቋረጥ መወሰኔን በሚደረግልኝ የህክምና ክትትል እና ክንውን ላይ ምንም አይነት ተጽእኖ እንደማይኖረው ተነግሮኛል፡፡ ከዚህም ሌላ ተጨማሪ ማብራሪያ እንዲሰጠኝ በጠየቅኳቸው ላይ ማብራሪያ ተሰጥቶኛል፡፡ በመሆኑም በዚህ ጥና ውስጥ ለመሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡ እነኝህም፤ሶስት አክታ ናሙና እንደምሰጥ፤ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆች እንደሚደረግልኝ፤ የኤች አይቪ ምርመራ ዉጤትን ጨምሮ የበሽታዬን ሁኔታ የሚገልጽ መረጃ ለጥናቱ እንደሚውል ተረድቻለሁ፡፡ ከእኔ የሚወሰደው የግል መረጃ በሚስጥራዊነት እንደሚጠበቅም ተገልፆልኛል፡፡ በመሆኑም ይህን ተረድቼ በዚህ ጥናት ውስጥ ለመሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡

የተሳታፊ ስም----------ፊርማ---------- ቀን--------

የህኪሙ ስም ----------ፊርማ--------ቀን----------

የምስክሩ ስም---------- ፊርማ ------ቀን----------

<u>በማወቅ የሚሰጥ የፈቃደኝነ ቅጽ (ለወላጅ /አሳዳጊ)</u>

አዲስ አበባ ዩኒቨርሲቲ ከአርሙር ሀንሰን የምርምር ተቋም፣ ከኦሮሚያ እና ደቡብ ጤና ቢሮዎች ጋር በመተባበር በቲቢ በሽታ ስርጭት አና መድሃኒቱን በተላመደ የቲቢ በሽታ ላይ ጥናት ለማድረግ አቅዷል፡፡

ልጄ በዚህ ጥናት ውስጥ እንዲሳተፍ ጥያቄ ቀርቦልኛል፡፡ ልጄ በዚህ በሽታ ተይዞ ከሆነና በሀኪሙ ከታዘዘ አክታ እንደሚሰጥ ከተብራራልኝ በኋላ ተረደረቼአለሁ፡፡ በዚህ ጥናት ልጄ እንዲሳተፍም ሆነ እንዳይሳተፍ የማድረግ መብት እንዳለኝም ዝርዝር መረጃ ተሰጥቶኛል፡፡ ከዚህም ሌላ ልጄ በጥናት ውስጥ በተሳታፊነት ለመቀጠል ፍላጎት ከሌለኝ በማንኛውም ግዜ ጥናቱን ለማቋረጥ እንደምችልና ጥናቱን እንዲያቋርጥ በመወሰኔ በሚደረግለት የህክምና ክትትል እና ክንውን ላይ ምንም አይነት ተጽእኖ እንደማይኖረው ተነግሮኛል፡፡ ከዚህም ሌላ ተጨማሪ ማብራያ እንዲሰጠኝ በጠየቅኳቸው ጉዳዮች ላይ ማብራሪያ ተሰጥቶኛል፡፡ እነኝህም፤ልጄ ሶስት አክታ ናሙና እንደሚሰጥ፤ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆች እንደሚደረግለት ፤ የኤች አይቪ ምርመራ ዉጤትን ጨምሮ የልጄን የበሽታ ሁኔታ የሚገልጽ መረጃ ለጥናቱ እንደሚውል ተረድቻለሁ፡፡ ከልጄ የሚወሰደው የግል መረጃ በሚስጥራዊነት እንደሚጠበቅም ተገልፆልኛል፡፡ በመሆኑም ይህን ተረድቼ ልጄ በዚህ ጥናት ውስጥ እንዲሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡

የወላጅ /አሳዳጊ ስም----------ፊርማ----------ቀን----------

የህኪሙ ስም ----------ፊርማ--------ቀን----------

የምስክሩ ስም---------- ፊርማ ------ቀን----------

<u>በማወቅ የሚሰጥ የፈቃደኝነት ቅጽ (ለህፃናት የጥናት ተሳታፊ)</u>

አዲስ አበባ ዩኒቨርሲቲ ከአርሙር ሀንሰን የምርምር ተቋም፣ ከኦሮሚያ እና ደቡብ ጤና ቢሮዎች ጋር በመተባበር በቲቢ በሽታ ስርጭት አና መድሃኒቱን በተላመደ የቲቢ በሽታ ላይ ጥናት ለማድረግ አቅዷል፡፡

በዚህ ጥናት ውስጥ እንድሳተፍ ጥያቄ ቀርቦልኛል፡፡ በበሽታው ተይዤ የታመምኩ ከሆነ እና በሀኪሜ ከታዘዘ አክታ እንደምሰጥ በሚገባ ከተብራራልኝ በኋላ ተረድቼአለሁ፡፡ በዚህ ጥናት የመሳተፍም ሆነ ያለመሳተፍ መብት እንዳለኝ ዝርዝር መረጃ ተሰጥቶኛል፡፡ ከዚህም ሌላ በጥናቱ ውስጥ በተሳታፊነት ለመቀጠል ፍላጎት ከሌለኝ በማንኛውም ጊዜ ጥናቱን ለማቋረጥ እንደምችል እና ጥናቱን ለማቋረጥ መወሰኔን በሚደረግልኝ የህክምና ክትትል እና ክንውን ላይ ምንም አይነት ተጽእኖ እንደማይኖረው ተነግሮኛል፡፡ ከዚህም ሌላ ተጨማሪ ማብራሪያ እንዲሰጠኝ በጠየቅኳቸው ላይ ማብራሪያ ተሰጥቶኛል፡፡ በመሆኑም በዚህ ጥና ውስጥ ለመሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡ እነኝህም፤ሶስት አክታ ናሙና እንደምሰጥ፤ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆች እንደሚደረግልኝ፤ የኤች አይቪ ምርመራ ዉጤትን ጨምሮ የበሽታዬን ሁኔታ የሚገልጽ መረጃ ለጥናቱ እንደሚውል ተረድቻለሁ፡፡ ከእኔ የሚወሰደው የግል መረጃ በሚስጥራዊነት እንደሚጠበቅም ተገልፆልኛል፡፡ በመሆኑም ይህን ተረድቼ በዚህ ጥናት ውስጥ ለመሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡

የተሳታፊ ስም----------ፊርማ------ቀን----------

የሀኪሙ ስም ----------ፊርማ----------ቀን----------

የምስክሩ ስም----------ፊርማ ------ቀን----------

Consent form for Community Study (Amharic version)

<u>በማወቅ የሚሰጥ የፈቃደኝነት ቅጽ (ለአዋቂ _>18 አመት)</u>

አዲስ አበባ ዩኒቨርሲቲ ከአርሙር ሀንሰን የምርምር ተቋም፣ ከኦሮሚያ እና ደቡብ ጤና ቢሮዎች ጋር በመተባበር በቲቢ በሽታ ስርጭት አና መድሃኒቱን በተላመደ የቲቢ በሽታ ላይ ጥናት ለማድረግ አቅዷል፡፡

