GENETICAL STUDIES ON PHENOTYPIC STABILITY AND ADAPTABILITY FOR YIELD AND ITS COMPONENTS OF DURUM WHEAT *(Triticum turgidum L. var. durum)* GENOTYPES IN SHOA REGION OF ETHIOPIA

By

Jemanesh Kifetew Haile

A thesis submitted to the School of Graduate Studies of Addis Ababa University in partial fulfillment of the requirements for the Degree of Master of Science in Biology (Applied Genetics)

Major advisor: Dr. Ashok Kumar Sarial (AAU)
Co-advisor: Dr. Solomon Assefa (EARO)

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Moreover, I gratefully acknowledge the National Durum Wheat Research Project (NDWRP) for financial, experimental materials, logistics and manpower support. My special thanks goes to the staff of NDWRP for handling the field works and helping me in data collection. Amongst those I particularly thank Bemnet, Gashawbeza, Coordinator of the NDWRP, and Mr. Alemayehu, Zemede for their valuable advice, constructive comments, reference material provision and continuous encouragement and inspiration.

I am also very thankful to Mr. Assefa, Funga for his assistance in data analysis, Mr. Demissew, Negussie and Mrs. Tsehay, Bekele for their help in sample collection. None of the work reported here would have been possible without the continuing support of NDWRP.

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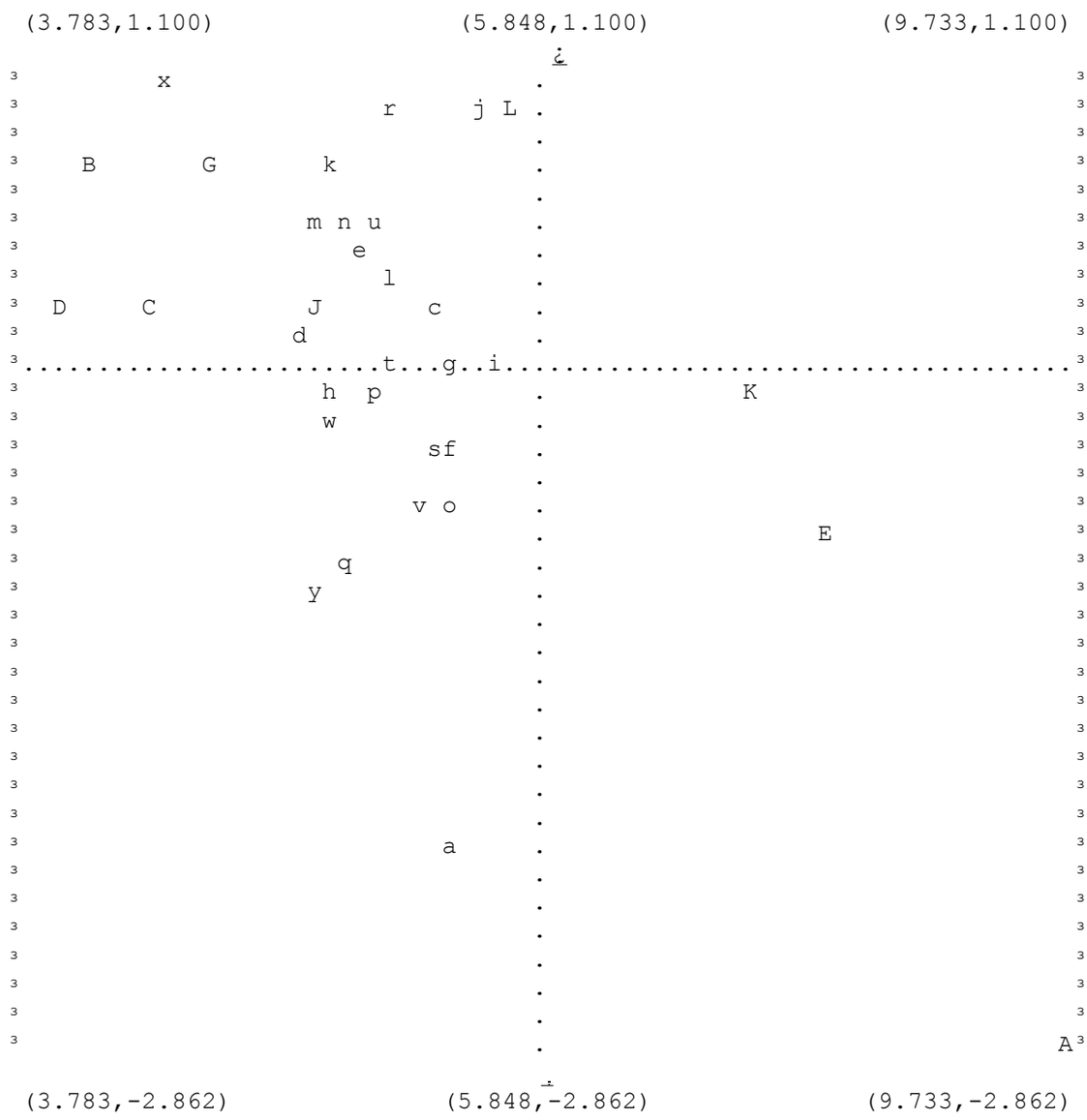

Figure 1 AMMI Biplot graph for grain yield per plant. Biplot with abscissa (X-axis) plotting means from 3.783 to 9.733 and with ordinate (Y-axis) plotting IPCA1 from -2.862 to 1.100. Genotypes plotted as lower cases and environments as upper case. Where, A=DZB, B=SER, C=MNR, D=SEB, E=DZR, F=CDR, G=ATB, H=MNB, I=ATR, J=AKR, k=CDB and L=AKB environments; and a=CDSS92B1467, **b=**CD91Y7, **c=**CD94523, **d=**CDSS93Y33, **e=**CD91989, **f=**CDSS92B193, **g=**CD97383, **h=**CD98206, **i=**CIGM91-349, **j=**CIGM91-347, **k=**CD94545-A, **l=**DZ2234, **m=**CD95294-1Y, **n=**DZ2212-1BS, **o=**DZ2293-2DZR, **p=**DZ1675-1AK, **q=**DZ1669-1AK, **r=**CD91313, **s=**DUKEM/3/RUF, **t=**DZ3117, **u=**Yerer, **v=**CDSS93Y545, **w=**Gerardo, **x=**DZ-04-118(local check)and **y=**Ude(standard check) genotypes.

Note: Three environments in place of others with similar means are not shown.

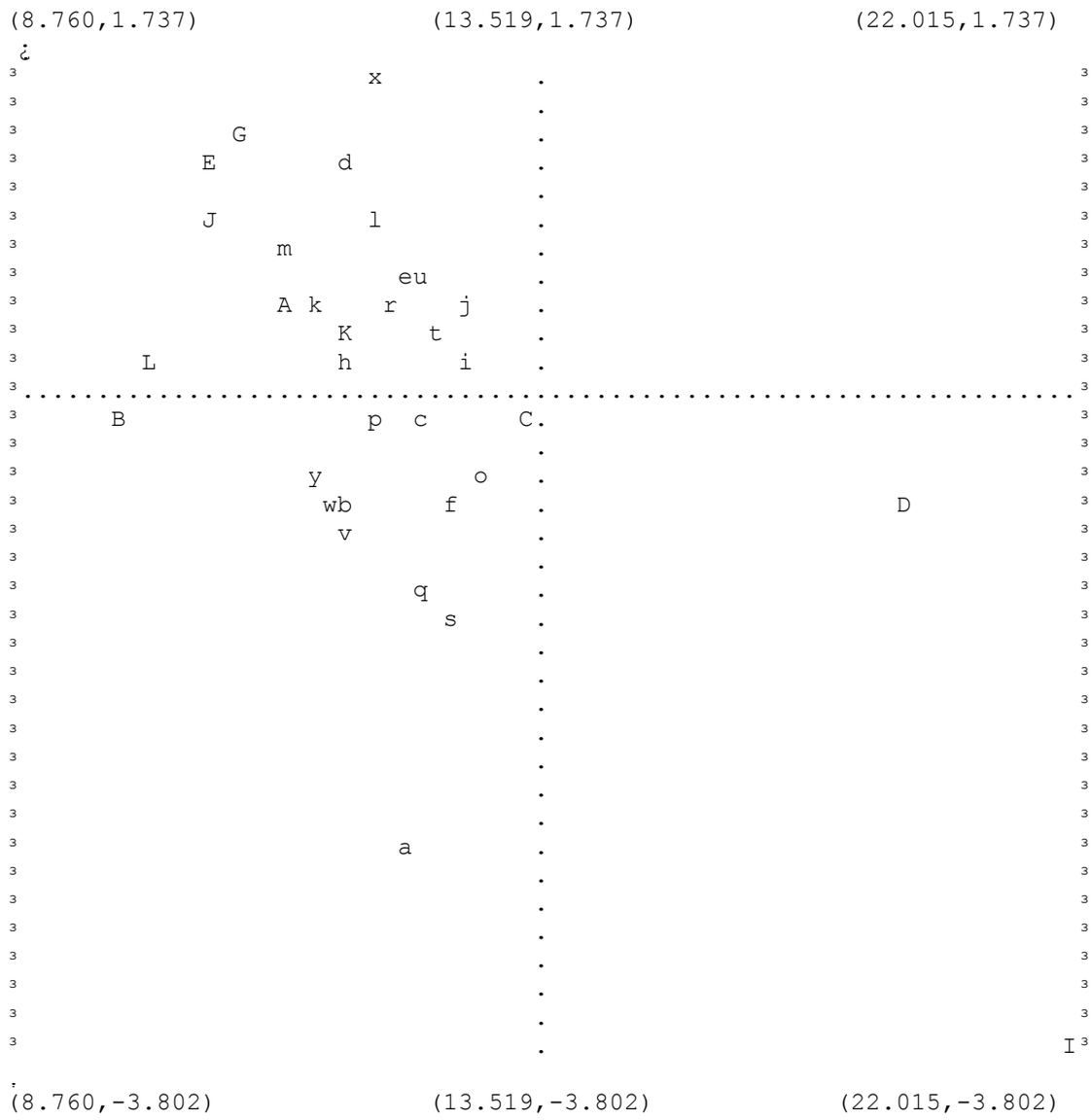

Fig 2. AMMI biplot model for biological yield per plant. Biplot with abscissa (X-axis) plotting means from 8.760 to 22.015 and with ordinate (Y-axis) plotting IPCA1 from -3.802 to 1.737. Genotypes plotted as lower cases and environments as upper case. Where, A=AKR, B=ATR, C=CDR, D=DZR, E=MNR, F=SEB, G=SER, H=CDB, I=DZB, J=ATB, k=AKB and L=MNB environments;
and a=CDSS92B1467, **b=**CD91Y7, **c=**CD94523, **d=**CDSS93Y33, **e=**CD91989, **f=**CDSS92B193, **g=**CD97383, **h=**CD98206, **i=**CIGM91-349, **j=**CIGM91-347, **k=**CD94545-A, **l=**DZ2234, **m=**CD95294-1Y,

n=DZ2212-1BS, **o=**DZ2293-2DZR, **p=**DZ1675-1AK, **q=**DZ1669-1AK, **r=**CD91313, **s=**DUKEM/3/RUF, **t=**DZ3117, **u=**Yerer, **v=**CDSS93Y545, **w=**Gerardo, **x=**DZ-04-118(local check)and **y=**Ude (standard check)genotypes

Note: Two environments in place of others with similar means are not shown.

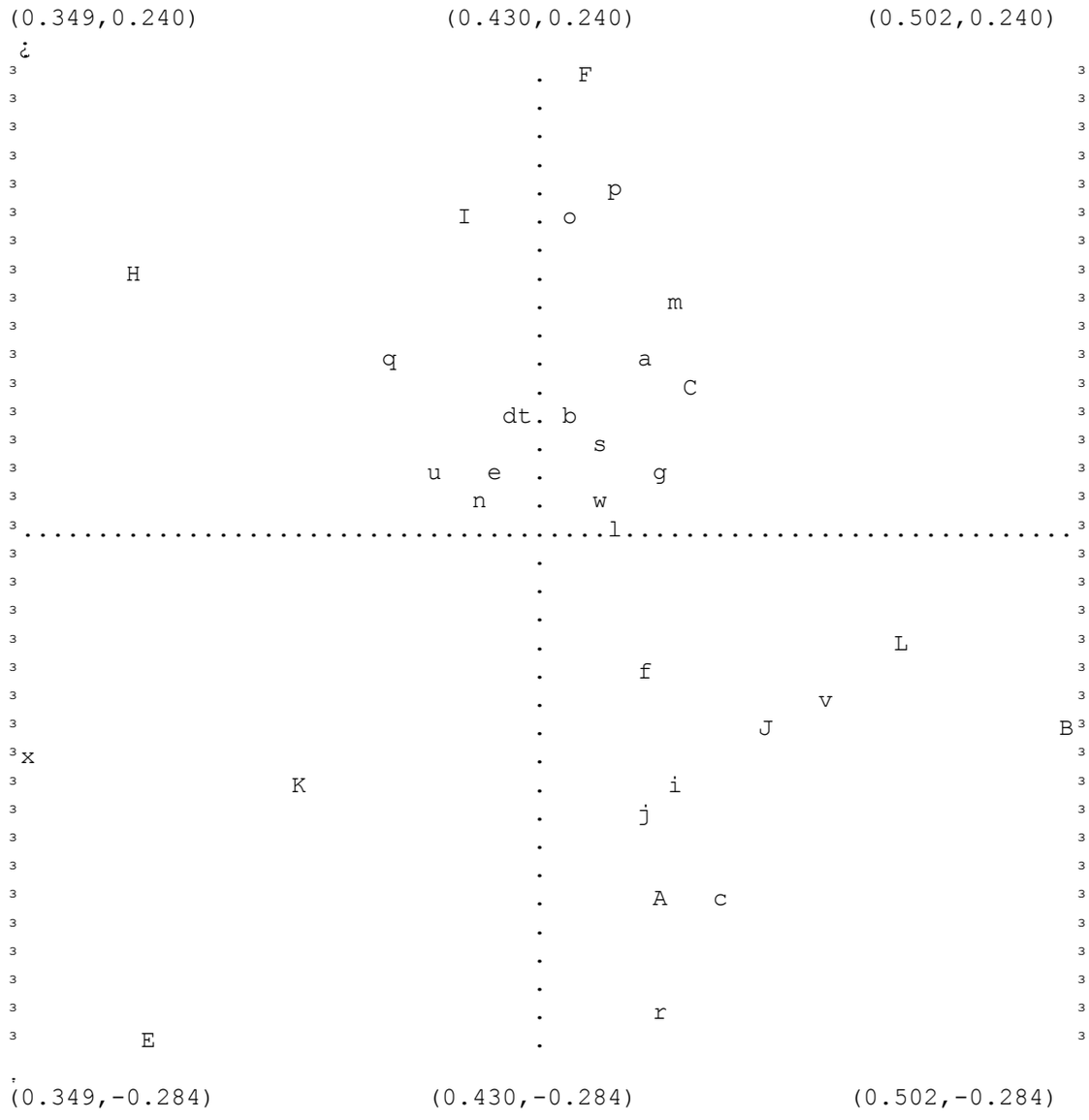

Fig 3. AMMI biplot graph for Harvest index. Biplot with abscissa (X-axis) plotting means from 0.349 to 0.502 and with ordinate (Y-axis) plotting IPCA1 from -0.284 to 0.240. Genotypes plotted as lower cases and environments as upper case. Where, A=CDR, B=AKB, C=AKR, D=ATB, E=ATR, F=DZB, G=DZR, H=MNB, I=MNR, J=SEB, k=SER and L=CDB environments; and a=CDSS92B1467, **b=**CD91Y7, **c=**CD94523, **d=**CDSS93Y33, **e=**CD91989, **f=**CDSS92B193, **g=**CD97383, **h=**CD98206, **i=**CIGM91-349, **j=**CIGM91-347, **k=**CD94545-A, **l=**DZ2234, **m=**CD95294-1Y, **n=**DZ2212-1BS, **o=**DZ2293-2DZR, **p=**DZ1675-1AK, **q=**DZ1669-1AK, **r=**CD91313, **s=**DUKEM/3/RUF, **t=**DZ3117, **u=**Yerer, **v=**CDSS93Y545, **w=**Gerardo, **x=**DZ-04-118(local check)and **y=**Ude (standard check) genotypes.

Note: Three genotypes in place of others with similar means are not shown.
Note: One environment in place of others with similar means is not shown.