በዚህ ጥናት ውስጥ እንድሳተፍ ጥያቄ ቀርቦልኛል፡፡ የቲቢ በሽታ እንዳለብኝ በሃኪም ከተገመተ አከታ እንደምሰጥ በሚገባ ከተብራራልኝ በኋላ ተረድቼአለሁ፡፡ የምርመራው ዉጤት የ ቲቢ በሽታ እንዳለብኝ ካረጋገጠ የ ኤች አይ ቪ ምርመራ እንደማደርግልኝና ዉጤቱም ለጥናቱ አገልግሎት እንደሚውል ተገልፆልኛል፡፡ በዚህ ጥናት የመሳተፍም ሆነ ያለመሳተፍ መብት እንዳለኝ ዝርዝር መረጃ ተሰጥቶኛል፡፡ ከዚህም ሌላ በጥናቱ ውስጥ በተሳታፊነት ለመቀጠል ፍላጎት ከሌለኝ በማንኛውም ጊዜ ጥናቱን ለማቋረጥ እንደምችል እና ጥናቱን ለማቋረጥ መወሰኔን በሚደረግልኝ የህክምና ክትትል እና ክንውን ላይ ምንም አይነት ተጽእኖ እንደማይኖረው ተነግሮኛል፡፡ ከዚህም ሌላ ተጨማሪ ማብራሪያ እንዲሰጠኝ በጠየቅኳቸው ላይ ማብራሪያ ተሰጥቶኛል፡፡ በመሆኑም በዚህ ጥና ውስጥ ለመሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡ እነኝህም፤ሁለት አከታ ናሙና እንደምሰጥ፤ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆች እንደሚደረግልኝ፤ የኤች አይቪ ምርመራ ዉጤትን ጨምሮ የበሽታዬን ሁኔታ የሚገልጽ መረጃ ለጥናቱ እንደሚውል ተረድቻለሁ፡፡ ከእኔ የሚወሰደው የግል መረጃ በሚስጥራዊነት እንደሚጠበቅም ተገልፆልኛል፡፡ በመሆኑም ይህን ተረድቼ በዚህ ጥናት ውስጥ ለመሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡

የተሳታፊ ስም----------ፊርማ-------ቀን----------

የህኪሙ ስም ----------ፊርማ-------ቀን----------

የምስክሩ ስም----------ፊርማ -------ቀን----------

<u>በማወቅ የሚሰጥ የፈቃደኝን ቅጽ (ለወላጅ /አሳዳጊ 5-11 አመት)</u>

አዲስ አበባ ዩኒቨርሲቲ ከአርሙር ሀንሰን የምርምር ተቋም፣ ከአሮሚያ እና ደቡብ ጤና ቢሮዎች ጋር በመተባበር በቲቢ በሽታ ስርጭት አና መድሃኒቱን በተላመደ የቲቢ በሽታ ላይ ጥናት ለማድረግ አቅዷል፡፡

ልጄ በዚህ ጥናት ውስጥ እንዲሳተፍ ጥያቄ ቀርቦልኛል፡፡ ልጄ የቲቢ በሽታ እንዳለነት በሃኪም ከተገመተ አክታ እንደምሰጥ በሚገባ ከተብራራልኝ በኋላ ተረድቼአለሁ፡፡ የምርመራው ዉጤት የ ቲቢ በሽታ እንዳለበት ካረጋገጠ ልጄ የ ኤች አይ ቪ ምርመራ እንደማደለግለትና ዉጤቱም ለጥናቱ አገልግሎት እንደሚውል ተገልፆልኛል፡፡ በዚህ ጥናት ልጄ እንዲሳተፍም ሆነ እንዳይሳተፍ የማድረግ መብት እንዳለኝም ዝርዝር መረጃ ተሰጥቶኛል፡፡ ከዚህም ሌላ ልጄ በጥናት ውስጥ በተሳታፊነት ለመቀጠል ፍላጎት ከሌለኝ በማንኛውም ግዜ ጥናቱን ለማቋረጥ እንደምችልና ጥናቱን እንዲያቋርጥ በመወሰኔ በሚደረግለት የህክምና ክትትል እና ክንውን ላይ ምንም አይነት ተጽእኖ እንደማይኖረው ተነግሮኛል፡፡ ከዚህም ሌላ ተጨማሪ ማብራያ እንዲሰጠኝ በጠየቅኳቸው ጉዳዮች ላይ ማብራሪያ ተሰጥቶኛል፡፡ እነኝህም፤ልጄ ሁለት አክታ ናሙና እንደሚሰጥ፤ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆች እንደሚደረግለት ፤ የኤች አይቪ ምርመራ ዉጤትን ጨምሮ የልጄን የበሽታ ሁኔታ የሚገልጽ መረጃ ለጥናቱ እንደሚውል ተረድቻለሁ፡፡ ከልጄ የሚወሰደው የግል መረጃ በሚስጥራዊነት እንደሚጠበቅም ተገልፆልኛል፡፡ በመሆኑም ይህን ተረድቼ ልጄ በዚህ ጥናት ውስጥ እንዲሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡

የወላጅ /አሳዳጊ ስም---------- ፊርማ----------
--------ቀን----------

የህኪሙ ስም ----------ፊርማ------ ቀን----------

የምስክሩ ስም----------ፊርማ -------ቀን----------

<u>በማወቅ የሚሰጥ የፈቃደኝነት ቅጽ (ለህፃናት የጥናት ተሳታፊ-12-17 አመት)</u>

አዲስ አበባ ዩኒቨርሲቲ ከአርሙር ሀንሰን የምርምር ተቋም፣ ከኦሮሚያ እና ደቡብ ጤና ቢሮዎች ጋር በመተባበር በቲቢ በሽታ ስርጭት አና መድሃኒቱን በተላመደ የቲቢ በሽታ ላይ ጥናት ለማድረግ አቅዷል፡፡

በዚህ ጥናት ውስጥ እንድሳተፍ ጥያቄ ቀርቦልኛል፡፡ የቲቢ በሽታ እንዳለብኝ በሃኪም ከተገመተ አከታ እንደምሰጥ በሚገባ ከተብራራልኝ በኋላ ተረድቼአለሁ፡፡ የምርመራው ዉጤት የ ቲቢ በሽታ እንዳለብኝ ካረጋገጠ የ ኤች አይ ቪ ምርመራ እንደማደርግልኝና ዉጤቱም ለጥናቱ አገልግሎት እንደሚውል ተገልፆልኛል፡፡ በዚህ ጥናት የመሳተፍም ሆነ ያለመሳተፍ መብት እንዳለኝ ዝርዝር መረጃ ተሰጥቶኛል፡፡ ከዚህም ሌላ በጥናቱ ውስጥ በተሳታፊነት ለመቀጠል ፍላጎት ከሌለኝ በማንኛውም ጊዜ ጥናቱን ለማቋረጥ እንደምችል እና ጥናቱን ለማቋረጥ መወሰኔን በሚደረግልኝ የህክምና ክትትል እና ክንውን ላይ ምንም አይነት ተጽእኖ እንደማይኖረው ተነግሮኛል፡፡ ከዚህም ሌላ ተጨማሪ ማብራሪያ እንዲሰጠኝ በጠየቅኳቸው ላይ ማብራሪያ ተሰጥቶኛል፡፡ በመሆኑም በዚህ ጥና ውስጥ ለመሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡ እነኝህም፤ሁለት አከታ ናሙና እንደምሰጥ፤ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆች እንደሚደረግልኝ፤ የኤች አይቪ ምርመራ ዉጤትን ጨምሮ የበሽታዬን ሁኔታ የሚገልጽ መረጃ ለጥናቱ እንደሚውል ተረድቻለሁ፡፡ ከእኔ የሚወሰደው የግል መረጃ በሚስጥራዊነት እንደሚጠበቅም ተገልፆልኛል፡፡ በመሆኑም ይህን ተረድቼ በዚህ ጥናት ውስጥ ለመሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡