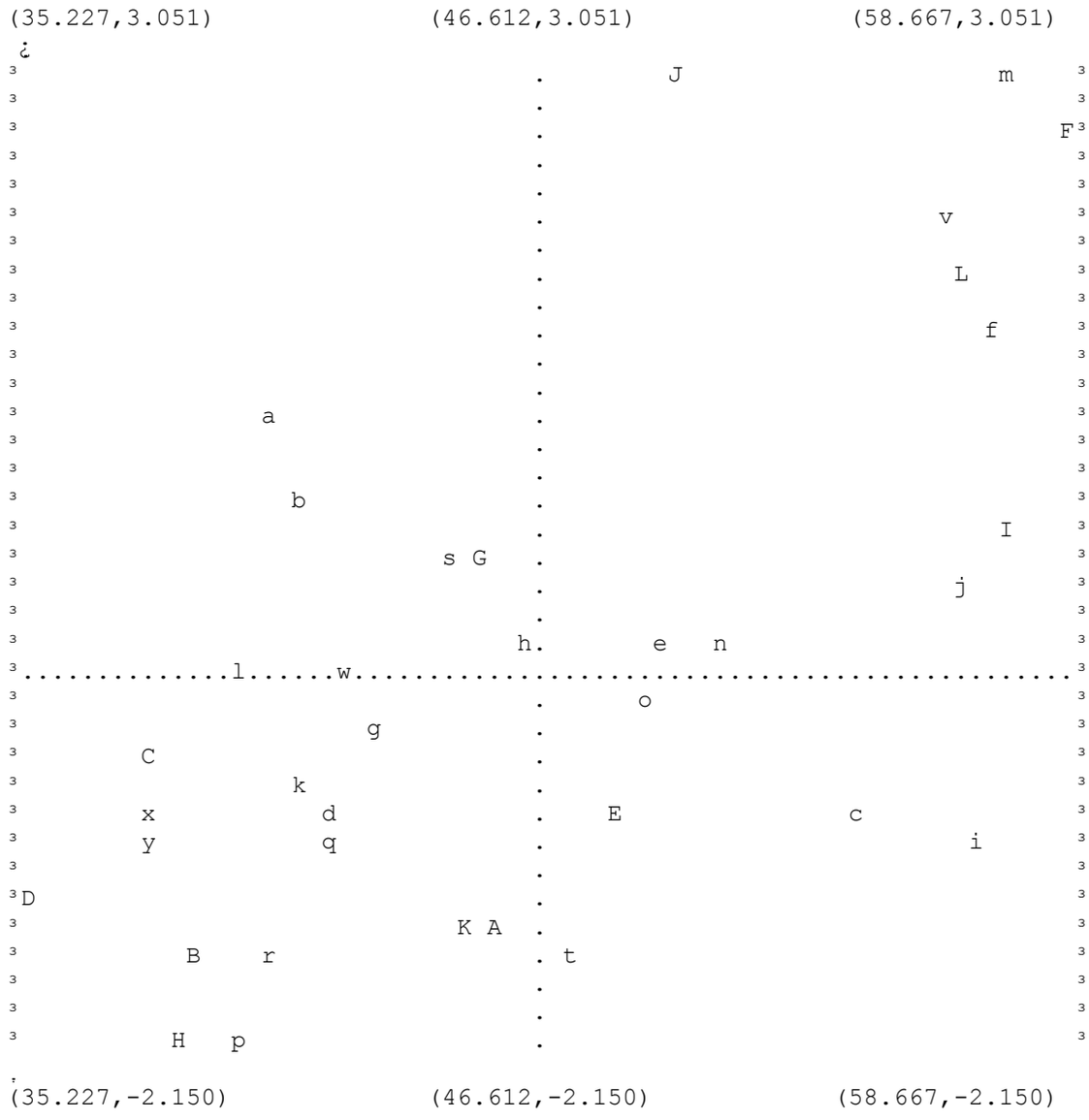

Fig 4. AMMI biplot graph for number of grains per spike. Biplot with abscissa (X-axis) plotting means from 35.227 to 58.667 and with ordinate (Y-axis) plotting IPCA1 from -2.150 to 3.051. Genotypes plotted as lower cases and environments as upper case. Where, A=AKR, B=SER, C=ATB, D=ATR, E=CDR, F=DZR, G=MNR, H=SEB, I=DZB, J=AKB, k=MNB and L=CDB environments; and a=CDSS92B1467, **b=**CD91Y7, **c=**CD94523, **d=**CDSS93Y33, **e=**CD91989, **f=**CDSS92B193, **g=**CD97383, **h=**CD98206, **i=**CIGM91-349, **j=**CIGM91-347, **k=**CD94545-A, **l=**DZ2234, **m=**CD95294-1Y, **n=**DZ2212-1BS, **o=**DZ2293-2DZR, **p=**DZ1675-1AK, **q=**DZ1669-1AK, **r=**CD91313, **s=**DUKEM/3/RUF, **t=**DZ3117, **u=**Yerer, **v=**CDSS93Y545, **w=**Gerardo, **x=**DZ-04-118(local check)and **y=**Ude (standard check) genotypes.

Note: One genotype in place of others with similar means is not shown.

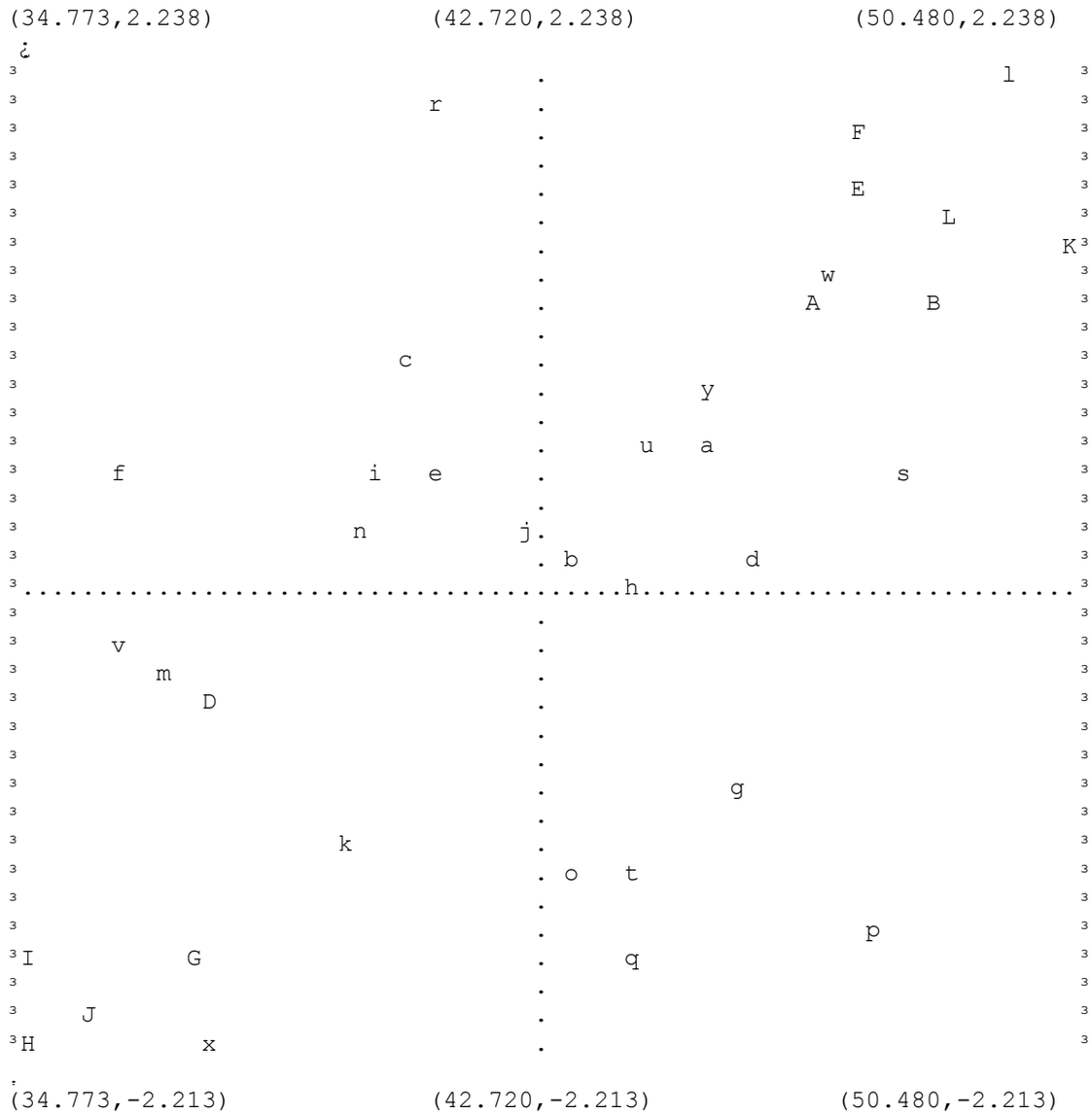

fig 5. AMMI biplot graph for 1000-kernel weight. Biplot with abscissa (X-axis) plotting means from 34.773 to 50.480 and with ordinate (Y-axis) plotting IPCA1 from -2.213 to 2.238. Genotypes plotted as lower cases and environments as upper case. Where, A=AKB, B=AKR, C=ATB, D=ATR, E=CDB, F=CDR, G=DZB, H=DZR, I=MNB, J=MNR, k=SEB and L=SER environments; and a=CDSS92B1467, **b=**CD91Y 7, **c=**CD94523, **d=**CDSS93Y33, **e=**CD91989, **f=**CDSS92B193, **g=**CD97383, **h=**CD98206, **i =**CIGM91 -349, **j=**CIGM91-347, **k=**CD94545-A, **l=**DZ2234, **m=**CD95294-1Y, **n=**DZ2212-1BS, **o=**DZ2293- 2DZR, **p=**DZ1675-1AK, **q=**DZ1669-1AK, **r=**CD91313, **s=**DUKEM/3/RUF, **t=**DZ3117, **u=**Yerer, **v=**CDSS93Y545, **w=**Gerardo, **x=**DZ-04-118(local check)and **y=**Ude (standard check) genotypes.

Note: One environment in place of others with similar means is not shown.

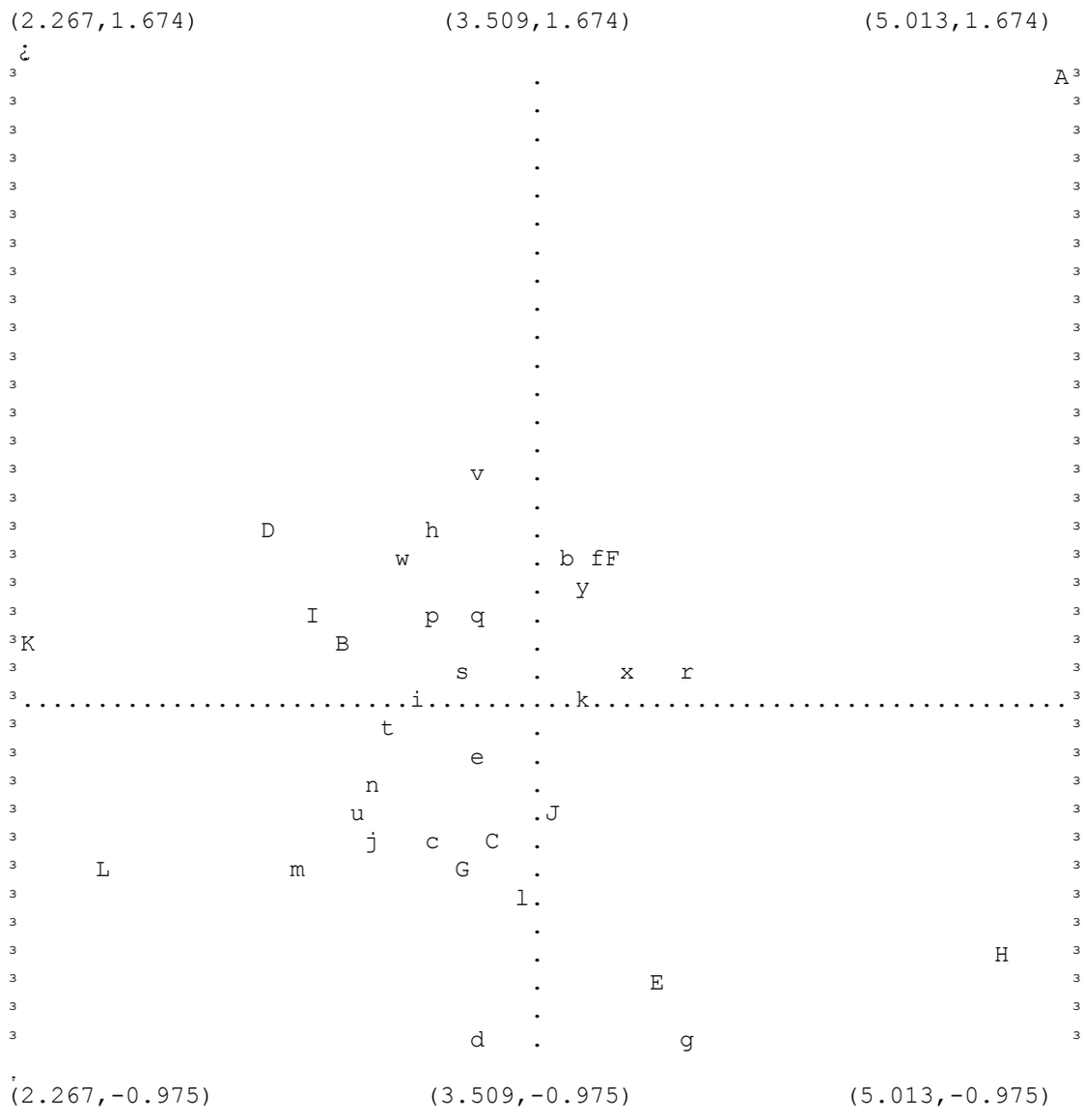

Fig 6. AMMI biplot graph for number of effective tillers per plant. Biplot with abscissa (X-axis) plotting means from 2.267 to 5.013 and with ordinate (Y-axis) plotting IPCA1 from -0.975 to 1.674. Genotypes plotted as lower cases and environments as upper case. Where, A=DZB, B=AKB, C=CDR, D=AKR, E=ATB, F=ATR, G=CDB, H=DZR, I=MNB, J=MNR, k=SEB and L=SER environment; and a=CDSS92B1467, **b=**CD91Y7, **c=**CD94523, **d=**CDSS93Y33, **e=**CD91989, **f=**CDSS92B193, **g=**CD97 383, **h=**CD98206, **i=**CIGM91-349, **j=**CIGM91-347, **k=**CD94545-A, **l=**DZ2234, **m=**CD95294-1Y, **n=**DZ2212-1BS, **o=**DZ2293-2DZR, **p=**DZ1675-1AK, **q=**DZ1669-1AK, **r=**CD91313, **s=**DUKEM/3/RUF, **t=**DZ3117, **u=**Yerer, **v=**CDSS93Y545, **w=**Gerardo, **x=**DZ-04-118(local check)and **y=**Ude (standard check) genotypes.

Note: Two genotypes in place of others with similar means are not shown.

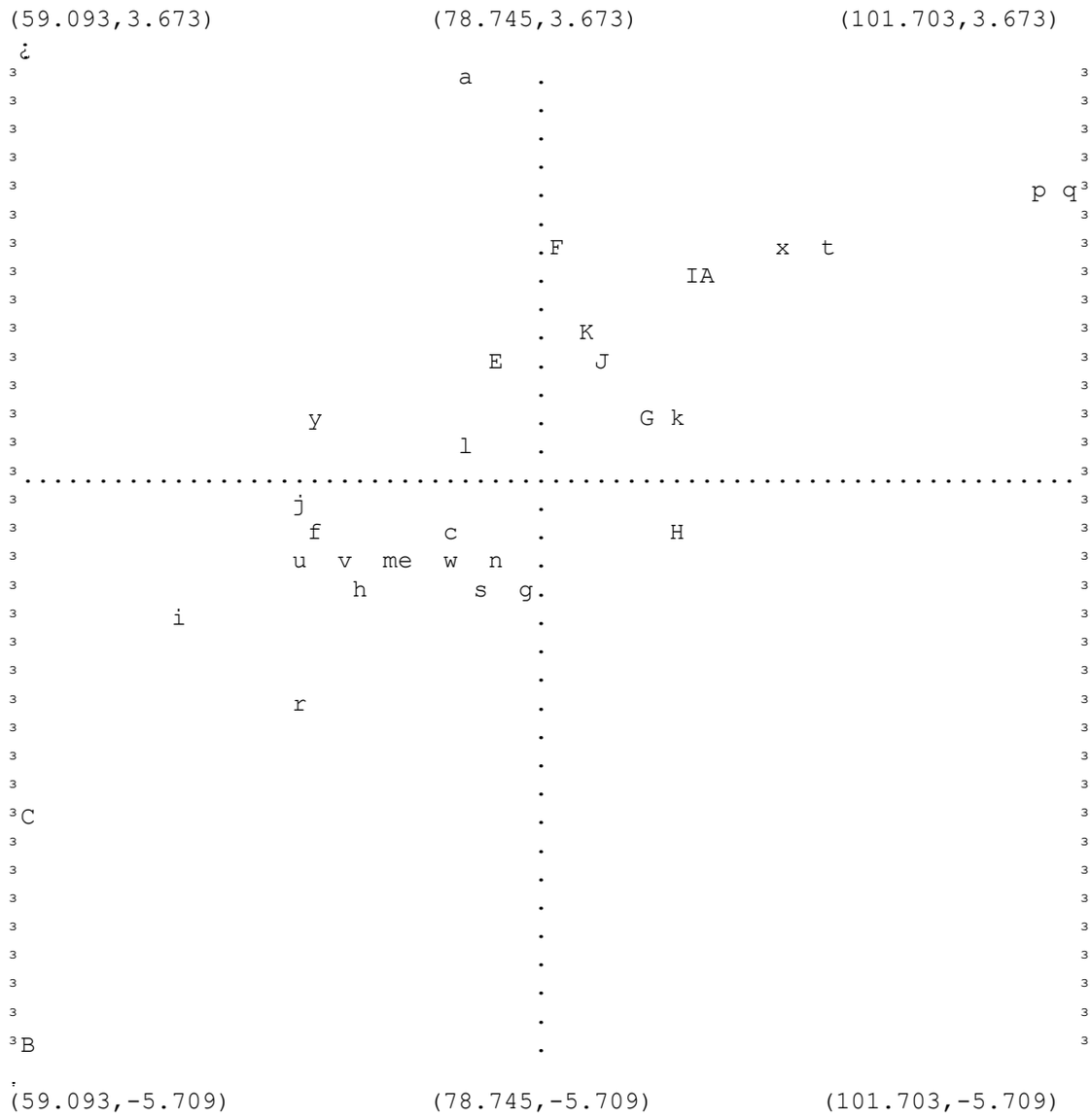

Fig 7. AMMI biplot graph for plant height. Biplot with abscissa (X-axis) plotting means from 59.093 to 101.703 and with ordinate (Y-axis) plotting IPCA1 from -5.709 to 3.673. Genotypes plotted as lower cases and environments as upper case. Where, A=AKR, B=ATB, C=ATR, D=MNB, E=MNR, F=SEB, G=SER, H=DZB, I=DZR, J=CDR, k=AKB and L=CDB environments; and a=CDSS92B1467, **b=**CD91Y7, **c=**CD94523, **d=**CDSS93Y33, **e=**CD91989, **f=**CDSS92B193, **g=**CD97383, **h=**CD98206, **i=**CIGM91-349, **j=**CIGM91-347, **k=**CD94545-A, **l=**DZ2234, **m=**CD95294-1Y, **n=**DZ2212-1BS, **o=**DZ2293-2DZR, **p=**DZ1675-1AK, **q=**DZ1669-1AK, **r=**CD91313, **s=**DUKEM/3/RUF, **t=**DZ3117, **u=**Yerer, **v=**CDSS93Y545, **w=**Gerardo, **x=**DZ-04-118(local check)and **y=**Ude (standard check) genotypes.

Note: Two environments in place of others with similar means are not shown.