የተሳታፊ ስም----------ፊርማ----------ቀን-------

የህኪሙ ስም ----------ፊርማ--------ቀን----------

የምስክሩ ስም----------ፊርማ --------ቀን----------

Consent form for Prison study (Amharic version)

<u>በማወቅ የሚሰጥ የፈቃደኝነት ቅጽ (ለአዋቂ የጥናት ተሳታፊ _>18 አመት))</u>

አዲስ አበባ ዩኒቨርሲቲ ከአርሙር ሀንሰን የምርምር ተቋም፣ ከኦሮሚያ እና ደቡብ ጤና ቢሮዎች ጋር በመተባበር በቲቢ በሽታ ስርጭት አና መድሃኒቱን በተላመደ የቲቢ በሽታ ላይ ጥናት ለማድረግ አቅዷል፡፡

በዚህ ጥናት ውስጥ እንድሳተፍ ጥያቄ ቀርቦልኛል፡፡ የቲቢ በሽታ እንዳለብኝ በሃኪም ከተገመተ አከታ እንደምሰጥ በሚገባ ከተብራራልኝ በኋላ ተረድቼአለሁ፡፡ የምርመራው ዉጤት የ ቲቢ በሽታ እንዳለብኝ ካረጋገጠ የ ኤች አይ ቪ ምርመራ እንደማደርግልኝና ዉጤቱም ለጥናቱ አገልግሎት እንደሚውል ተገልፆልኛል፡፡ በዚህ ጥናት የመሳተፍም ሆነ ያለመሳተፍ መብት እንዳለኝ ዝርዝር መረጃ ተሰጥቶኛል፡፡ ከዚህም ሌላ በጥናቱ ውስጥ በተሳታፊነት ለመቀጠል ፍላጎት ከሌለኝ በማንኛውም ጊዜ ጥናቱን ለማቋረጥ እንደምችል እና ጥናቱን ለማቋረጥ መወሰኔን በሚደረግልኝ የህክምና ክትትል እና ክንውን ላይ ምንም አይነት ተጽእኖ እንደማይኖረው ተነግሮኛል፡፡ ከዚህም ሌላ ተጨማሪ ማብራሪያ እንዲሰጠኝ በጠየቅኳቸው ላይ ማብራሪያ ተሰጥቶኛል፡፡ በመሆኑም በዚህ ጥና ውስጥ ለመሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡ እነኝህም፤ሶስት አከታ ናሙና እንደምሰጥ፤ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆች እንደሚደረግልኝ፤ የኤች አይቪ ምርመራ ዉጤትን ጨምሮ የበሽታዬን ሁኔታ የሚገልጽ መረጃ ለጥናቱ እንደሚውል ተረድቻለሁ፡፡ ከእኔ የሚወሰደው የግል መረጃ በሚስጥራዊነት እንደሚጠበቅም ተገልፆልኛል፡፡ በመሆኑም ይህን ተረድቼ በዚህ ጥናት ውስጥ ለመሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡

የተሳታፊ ስም----------ፊርማ----------ቀን-------

የህኪሙ ስም ----------ፊርማ------ቀን-------

የምስክሩ ስም---------- ፊርማ --------ቀን-------

<u>በማወቅ የሚሰጥ የፈቃደኝን ቅጽ (ለወላጅ /አሳዳጊ, 5-11 አመት)</u>

አዲስ አበባ ዩኒቨርሲቲ ከአርሙር ሀንሰን የምርምር ተቋም፣ ከአሮሚያ እና ደቡብ ጤና ቢሮዎች ጋር በመተባበር በቲቢ በሽታ ስርጭት አና መድሃኒቱን በተላመደ የቲቢ በሽታ ላይ ጥናት ለማድረግ አቅዷል፡፡

ልጄ በዚህ ጥናት ውስጥ እንዲሳተፍ ጥያቄ ቀርቦልኛል፡፡ ልጄ የቲቢ በሽታ እንዳለነት በሃኪም ከተገመተ አክታ እንደምሰጥ በሚገባ ከተብራራልኝ በኋላ ተረድቼአለሁ፡፡ የምርመራው ዉጤት የ ቲቢ በሽታ እንዳለበት ካረጋገጠ ልጄ የ ኤች አይ ቪ ምርመራ እንደማደለግለትና ዉጤቱም ለጥናቱ አገልግሎት እንደሚውል ተገልፆልኛል፡፡ በዚህ ጥናት ልጄ እንዲሳተፍም ሆነ እንዳይሳተፍ የማድረግ መብት እንዳለኝም ዝርዝር መረጃ ተሰጥቶኛል፡፡ ከዚህም ሌላ ልጄ በጥናት ውስጥ በተሳታፊነት ለመቀጠል ፍላጎት ከሌለኝ በማንኛውም ግዜ ጥናቱን ለማቋረጥ እንደምችልና ጥናቱን እንዲያቋርጥ በመወሰኔ በሚደረግለት የህክምና ክትትል እና ክንውን ላይ ምንም አይነት ተጽእኖ እንደማይኖረው ተነግሮኛል፡፡ ከዚህም ሌላ ተጨማሪ ማብራያ እንዲሰጠኝ በጠየቅኳቸው ጉዳዮች ላይ ማብራሪያ ተሰጥቶኛል፡፡ እነኝህም፤ልጄ ሶስት አክታ ናሙና እንደሚሰጥ፤ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆች እንደሚደረግለት ፤ የኤች አይቪ ምርመራ ዉጤትን ጨምሮ የልጄን የበሽታ ሁኔታ የሚገልጽ መረጃ ለጥናቱ እንደሚውል ተረድቻለሁ፡፡ ከልጄ የሚወሰደው የግል መረጃ በሚስጥራዊነት እንደሚጠበቅም ተገልፆልኛል፡፡ በመሆኑም ይህን ተረድቼ ልጄ በዚህ ጥናት ውስጥ እንዲሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡