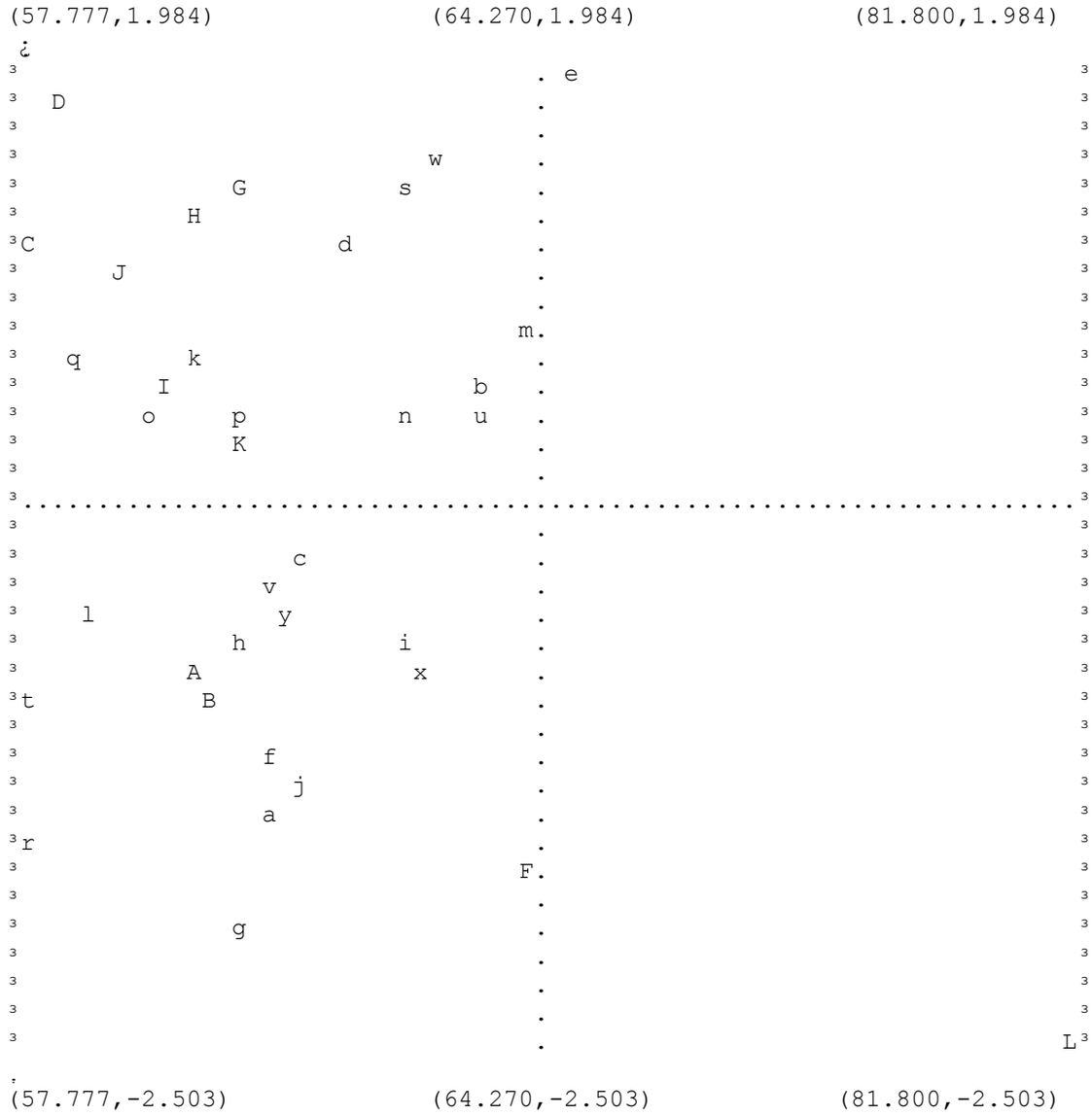

Fig 8. AMMI biplot graph for days to 50% heading. Biplot with abscissa (X-axis) plotting means from 57.777 to 81.800and with ordinate (Y-axis) plotting IPCA1 from -2.503 to 1.984. Genotypes plotted as lower cases and environments as upper case. Where, A=AKB, B=AKR, C=ATB, D=ATR, E=CDB, F=CDR, G=DZB, H=DZR, I=MNB, J=MNR, k=SEB and L=SER environments; and a=CDSS92B1467, **b=**CD91Y 7, **c=**CD94523, **d=**CDSS93Y33, **e=**CD91989, **f=**CDSS92B193, **g=**CD97383, **h=**CD98206,**i=** CIGM91- 349, **j=**CIGM91-347, **k=**CD94545-A, **l=**DZ2234, **m=**CD95294-1Y, **n=**DZ2212-1BS, **o=**DZ2293-2DZR, **p=**DZ1675-1AK, **q=**DZ1669-1AK, **r=**CD91313, **s=**DUKEM/3/RUF, **t=**DZ3117, **u=**Yerer, **v=**CDSS93Y545, **w=**Gerardo, **x=**DZ-04-118(local check)and **y=**Ude (standard check) genotypes.

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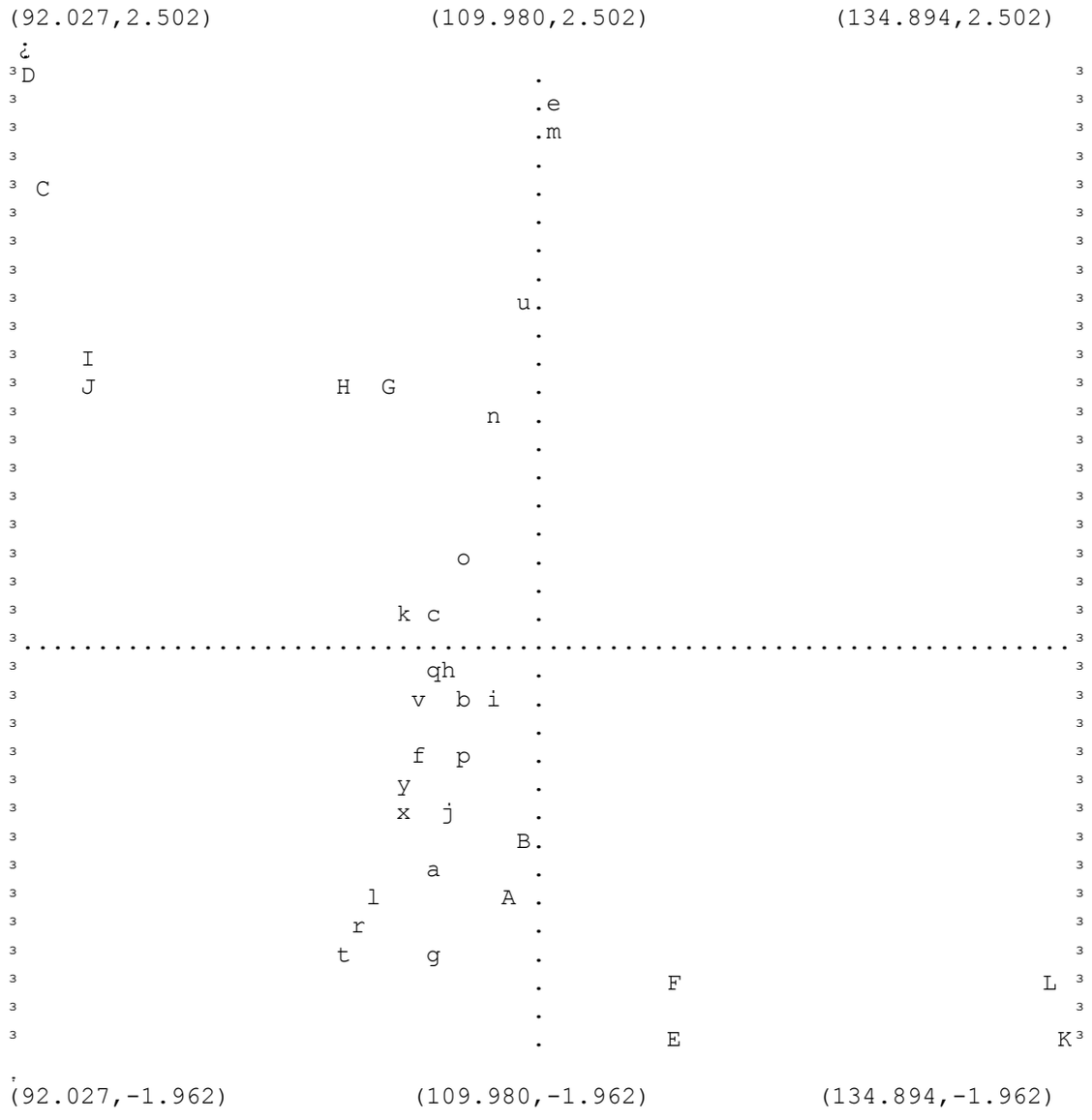

Fig 9 AMMI biplot graph for days to 75% maturity. Biplot with abscissa (X-axis) plotting means from 92.027 to 134.894 and with ordinate (Y-axis) plotting IPCA1 from -1.962 to 2.502. Genotypes plotted as lower cases and environments as upper case. Where, A=AKB, B=AKR, C=ATB, D=ATR, E=CDB, F=CDR, G=DZB, H=DZR, I=MNB, J=MNR, k=SEB and L=SER environments; and a=CDSS92B1467, **b=**CD91Y7, **c=**CD94523, **d=**CDSS93Y33, **e=**CD91989, **f=**CDSS92B193, **g=**CD97383, **h=**CD98206, **i=**CIGM91-349, **j=**CIGM91-347, **k=**CD94545-A, **l=**DZ2234, **m=**CD95294-1Y, **n=**DZ2212-1BS, **o=**DZ2293-2DZR, **p=**DZ1675-1AK, **q=**DZ1669-1AK, **r=**CD91313, **s=**DUKEM/3/RUF, **t=**DZ3117, **u=**Yerer, **v=**CDSS93Y545, **w=**Gerardo, **x=**DZ-04-118(local check)and **y=**Ude (standard check) genotypes.

Note: Two genotypes in place of others with similar means are not shown.

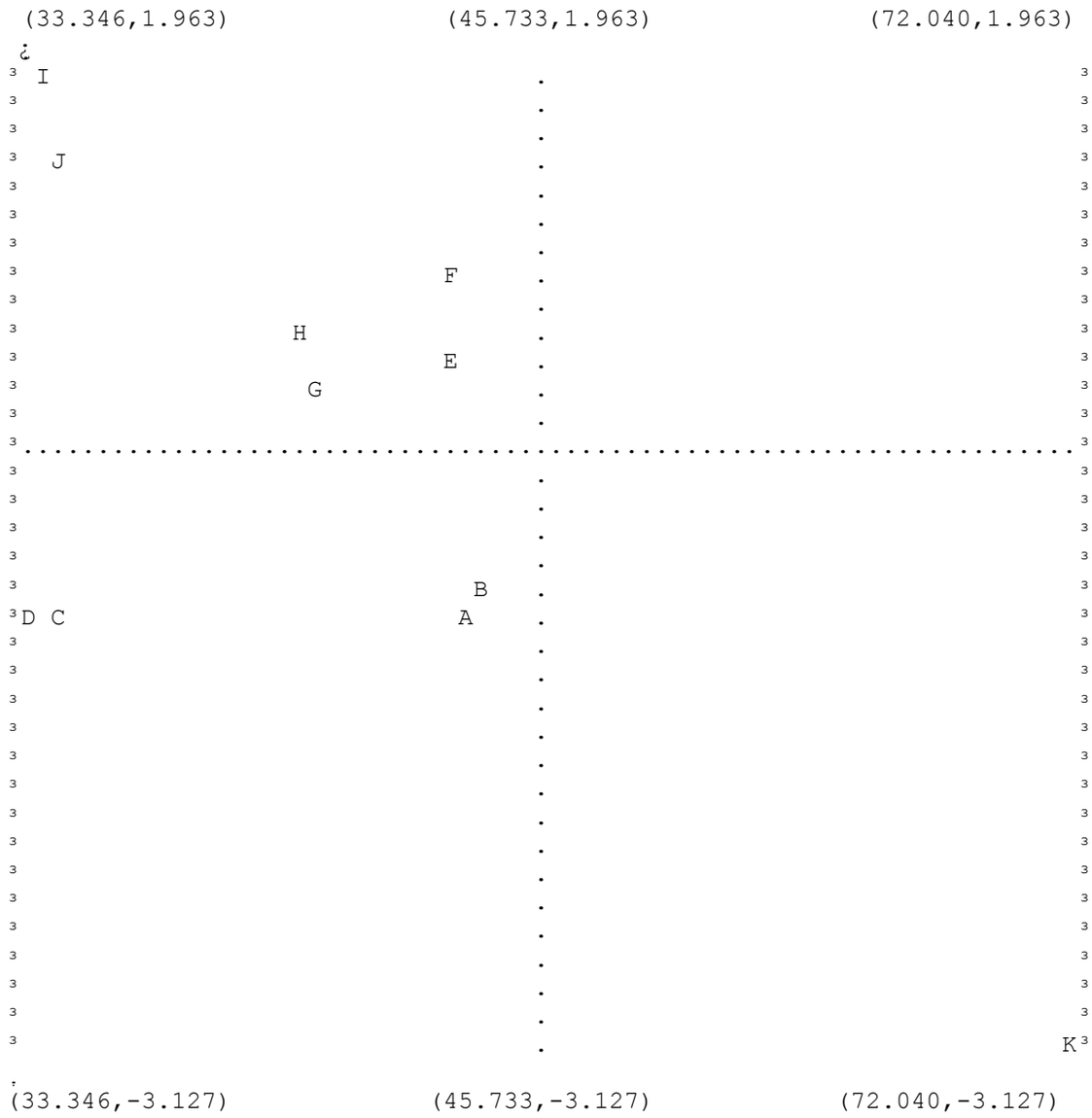

Fig 10. AMMI biplot graph for grain filling period. Biplot with abscissa X-axis) plotting means from 33.346 to 72.040 and with ordinate (Y-axis) plotting IPCA1 from -3.127 to 1.963. Genotypes plotted as lower cases and environments as upper case. Where, A=AKB, B=AKR, C=ATB, D=ATR, E=CDB, F=CDR, G=DZB, H=DZR, I=MNR, J=MNB, k=SEB and L=SER environments and a=CDSS92B1467, **b=**CD91Y7, **c=**C D94523, **d=**CDSS93Y33, **e=**CD91989, **f=**CDSS92B193, **g=**CD97383, **h=**CD98206, **i=**CIGM91-349, **j=**CIGM91-347, **k=**CD94545-A, **l=**DZ2234, **m=**CD95294-1Y, **n=**DZ2212-1BS, **o=**DZ2293-2DZR, **p=**DZ1675-1AK, **q=**DZ1669-1AK, **r=**CD91313, **s=**DUKEM/3/RUF, **t=**DZ3117, **u=**Yerer, **v=**CDSS93Y545, **w=**Gerardo, **x=**DZ-04-118(local check)and **y=**Ude (standard check) genotypes.

Note: Twenty-five genotypes in place of others with similar means are not shown.
Note: One environment in place of others with similar means is not shown.

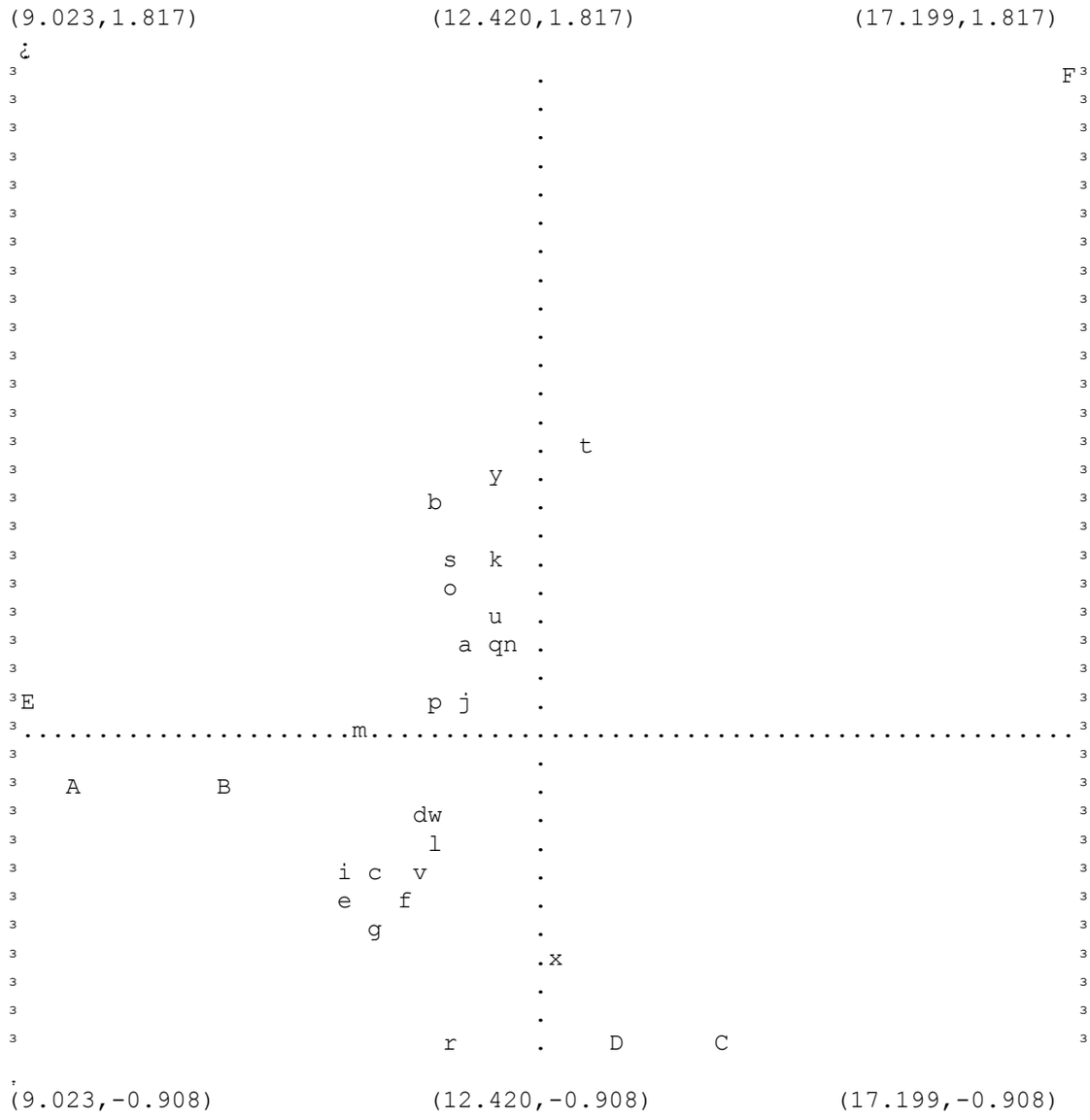

Fig 11. AMMI biplot graph for grain protein content. Biplot with abscissa (X-axis) plotting means from 9.023 to 17.199 and with ordinate (Y-axis) plotting IPCA1 from -0.908 to 1.817. Genotypes plotted as lower cases and environments as upper case. Where, A=AK, B=CD, C=DZ, D=MN, E=SE and F=AT environments; and a=CDSS92B1467, **b=**CD91Y7, **c=**CD94523, **d=**CDSS93Y33, **e=**CD91989, **f=**CDSS92B193, **g=**CD97383, **h=**CD98206, **i=**CIGM91-349, **j=**CIGM91-347, **k=**CD94545-A, **l=**DZ2234, **m=**CD95294-1Y, **n=**DZ2212-1BS, **o=**DZ2293-2DZR, **p=**DZ1675-1AK, **q=**DZ1669-1AK, **r=**CD91313, **s=**DUKEM/3/RUF, **t=**DZ3117, **u=**Yerer, **v=**CDSS93Y545, **w=**Gerardo, **x=**DZ-04-118(local check)and **y=**Ude (standard check) genotypes.