የወላጅ /አሳዳጊ ስም----------ፊርማ----------ቀን-------

የህኪሙ ስም ---------- ፊርማ-------ቀን-------

የምስክሩ ስም----------ፊርማ ---------ቀን-------

<u>በማወቅ የሚሰጥ የፈቃደኝነት ቅጽ (ለህፃናት የጥናት ተሳታፊ,12-17 አመት))</u>

አዲስ አበባ ዩኒቨርሲቲ ከአርሙር ሀንሰን የምርምር ተቋም፣ ከኦሮሚያ እና ደቡብ ጤና ቢሮዎች ጋር በመተባበር በቲቢ በሽታ ስርጭት አና መድሃኒቱን በተላመደ የቲቢ በሽታ ላይ ጥናት ለማድረግ አቅዷል፡፡

በዚህ ጥናት ውስጥ እንድሳተፍ ጥያቄ ቀርቦልኛል፡፡ በዚህ ጥናት ውስጥ እንድሳተፍ ጥያቄ ቀርቦልኛል፡፡ የቲቢ በሽታ እንዳለብኝ በሃኪም ከተገመተ አከታ እንደምሰጥ በሚገባ ከተብራራልኝ በኋላ ተረድቼአለሁ፡፡ የምርመራው ዉጤት የ ቲቢ በሽታ እንዳለብኝ ካረጋገጠ የ ኤች አይ ቪ ምርመራ እንደማደርግልኝና ዉጤቱም ለጥናቱ አገልግሎት እንደሚውል ተገልፆልኛል፡፡ በዚህ ጥናት የመሳተፍም ሆነ ያለመሳተፍ መብት እንዳለኝ ዝርዝር መረጃ ተሰጥቶኛል፡፡ ከዚህም ሌላ በጥናቱ ውስጥ በተሳታፊነት ለመቀጠል ፍላጎት ከሌለኝ በማንኛውም ጊዜ ጥናቱን ለማቋረጥ እንደምችል እና ጥናቱን ለማቋረጥ መወሰኔን በሚደረግልኝ የህክምና ክትትል እና ክንውን ላይ ምንም አይነት ተጽእኖ እንደማይኖረው ተነግሮኛል፡፡ ከዚህም ሌላ ተጨማሪ ማብራሪያ እንዲሰጠኝ በጠየቅኳቸው ላይ ማብራሪያ ተሰጥቶኛል፡፡ በመሆኑም በዚህ ጥና ውስጥ ለመሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡ እነኝህም፤ሶስት አከታ ናሙና እንደምሰጥ፤ስለ ግላዊና ማህበራዊ ጉዳዮች እና ስለ ቲቢ በሽታ መጠይቆች እንደሚደረግልኝ፤ የኤች አይቪ ምርመራ ዉጤትን ጨምሮ የበሽታዬን ሁኔታ የሚገልጽ መረጃ ለጥናቱ እንደሚውል ተረድቻለሁ፡፡ ከእኔ የሚወሰደው የግል መረጃ በሚስጥራዊነት እንደሚጠበቅም ተገልፆልኛል፡፡ በመሆኑም ይህን ተረድቼ በዚህ ጥናት ውስጥ ለመሳተፍ በራሴ ፈቃደኝነት ተስማምቻለሁ፡፡

የተሳታፊ ስም----------ፊርማ------ቀን----------

የህኪሙ ስም ----------ፊርማ------ቀን----------

የምስክሩ ስም----------ፊርማ ------ቀን----------

Questioners (Amharic version)

የአማርኛ ቃለ መጠየቅ

ምህጻረ ቃል_____ የጥናቱ ኮድ_____ ካርድ ቁጥር._____]

<u>ክፍል አንድ አጠቃላይ ጥያቄ</u>

ተ.ቁ	ጥያቄዎች	መልስ	ዝለል
1	እድሜ በአመት	----------አመት	
2	ጾታ	2. ሴት 3. ወንድ	
3	ቋሚ የመኖሪያ ቦታ	1. ከተማ ወረዳ.....) ቀበሌ.....) 2. ገጠር ወረዳ.....) ገጠር.....)	
4	የጋብቻ ሁኔታ	5. ያላገባ 6. ያገባ 7. የፈታ 8. የሞተበት 9. የተለያዩ 10. ሌላ ካለ….	
5	የትምህርት ሁኔታ	5. ያልተማረ 6. አንደኛ ደረጃ (1-8) 7. ሁለተኛ ደረጃ (9-10/12) 8. ኮሌጅ (10+ or 12+) 9. የተለየ ካለ	
6	የስራ ሁኔታ (ይህ ጥያቄ የሚቀርበው ለታራሚ ከሆነ የስራ ሁኔታ ከማረሚያ በፊት ያለውን ይመለከታል)	8. የመንግስት ሰራተኛ 9. ገበሬ 10. የቀን ሰራተኛ 11. ተማሪ የቤት እመቤት 12. ስራ ፈላጊ/ስራ የሌለው/ 13. ነጋዴ 14. ሌላ	

ክፍል ሁለት የቲቢ በሽታ ምልክቶች

1	ለሁለት ሳምንት እና ከዛ በላይ የቆየ ሳል አለብህ/ሽ?	2. የለም 3. አለ	
2	ለጥያቄው መልሱ አለ ከሆነ ለምን ያህል ሳምንት?	---------- ሳምንት	
3	ሳሉ አክታ አለው?	2. የለውም 3. አለው	
4	መልሱ አለው ከሆነ አክታው ደም የተቀላቀለበት ነው	2. አዎ 3. አይደለም	
5	ትኩሳት አለህ/ሽ?	2. የለም 3. አለ	
6	ትኩሳት ካለ ለምንያህል ሳምንት ቆየብህ/ሽ	---------- ሳምንት	
7	ማታ ማታ ላይ ያልብህል?	1. የለም 2. አለ	
8	ላብ ካለ ለምን ያህል ሳምንት ቆየብህ/ሽ?	---------- ሳምንት	
9	የምግብ ፍላጎትህ/ሽ ቀንሷል?	2. አልቀነሰም 3. አለ	
10	የምግብ ፍላጎትህ/ሽ ቀንሶ ከሆነ ይህ ከሆነ ምን ያህል ሳምንት ሆነው?	---------- ሳምንት	
11	ክብደት ቀንሰህል/ሻል?	2. አልቀነሰም 3. ቀንሷል	
12	የደረት ህመም አለብህ/ሽ?	2. የለብኝም 3. አለብኝ	
13	የደረት ህመም ካለብህ/ሽ ለምን ያህል ሳምንት ቆየብህ/ሽ?	---------- ሳምንት	
14	የመተንፈስ ችግር አለብህ/ሽ?	2. የለብኝም 3. አለብኝ	
15	የመተንፈስ ችግር ካለብህ/ሽ ለምን ያህል ሳምንት ቆየብህ/ሽ?	---------- ሳምንት	