Note: One genotype in place of others with similar means is not shown .

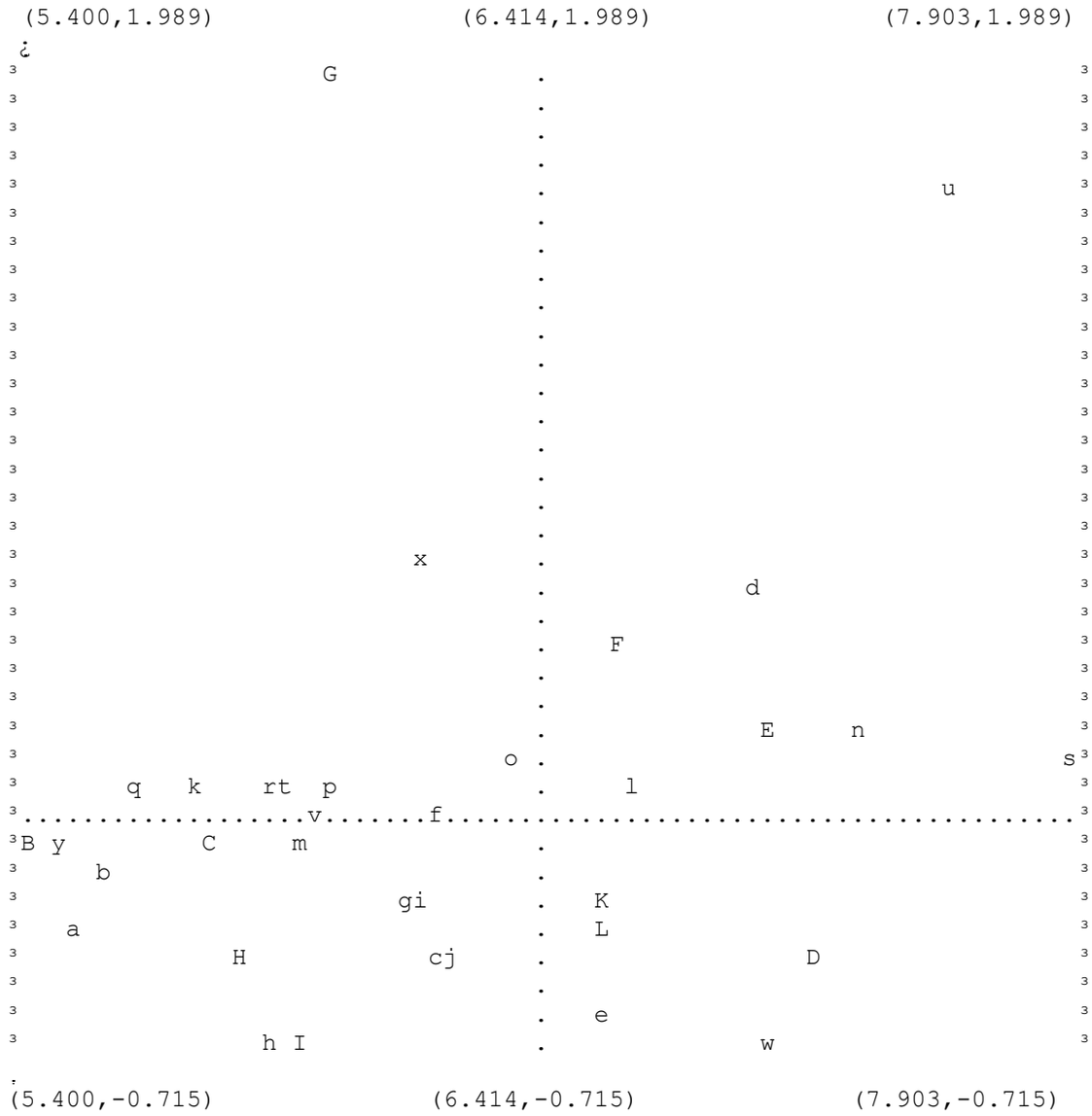

Fig 12. AMMI biplot graph for spike length. Biplot with abscissa (X-axis) plotting means from 5.400 to 7.90 and with ordinate (Y-axis) plotting IPCA1 from -0.715 to 1.989. Genotypes plotted as lower cases and environments as upper case. Where, A=AKR, B=ATB, C=ATR, D=CDB, E=DZB, F=DZR, G=MNB, H=SEB, I=SER, J= MNR, k=DZR and L=AKB environments and a=CDSS92B1467, b=CD91Y7, c=CD94523, d=CDSS93Y3 3, e=CD91989, f=CDSS92B193, g=CD97383, h=CD98206, i=CIGM91-349, j=CIGM91-347, k=CD94545-A, l=DZ2234, m=CD95294-1Y, n=DZ2212-1BS, o=DZ2293-2DZR, p=DZ1675-1AK, q=DZ1669-1AK, r=CD91313, s=DUKEM/3/RUF, t=DZ3117, u=Yerer, v=CDSS93Y545, w=Gerardo, x=DZ-04-118(local check)and y=Ude (standard check) genotypes.

Note:1 environments in place of others with similar means and not shown.

Appendix 2a. Analysis of variance (ANOVA) for different traits in durum wheat studied at Alem Tena planted in row method of sowing

Source	df	Mean sum of squares											
		Grain yield per plant (gm)	Biol. yield per plant (gm)	Harvest index	No. of effective tillers /plant	No. of kernels per spike	1000 kernel weight (gm)	Spike length (cm)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling duration	Grain protein (%)
Replication	2	14.23**	71.47**	0.005	1.56	89.05*	35.77	2.25**	182.07*	1.48	26.81	40.41*	17.98**
Genotype	24	2.27	5.74	0.010*	0.64	130.60**	41.04**	1.25**	116.15**	71.93**	93.14**	28.21**	4.38**
Error	48	1.54	6.23	0.005	0.62	28.97	15.61	0.48	53.59	4.05	10.65	12.61	1.83
CV (%)		**32.6**	**24.5**	**19.5**	**20.4**	**15.3**	**10.5**	**11.8**	**12.4**	**3.4**	**3.6**	**10.7**	**7.9**

Appendix 2b. ANOVA for different traits in durum wheat studied at Alem Tena planted in broadcasting method of sowing

Source	df	Mean sum of squares										
		Grain yield per plant (gm)	Biological yield per plant (gm)	Harvest index	No. of effective tillers per plant	No. of kernels per spike	1000 kernel weight (gm)	Spike length (cm)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling duration
Replication	2	4.93**	1.49	0.024*	0.21	42.65	7.05	0.36	76.21	10.92	2.56	4.84
Genotype	24	2.32**	9.05	0.011	1.10	128.53**	49.63**	1.22**	80.05**	54.07**	76.64**	36.91**
Error	48	0.98	6.10	0.007	0.69	20.15	21.01	0.25	33.71	4.42	7.49	8.80
CV (%)		**20.4**	**21.9**	**19.1**	**21.0**	**11.8**	**10.8**	**9.2**	**9.7**	**3.6**	**2.9**	**8.5**

Appendix 2c. ANOVA for different traits in durum wheat at Minjar planted in row method of sowing

Source	df	Mean sum of squares											
		Grain yield per plant (gm)	Biol. yield per plant (gm)	Harvest index	No. of effective tillers per plant	No. of kernels per spike	1000 kernel weight (gm)	Spike length (cm)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling duration	Grain protein (%)
Replication	2	11.22**	32.76*	0.013	1.65	38.41	13.61	0.73	118.13*	2.65**	12.41**	10.72**	0.54
Genotype	24	1.33	14.26	0.007 *	1.47*	150.79**	63.06**	1.46**	355.56**	67.29**	42.29**	27.75**	1.80
Error	48	1.57	9.85	0.004	0.83	25.47	7.25	0.32	28.84	0.45	2.05	1.93	1.87
CV (%)		**27.3**	**27.9**	**16.1**	**24.9**	**11.0**	**7.5**	**9.4**	**6.8**	**1.1**	**1.5**	**4.0**	**4.0**

*, ** Significant at P $\leq$ 0.05, and 0.01 respectively

Appendix 2d. ANOVA for different traits in durum wheat at Minjar planted in broadcasting method of sowing

Source	df	Mean sum of squares										
		Grain yield per plant (gm)	Biological yield per plant (gm)	Harvest index	No. of effective tillers per plant	No. of kernels per spike	1000 kernel weight (gm)	Spike length (cm)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling duration
Replication	2	5.65**	5.80	0.023**	1.12	43.32	67.57**	6.41	21.30	2.77	4.41	8.68
Genotype	24	1.50	8.81	0.005 *	0.68	81.86**	67.33**	5.25	394.85**	49.42**	46.07**	19.01**
Error	48	1.17	7.02	0.003	0.55	18.56	11.38	3.59	41.66	2.12	5.23	4.96
CV (%)		**28.5**	**2.5**	**15.0**	**24.4**	**9.5**	**9.7**	**30.8**	**8.5**	**2.4**	**2.4**	**6.5**

Appendix 2e. ANOVA for different traits in durum wheat at Debre Zeit planted in row method of sowing