ክፍል ሶስት ለቲቢ በሽታ የሚያጋጡ ሁኔታዎች

1	ከዚህ በፊት የቲቢ በሽታ ይዞህ/ሽ/ያውቃል?	2. አልያዘኝም 3. ይዞኛል	
2	ከታወቀ የቲቢ በሽተኛ ጋር የቅርብ ግንኙነት ነበረህ /ሽ?	2. አልነበረኝም 3. ነበረኝ	
3	በቤተሰብ ውስጥ የቲቢ በሽታ የያዘው ሰው አለ?	1. የለም 2. አለ	
4	የስኳር በሽታ አለብህ/ሽ/?	2. የለብኝም 3. አለብኝ	
5	ሲጋራ ታጨሳለህ/ሽ?	2. አላጨስም 3. አጨሳለሁ	
6	የምታጨስ/ሺ ከሆነ ለምን ያህል አመት?	---------- አመት	
7	ጫት ትቅማለህ/ሽ?	2. አልቅምም 3. እቅማለሁ	
8	የምትቅም/ ሚ ከሆነ ለምን ያህል ዓመት?	---------- አመት	
9	የአልኮል መጠጥ ትጠጣለህ/ሽ ?	2. አልጠጣም 3. እጠጣለሁ	
10	የምትጠጣ/ጪ/ ከሆነ ምን ያህል ጠርሙስ/ብርጭቆ በቀን /በሳምንት ትጠጣለህ/ሽ?	----------ቀን/ሳምንት	
11	ለምን ያህል አመታት ጠጣህ/ጠጣሽ?	---------- አመት	
12	የአስም በሽታ አለብህ/ሽ?	2. የለብኝም 3. አለብኝ	
13	የምትኖርበት ቤት ግርግዳው በምንድ ነው የተሰራው ?	2. በጭቃ/በጭቃ ጡብ 3. ሲሚንቶ	
14	የምትኖርበት ወለል በምድነው የተሰራው?	2. አፈር 3. ሲሚንቶ 4. ጣውላ 5. ሌላ------	
16.	የቤተሰብ አባላት ብዛት	----------	
17	የምትኖርበት ቤት መስኮት አለው?	2. የለውም 3. አለው	
18.	መስኮት ካለው መስኮቱ በምን ያህል ግዜ ነው የሚከፈተው?	3. አልፎ አልፎ 4. አንዳንድ ግዜ 5. ሁል ግዜ	
19.	የኤችአይቪ ውጤት (ከመዝገብ ላይ ተወስዶ የሚሞላ)	1. ፖዝቲቭ 2. ኔጋቲቭ	

ክፍል አራት፣ መድሀኒቱ ለተላመደ ቲቢ በሽታ የሚያጋልጡ ሁኔታዎች

1	ከዚህ ቀደም ለቲቢ በሽታ መድሀኒት ወስደህ/ሽ ታውቃለህ/ሽ?	2. አልወሰድኩም 3. ወስጃለሁ	
2	ለጥያቄ ቁጥር አንድ መልስህ/ሽ ወስጃለሁ ከሆነ የህክምናው ውጤት ምን ነበር?	4. መዳን 5. መድሀኒት መጨረስ 6. የመድሀኒት አለመስራት 7. መድሀኒት ማቋረጥ	
3	ለጥያቄ ቁጥር አንድ መልስህ /ሽ ወስጃለሁ ከሆነ በየትኛው ጤና ተቋም ነው ህክምናውን የተከታተልከው/ሽው?	3. በጤናጣቢያ 4. በሆስፒታል 5. በጤና ኬላ	
4	ህክምናውን የተከታተልከው በየት ህክምና ተቋም ነው?	2. በመንግስት 3. በግል	
5	ከዚህ ቀደም በማረሚያ ቤት ታስረህ ታውቃለህ?	2. አልታሰርኩም 3. ታስሬአለሁ	
6	ለጥያቄ ቁ.5 መልስህ ታስሬአለሁ ከሆነ ለምን ያህል ወር/አመት ?	---------- ወር/አመት	
7	ከዚህ ቀደም ሆስፒታል ተኝተህ /ሽ ታውቃለህ/ሽ?	2. አልተኛሁም 3. ተኝቻለሁ	
8	ለጥያቄ ቁ.7ተኝቼ ነበር ከሆነ ለምን ያህል ወር/አመት?	---------- አመት/ወር	
9	ለጥያቄ ቁ.7 መልስህ ተኝቼ ነበር ከሆነ በምን ምክንያት?	_____	
10	ከታወቀ መድሀኒቱ የተላመደ የቲቢ በሽተኛ ጋር የቅርብ ግንኙነት ነበረህ /ሽ?	3. አልነበረኝም 4. ነበረኝ 5. አላስታውስም	
11	በቤተሰቡ ውስጥ መድሀኒቱ የተላመደ የቲቢ በሽተኛ አለ ?	2. የለም 3. አለ	
12	የት ነው የምትኖረው/የምትኖሪው/?	5. በግሌ የመኖሪያ ቤት 6. ተከራይቼ 7. በዶርሜተሪ 8. ቤት አልባ 9. ሌላ-----	

ክፍል አምስት ፡ የማረሚያ ቤት ታሪክ እና ሁኔታ

1	ከቤተሰብ የምታገኘዉ/ኚው/ ጉብኝት እና ምግብ አለ?	1.የለም 2. ጉብኝት ብቻ 3. ምግብ ብቻ 4. ጉብኝት እና ምግብ	ወደ ጥያቄ ቁጥር-3
2	የቤተሰብ ጉብኝት እና ምግብ የሚመጣለህ /ሽ/ ከሆነ በሳምንት ስንት ቀን ምግብ ይመጣልሃ/ሻል/?	በ ----------ሳምንት	
3	በዚህ ማረሚያ ቤት ምን ያህል ጊዜ ቆይተሃል?	----------በወር	
4	በዚህ ማረሚያ ቤት ምን ያህል ጊዜ በተደጋጋሚ ጉበተሃል?	----------በጊዜ	
5	በሌላ ማረሚያ ቤት ጉበተህ ታውቃለህ?	1.አልገባሁም 2.ጉብቻለው	ወደ ጥያቄ ቁጥር-8
6	የጥያቄ ቁጥር 5 መልስ ጉብቻለው ከሆነ ስንት ጊዜ?	----------በጊዜ	
7	የጥያቄ ቁጥር 5 መልስ ጉብቻለው ከሆነ ምን ያህል ጊዜ ቆይተሃል?	----------በወር	
8	በአንድ ክፍል ውስጥ ከታወቀ የቲቢ (ሳንባ ቲቢ) በሽተኛ ጋር ነበርክ (ሽ) ወይም አሁን አለ?	1.አልነበርኩም 2.ነበርኩ 3.አላውቅም	ወደ ጥያቄ ቁጥር- 10
9	ለጥያቄ ቁጥር 8 መልስህ ነበርኩ ከሆነ ለምን ያህል ጊዜ?	----------በወር/በአመት	
10	በክፍልህ/ሽ/ ውስጥ በጣም የሚያስለው ሰው ነበር ወይም አለ?	1.የለም 2.አለ	ወደ ጥያቄ ቁጥር-12
11	ጥያቄ ቁጥር 10 መልስ አለ ከሆነ መልስህ/ሽ/ ለምን ያህል ጊዜ?	----------ሳምንት/ወር	
12	በአንተ/ቺ/ ክፍል ዉስጥ ምን ያህል ብዛት ያላቸው ታራሚዎች አሉ?	በ ----------ክፍል	
13	ክፍልህ/ሽ/ መስኮት አለው?	1.የለውም 2. አለው	ወደ ጥያቄ ቁጥር-15
14	ለጥያቄ ቁጥር 13 መልስህ/ሽ/ አለ ከሆነ ምን ያህል ጊዜ መስኮት ትከፍታለህ/ሽ/?	1.አልፎ አልፎ 2.አንዳንድ ጊዜ 3.ሁል ጊዜ	
15	በየምን ያህል ጊዜ ድግግሞሽ ከክፍል ውጭ ታሳልፋለህ/ለሽ/?	1.በፍፁም 2.አንዳንድ ጊዜ 3.በየቀኑ	
16	የመጠጫ ና የመመገቢያ እቃዎች በጋራ ወይስ በመዋዋስ ትጠቀማለህ/ሽ/?	1.አልጠቀምም 2. እጠቀማለው	

ክፍል ስድስት :- የህመም ታሪክ ሁኔታ

1	በአሁን ሰዓት የሚሰማህ ና የሚታይብህ የህመም ምልክቶች አሉህ/ሽ/?	1. የሉም 2. አሉ 3. ለይቼ መናገር አልችልም	
2	ለጥያቄ ቁ.1 መልስህ አሉ ከሆነ ምን አይነት ምልክቶች ናቸው ..... **አስተውል**:- እነዚህን ምልክቶች አትግለፃቸው እንደሁኔታዉ ግን ምርጫ ልትሰጥ ትችላላህ	1.ሳል 2.የደረት ህመም 3.የመተንፈስ ችግር 4.ትኩሳት 5.ከብደት መቀነስ 6.ማታማታ ማላብ 7.የምግብ ፈላጎት መቀነስ 8.ማቅለሽለሽ 9.ድካም 10.ሌላ...	
3	ሳል ከጀመረህ /ሽ/ ምን ያህል ጊዜ ሆነህ/ሽ/?	በ ---------ሳምንት	
4	አሁን ላለህ የህመም ምልክት ህክምና አግኝተሃል/ሻል/?	1.አላገኘውም ⟶ 2. አግንቻለው	ወደ ጥያቄ ቁጥር-5
5	ለጥያቄ ቁጥር 4 መልስህ/ሽ/ አግንቻለው ከሆነ የት?	1.ከማረሚያ ቤት ውስጥ ያለ ጤና ድርጅት 2. ማረሚያ ቤት ውጭ ያለ ክሊኒክ 3. ሁለቱም ጋር 4.ሌላ----------	
6	ምን ያህል ጊዜ በነዚህ መልክቶች ምክንያት ታይተሃል(በቁጥር 2 ጥያቄ በተዘረዘሩት)?	-------ጊዜ	
7	ለጥያቄ ቁጥር 4 መልስህ አላገኘሁም ከሆነ ለምን እንደሆነ ግለፅ?	----------	
8	በጥያቄ ቁጥር 2 ላይ የተገለፁት ምልክቶች እዚህ ማረሚያ ቤት ከመግባት/ሽ/ በፊት ነበሩ?	1.የሉም 2.አሉ	

9	ቲቢ በሽታ ተመርምረህ/ሽ/ ታውቃለህ/ሽ/?	1.አልተመረመርኩም 2.ተመርምሬአለው	
10	ለጥያቄ ቁጥር 9 መልስህ/ሽ/ ተመርምሬአለው ከሆነ መቼ?	1.ከማረሚያ ቤት በፊት 2.ማረሚያ ቤት ውስጥ 3.አላስታውስም	
11	ለጥያቄ ቁጥር 9 መልስህ/ሽ/ ተመርምሬአለው ከሆነ ህክምና ወስደሃል/ሻል/	1.አልወሰድኩም 2. ወስጃለው	
12	ለጥያቄ ቁጥር 11 መልስህ/ሽ/ ወስጃለው ከሆነ ሁሉንም እስከ መጨረሻው ወስድሃል/ሻል/?	1.አልጨረስኩም 2.ጨርሻለው	
13	ለጥያቄ ቁጥር 12 አልጨረስኩም ከሆነ ለምን?	———	
14	የታወቀ የጤና ችግር (ለምሳሌ ስኳር፣ደም ግፊት...ወዘተ) አለብህ/ሽ/?	1.የለም → 2.አለ 3.አላውቅም	ወደ ጥያቄ ቁጥር 16
15	ለጥያቄ ቁጥር 14 መልስህ/ሽ/ አለ ከሆነ ችግሮቹ ምንድናቸው?		
16	ለጥያቄ ቁጥር 14 መልስህ/ሽ/ አለ ከሆነ ህክምና እየወሰድክ /ሽ/ ነው?	1.አለወሰድኩም 2. ወስጃለው →	ወደ ጥያቄ ቁጥር 17
17	ለጥያቄ ቁጥር 16 መልስህ/ሽ/ አልወሰድኩም ከሆነ ለምን እንደሆነ ገለፅ?	———	

18	ሆስፒታል ተኝተህ ታውቃልህ/ሽ/?	1.አላውቅም ⟶ 2. አውቃለው	ወደ ቁጥር 21
19	ለጥያቄ ቁጥር 18 መልስህ/ሽ/ አውቃለው ከሆነ ለምን ያህል ጊዜ?	---------- ወር	
20	ለጥያቄ ቁጥር 18 መልስህ/ሽ/ አውቃለው በምን ምክንያት?	_____	
21	ከታወቀ የቲቢ በሽተኛ ጋር ግንኙነት በቤት ውስጥ ከማረሚያ ቤት በፊት ወይም ለጉበኝት በሚመጣበት ሰዓት አለህ/ሽ/?	1.የለም 2.አለ 3.አላስታውስም	
22	በአሁኑ ሰአት የቲቢ በሽታ መድሀኒት ትወስዳለህ(ሽ)	1.የለም 2.አለ	
23	መድሀኒቱን ከመጀመርህ በፊት የአክታ ምርመራ አድርገህ(ሽ) ዉጤት ተነግሮህል(ሻል)?	1.የለም 2.ተነግሮኛል 3.አላስታውስም	
24	ከተነገረህ(ሽ) ዉጤቱ ምን ነበር	----------	
25	አክታ አሰባሰብ(በናሙና ሰብሳቢዎች የሚሞላ) አስተውል:- ሲሰጡ ምልክት አድርግ !	1.ጠዋት 2.ከጠዋት ውጭ(2 ጊዜ) 3.አክታ የለም(ምክንያቱን ግለፅ)	

ክፍል ሰባት፡ የቲቢ በሽታን እውቀት በተመለከ

1. የቲቢ በሽታ መንስኤዎችን ያውቃሉ?

   ሀ. አላውቅም

   ለ. አውቃለሁ

4. መልስ አውቃለሁ ከሆነ መንስኤው ምንድነው?

   ----

5. የቲቢ በሽታ ከታመመ ሰው ወደ ጤነኛ ሰው ይተላለፋል ?

   ሀ. አይተላለፍም

   ለ. ይተላለፋል

6. መልሱ ይተላለፋ ከሆነ በምንድነው የሚተላፈው?

   ----

7. የቲቢ በሽታ ህክምና አለው?

   ሀ. የለውም

   ለ. አለው

8. ህክምና ካለው የቲቢ በሽታ ከታከመ ሙሉ ለሙሉ ለመዳን ይችላል?

   ሀ. አይችልም

   ለ. ይችላል

   ሐ. አላውቅም

9. የቲቢ በሽታ ካልታከመ የሚያመጣው ችግር አለ?

   ሀ. የለም

   ለ. አለ

10. ለጥያቄ 5 የመለሱት መልስ አለ ከሆነ የሚያመጣውችግር ምንድነው?

   ሀ. ለበሽተኛው ----------

ለ. ለአካባቢው ሰዎች----------

11. የቲቢ ህክምናን ማቋረጥ ችግር እንደሚያመጣ ያውቃሉ?

ሀ. አላውቅም

ለ. አውቃለሁ

12. ለጥያቄ ቁጥር 7 መልስ አውቃለሁ ከሆነ ምን አይነት ችግር ያመጣል?

_____

13. የቲቢ ህክምና ነጻ እንደሆነ ያውቃሉ?

ሀ. አላውቅም

ለ. አውቃለሁ

14. የቲቢ በሽታ መከላከያ መንገዶች ምንድናቸው?

_____

15. የቲቢ በሽታ ከማረሚያ ቤት ውስጥ እና ውጪ ያለውን የልዩነት ሁኔታን ያውቃሉ (ለማረሚያ ቤት እስረኛ ብቻ የሚቀርብ ጥያቄ)

_____

Gaaffilewwan

Ka'umsashakki _____kodiqoranno_____lakkkardii____

Kutaa 1. Amalawwanfakkihawwasumma

Lakki	Gaffi	Gareedeebii	Cheemsa
1	Umrii	--------	
2	Saala	0. Dhalaa 1. Dhiira	
3	Iddojireenya	0. Magaala 1. Baadiyya	
4.	Haalafudhaa	0. Qofaa 1. Kanfudhe 2. Walhiike 3. Irradu'e 4. Addanbahan	
5	Haalabarumsa	0. Hinbaranne 1. Sad.tokko.(1-8) 2. Sad.la(9-10ykn 12 3. Kolejii(10+ /12 4. Kan biro----	
6	Hojii/dalagaa	0. Kanmottumaa 1. Qoteebulaa 2. Hoj. Human 3. Hadhawaarra 4. Barata 5. Hinqabu 6. Daldalaa 7. Kan biro—	

Kutaa2ffa maalattowandhukaba TB

1	Qufaa turban lamaafi isaa ol ture qabduu	0. Lakii 1. Eeyye	
2	Yoo gaf.1 eeyyeta'etorbanmeeqa	Torban ---------	
3	Qufa kun isintutufsisaa	0. Lakki 1. Eeyye	
4	Yooisintutufsiseedhhiqaaqaba	0. Lakki 1. Eeyye	
5	Nafniikessanniho'aa	0. Lakki 1. Eyyee	
6	Yoo gaff. Eye ta'etorbaanmeeqaf	Turban-----	
7	Halkannidafqituu	0. Lakki 1. Eeyye	
8	Yoo gaff. 7fan eye ta'e turban meeqaf	Turban ---------	
9	Nyaataisinlagee/chufeebeeka	0. Lakki 1. Eeyye	
10	Yoo gaf.9 eye ta'e turban meeqa	Torba ----------	
11	Ulfatinehir'istanibeektuu	0. Lakki 1. Eye	
12	Hukkubiilapheeqabdu	0. Lakki 1. Eye	
13	Yoogaf.12 eye ta'e turban meeqa	Torba -------	
14	Affurriibafachuudadhabdaniibeektu	0. Lakki 1. Eye	
15	Yoogaf.14 eye ta'e turban meeqa	Turban ----------	

Kutaa 3ffa sababotadhukkuba Tb geessisan

1	Kanandura TB in qabamtanibeektuu	0. Lakki 1. eyyee	
2	Nama TB qabutidhiyeenaqabduu	0. lakki 1. eeyye	
3	Namni dhibee Tb qabu maati kessaa jiraa	0. lakki 1. eeye	
4	Dhukkuba sukaraa qabduu	0. lakki 1. eeye	
5	Sigaara ni aarsituu	0. lakkii 1. eyye	
6	Yoo ni aarsituta'ehangamiif	Bara ---------	
7	Jimaa ni qamaatu	0. lakki 1. eeyye	
8	Yoo ni qammatu ta 'e hangamiif	Bara ---------	
9	Alkooli ni dhugduu	0. lakki 1. eyye	
10	Yoo ni dhugduta'eguyyatihangam	Torbaniit ----/guyyati--	
11	Yerohangamiifdhugdan	Bara ------	
12	Asmiisombaa ni qabduu	0. lakki 1. eeyye	
13	Dagalee manni kessan maalin ijaarame	0. dhoqqe/- 1. simintoo	
14	Manii kessan lafi isa maali golgame	0. dhoqqee 1. simintoo	
15	Bayinni aati kessani meeqa	---------	
16	Mani kessan foddaa qabaa	0. lakki 1. eeyye	
17	Yoo qabate guyyati hangam bantuu	0. yeroo hunda 1. darbe darbe 2. turre	
18	Haala HIV (galmeef)	0. nagative 1. Pozeetive	

Kuta 4 haalawwan dhukkuba Tb qorichaan wal bare geessisan

1	Seena yalama Tb qabduu	0. Lakki 1. Eyye	
2	Yoo yalamtani beektan dhumni is akkam ture	0. Fayera 1. Fiteera 2. Hinfayinee 3. Gargar kuteni	
3	Yoo gaf.1 eye ta'e eessati yalamtani	0. Bufata fayya 1. Hospitala 2. ?	
4	Yoo yaalamtan yalichii enyuun isin keename	0. Motuma 1. Dhunfa	
5	Amala sirressa sentanii beektu	0. Lakki 1. Eeyye	
6	Hangamif amala siressa sentan	0. Bara -----	
7	Kana dura hospitala chistani beektuu	0. Lakki 1. Eeyye	
8	Yoo chiiftan ta'e hangamif	Bara/ji'a---------	
9	Yoo chiiftan ka'umsi isaa malii	----------	
10	Nama dhukuba TB qorichan wal bare qabu maati keessa walit dhiyodha	0. Lakkii 1. Eyyee 2. Hin yaadadhu	
11	Maati keessan kessa TB qorichan wal bare qabu jira	0. Lakki 1. eeyye	
12	Eessa jiraattu	0. man dhunfa kessa 1. kiraadhan 2. doormii 3. mana hin qabu 4. kan biiroo	

Kuta 5ffa wa'ee yaalaa TB beekuu

2. ka'umsa dhibee TB beektuu
   0. lakki 1. eyyee
3. yoo gaff.1ff eyye ta'e ka'umsi issa maal _____

4. dhiben Tb nama gara namatii ni dadarba jette ni yaadda
   _____

5. Tb qorich ni jiraa jette yaadda 0. lakki 1. eyyee

6. Gaffi 5faf yoo eyye jette namni qoricha TB fudhatee ni fayyaa jette yaadda_____

7. Balaa gahu jira jette yaadda yo namni Tbqabame hin yaalamin? 0. lakkii 1. eyyee

8. Yoo gaf 7 eyye jeette balaa akkami

   0. Dhukubsataa irrati _____
   1. Namoota nanoo dhukubsataa _____
9. Qoricha Tb gargar kutun rakkini ni dhufu
   0. Lakii
   1. Eyye
10. Yoo gaf.9fan eyye jette rakko akkmi _____
11. qorichi TB gatii akka kennamu ni beektaa
   0. lakki
   1. eeyye
   2. hin beekuu
12. dhibeen TB akkamiti dhorkamaa /itiifamaa _____

Laboratory forms

Study code: ..... **Card no.....**

Sputum	AFB result		Grading			
	Positive	Negative	Scanty	+1	+2	+3
1st spot						
Morning						
2nd spot						

I. Dire ct microscopy (AFB) result

II. Culture result

LJ medium	Positive	Negative	Remark
LJ + glycerol			
LJ + pyruvate			

Material Transfer Agreement

በኢትዮጵያ ፌዴራላዊ ዲሞክራሲያዊ ሪፐብሊክ
የኢትዮጵያ ብዝሀ ሕይወት ኢንስቲትዩት

The Federal Democratic Republic of Ethiopia
ETHIOPIAN BIODIVERSITY INSTITUTE (EBI)

ቁጥር ..EBI 71/1071/2017
Ref. No.
ቀን 07 JUL. 2017
Date

Armeuer Hansen Research Institute
Addis Ababa

Subject: - Material Export Permit

Dear Sir/Madam,

Reference is made to your letter of 30 June 2017 (AHRI-523/Tt/17) requesting export permit for Mr. Yared Merid Asfaw, a staff member at your institution, to take 175 eppendorf tubes of *Mycobacterium tuberculosis* DNA samples to London School of Hygiene and Tropical Medicine, London, UK, for a molecular genotyping study.

Convinced that the intended research is useful for molecular characterization of strains and having confirmed that your office has signed the Material Transfer Agreement (MTA) where in obligation is entered into to protect the national sovereignty and interest over the genetic materials. Therefore, we have consented to the export of the aforementioned samples to London School of Hygiene and Tropical Medicine, London, UK,

We would, once again, like to emphasize that the material should strictly be utilized for the said purpose only and the transfer to third party is not permitted. It should be recalled that future collection of genetic material for research purposes must be implemented according to the provisions in proclamation No.482/2006 (Access to genetic Resources and Community knowledge, and community Rights Proclamation).

We have enclosed here with the Material Transfer Agreement signed. We look forward to the progress of research work.

Yours Sincerely,

Melesse Menro Selamo (PhD
Director General

CC.
- Air Port Customs Office
- Lagar Customs Office
- Genetic Resources Access and Benefit Sharing Directorate
  Addis Ababa

ስልክ Tel. 011-6-612244 / 011-6-512023 / 011-6-615607 / 011-6-616643
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መልሱን በሚፅፉልን ጊዜ እባክዎን የእኛን ደብዳቤ ቁጥር ይጥቀሱልን
Please quote our Ref. No. when replying

Material Transfer Agreement

1. Formation

This material transfer agreement is made between the **Institute of Biodiversity Conservation** here in after referred to as the "Provider" of the one part and **Armaeuer Hansen Research Institute, here in after referred to as the "Sponsor" and Mr. Yared Merid Asfaw** hereinafter referred to as the **"Researcher".**

2. Purpose of Agreement

Whereas the Researcher, **Mr Yared Merid Asfaw** is undertaking a PhD research that intends to characterize the circulating bacterial strains in terms of the transmission dynamics and development and spread TB and MDR TB in the study sites and wants to take **175 DNA samples to London School of Hygiene and Tropical Medicine, London** for purpose of the said research;

Whereas the Researcher has confirmed that the research cannot be carried out here in Ethiopia due to **unavailability of laboratory set up to do WGS in Ethiopia.**

Whereas the Provider convinced that the intended research is useful for the **characterization of the circulating bacterial strains in relation to chain of transmission and development and spread of drug resistance TB** approved the exporting of the said 175 DNA samples.

Now, therefore, it is agreed as follows:

3. Descriptions and Quantity

Under this material transfer agreement the Researcher is allowed to export to **London School of Hygiene and Tropical Medicine, London, 175 DNA samples.**

4. Utilisation of Material

1. The Researcher shall utilize the material for said research program only.
2. The Researcher cannot use the material for commercial purpose nor can it obtain any intellectual property right on the material.
3. The Researcher retains the material for the period of the research in London where upon it shall return any remaining unused material to the Provider.

5. Other Obligations

4. The Researcher shall not transfer the material to any third party whosoever without first notifying to and securing explicit written agreement of the Provider.
5. Any third party that obtains the material from the Researcher in the absence of permission from the Provider shall not have any right whatsoever over the material and its components.
6. The Researcher shall notify the Provider the progress of its research through periodic research report.
7. The Researcher shall at the end of the research present to the Provider the hard and electronic copy of the research results.
8. Any benefit that accrues from the use of this material shall be subject to the relevant existing and future national and international laws.

Signature

On behalf of the Sponsor	On behalf of the Researcher
Name: **Dr. Abraham Aseffa**	Name: **Yared Merid**
Signature	Signature
Date June 27, 2017	Date June 27, 2017

Abraham Aseffa (MD/PhD)
A.D. Director General,
Research and Innovation

On behalf of the Provider

Melesse Maryo Belamo (PhD
Director General

Name

Signature

Date

DECLARATION

I the undersigned declare that this PhD Thesis is my own original work and has not been presented for a degree in any other university and all sources of materials used for the Thesis have been duly acknowledged.

Principal Investigator: Yared Merid

Signature: _____

Date of Submission _____

Supervisors

1. Dr. Yimtubezinash Woldeamanuel (MD, M.Sc., PhD)

   Signature_____ Date _____

2. Dr. Abraham Assefa (MD, PhD)

   Signature_____ Date _____

High utility of active tuberculosis case finding in an Ethiopian prison

International Journal of Infectious Diseases

Population-based screening for pulmonary tuberculosis utilizing community health workers in Ethiopia★

Yared Merid, Yimtubezinash Woldeamanuel Mulate, Mesay Hailu, Tsegaye Hailu, Getnet Habtamu, Markos Abebe, Daniel G. Datiko, Abraham Aseffa