Source	df	Mean sum of squares											
		Grain yield per plant (gm)	Biol. yield per plant (gm)	Harvest index	No. of effective tillers per plant	No. of kernels per spike	1000 kernel weight (gm)	Spike length (cm)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling duration	Grain protein (%)
Replication	2	0.85	6.04	0.010*	0.16	17.77	0.21	5.29**	0.56	0.57	13.96**	9.61*	0.74
Genotype	24	5.54**	14.52	0.006**	2.50	207.83**	60.41**	2.95**	477.58**	59.34**	41.45**	15.32**	1.99**
Error	48	1.77	11.38	0.002	1.99	22.56	5.12	0.61	18.52	8.49	3.17	2.71	1.87
CV (%)		**15.8**	**17.0**	**11.7**	**29.2**	**8.1**	**6.5**	**11.5**	**5.0**	**1.1**	**1.7**	**3.8**	**5.6**

Appendix 2f. ANOVA for different traits in durum wheat at Debre Zeit planted in broadcasting method of sowing

Source	df	Mean sum of squares										
		Grain yield per plant (gm)	Biological yield per plant (gm)	Harvest index	No. of effective tillers per plant	No. of kernels per spike	1000 kernel weight (gm)	Spike length (cm)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling duration
Replication	2	0.58	1.47	0.003	2.61	73.45	10.89	0.81	93.62	0.09	0.84	1.21
Genotype	24	12.04**	41.94*	0.006*	2.90**	204.72**	73.81**	3.28**	433.42**	63.50**	45.82**	14.26**
Error	48	5.73	21.08	0.003	1.34	27.68	5.45	0.30	154.06	1.97	7.53	4.45
CV (%)		**25.0**	**20.9**	**13.1**	**23.1**	**9.2**	**6.2**	**7.6**	**14.4**	**2.2**	**2.6**	**4.8**

*, ** Significant at P $\leq$ 0.05, and 0.01 respectively

Appendix 2g. ANOVA for different traits in durum wheat at Akaki planted in row method of sowing

		Mean sum of squares

Source	df	Grain yield per plant (gm)	Biological yield per plant (gm)	Harvest index	No. of effective tillers per plant	No. of kernels per spike	1000 kernel weight (gm)	Spike length (cm)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling duration	Grain protein (%)
Replication	2	9.17**	75.88**	0.003	3.57**	46.69	11.05	0.09	60.24*	4.65	4.96	9.45	0.92*
Genotype	24	2.85*	10.82	0.004	0.61*	189.41**	80.56**	1.21**	471.61**	18.96**	9.08*	18.86**	0.60**
Error	48	1.68	8.15	0.004	0.35	28.88	5.19	0.29	19.24	1.97	5.06	6.94	0.28
CV (%)		**23.7**	**23.3**	**13.7**	**20.2**	**11.7**	**4.7**	**8.1**	**5.0**	**2.3**	**2.0**	**5.2**	**5.5**

Appendix 2h. ANOVA for different traits in durum wheat at Akaki planted in broadcasting method of sowing

Source	df	Mean sum of squares										
		Grain yield per plant (gm)	Biological yield per plant (gm)	Harvest index	No. of effective tillers per plant	No. of kernels per spike	1000 kernel weight (gm)	Spike length (cm)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling duration
Replication	2	3.74	4.49	0.006	0.37	56.92	5.49	0.75	3.38	6.52	1.92	15.16*
Genotype	24	6.16	16.10	0.017	0.38	286.30**	62.81**	1.45**	390.99**	28.42**	10.09**	18.09**
Error	48	4.70	11.00	0.012	0.53	67.85	6.49	0.39	17.46	3.15	1.41	4.15
CV (%)		**32.8**	**25.8**	**21.0**	**23.4**	**16.4**	**5.5**	**9.2**	**5.1**	**2.9**	**1.1**	**4.1**

Appendix 2i. ANOVA for different traits in durum wheat at Chefe Donsa planted in row method of sowing

Source	df	Mean sum of squares											
		Grain yield per plant (gm)	Biological yield per plant (gm)	Harvest index	No. of effective tillers per plant	No. of kernels per spike	1000 kernel weight (gm)	Spike length (cm)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling duration	Grain protein (%)
Replication	2	15.63**	63.23**	0.003	0.65	473.08**	4.44	0.56	62.12**	4.173	7.09	2.25	0.41
Genotype	24	4.38 *	15.85*	0.005	0.42	209.14**	81.61**	1.45**	409.60**	33.54**	7.79	19.70**	1.48*
Error	48	2.67	8.60	0.003	0.40	57.41	13.91	0.36	11.48	2.76	5.48	4.30	0.80
CV (%)		**24.3**	**19.2**	**13.3**	**18.1**	**15.6**	**7.9**	**8.8**	**4.1**	**2.4**	**2.0**	**4.2**	**8.4**

*, ** Significant at P $\leq$ 0.05, and 0.01 respectively

Appendix 2j. ANOVA for different traits in durum wheat at Chefe Donsa planted in broadcasting method of sowing

		Mean sum of squares										
		Grain yield per plant	Biological yield	Harvest index	No. of effective	No. of kernels per spike	1000 kernel	Spike length	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling

	df	(gm)	per plant (gm)		tillers per plant		weight (gm)	(cm)				duration
Replication	2	5.63	22.74	0.000	0.49	64.00	3.04	0.41	24.85	2.08*	0.05	1.97
Genotype	24	4.42	13.00	0.005**	0.65*	262.31**	75.96**	0.86	303.63**	37.15**	6.93**	23.31**
Error	48	3.23	12.88	0.002	0.37	42.60	11.98	0.72	25.31	0.58	1.91	2.45
CV (%)		**22.7**	**21.7**	**9.5**	**17.7**	**11.6**	**7.3**	**11.6**	**6.2**	**1.1**	**1.2**	**3.2**

Appendix 2k. ANOVA for different traits in durum wheat at Selale planted in row method of sowing

Source	df	Mean sum of squares											
		Grain yield per plant (gm)	Biological yield per plant (gm)	Harvest index	No. of effective tillers per plant	No. of kernels per spike	1000 kernel weight (gm)	Spike length (cm)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling duration	Grain protein (%)
Replication	2	3.05	533.85**	0.302**	0.09	66.33*	4.97	1.77*	43.64	29.32**	18.84	17.08	0.89**
Genotype	24	1.79	10.64 *	0.006	0.34	104.66**	63.88**	1.74 **	370.84**	42.14**	18.08*	47.19**	0.81**
Error	48	1.59	6.16	0.007	0.55	20.44	7.06	0.44	31.14	6.75	10.13	11.40	0.21
CV (%)		**30.4**	**21.5**	**20.8**	**29.8**	**11.5**	**5.5**	**10.9**	**6.6**	**3.2**	**2.4**	**6.5**	**5.0**

Appendix 2l. ANOVA for different traits in durum wheat at Selale planted in broadcasting method of sowing

Source	df	Mean sum of squares										
		Grain yield per plant (gm)	Biological yield per plant (gm)	Harvest index	No. of effective tillers per plant	No. of kernels per spike	1000 kernel weight (gm)	Spike length (cm)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling duration
Replication	2	2.68	11.80	0.001	0.17	81.01**	4.96	1.05*	571.27**	1.77	2.77	10.92
Genotype	24	1.46	4.05	0.005**	0.31	94.63**	61.06**	1.38**	411.60**	38.21**	24.33**	59.65**
Error	48	1.17	4.80	0.001	0.31	17.43	16.24	1.30	110.93	13.26	8.87	10.61
CV (%)		**26.9**	**25.0**	**8.4**	**24.7**	**10.7**	**8.0**	**9.3**	**13.0**	**5.8**	**2.2**	**4.5**

*, ** Significant at P $\leq$ 0.05, and 0.01 respectively

Appendix 3. Combined analysis of variance for different traits in durum wheat over locations and method of sowing

Source	df	Mean sum of squares										
		Grain yield per plant	Biological yield per plant	Harvest index	Thousand kernel weight	No. of grains per spike	No. of effective tillers per plant	Spike length	Plant height	Days to 50% heading	Days to 75% maturity	Grain filling duration
Location	5	606.62**	2651.53**	0.174**	5876.45**	9609.37**	110.92**	52.00**	14758.70**	4496.06**	36517.10**	16957.74**
MOS	1	81.51**	14.03	0.228**	260.28**	946.59**	1.44	1.83	961.29**	1789.29**	97.35**	2756.25**
Loc by MOS	5	27.29**	120.12**	0.080**	231.60**	453.58**	3.63**	4.51**	129.41**	2314.06**	23.06**	2426.61**
Bloc (Loc x MOS)	24	6.45**	69.25**	0.033**	14.09	91.08**	1.06	1.71**	104.78**	5.58*	8.05	11.03**
Genotype	24	6.00**	16.41**	0.018**	486.76**	1504.40**	2.52**	14.91**	3159.03**	430.79**	209.93**	158.45**
Genotype by loc	120	4.46**	16.21**	0.006**	46.07**	55.24**	0.81	0.93**	112.51**	19.86**	35.01**	23.32**
Genotype by MOS	24	2.00	9.91	0.006	6.30	22.13	0.78	0.54	30.96	2.62	4.40	5.46
Genotype x loc x MOS	120	3.15**	11.48	0.006*	11.54	49.81**	0.94*	0.68	92.66**	6.26**	6.46	9.15**
Residual	576	2.32	9.44	0.005	10.56	31.50	0.71	0.67	45.50	3.50	5.75	6.27

*, ** **Significant at P ≤ 0.05, and 0.01 respectively**; where MOS is method of sowing

Appendix 4. Means and IPCA scores for the traits across environments

Environments	Grain yield/ plant (gm)		Biological yield/ plant (gm)		1000-kernel weight (gm)		Harvest index		Spike length (cm)		Plant height (cm)	
	Mean	IPCA score	Mean	IPCA score	Mean	IPCA score	Mean	IPCA score	Mean	IPCA score	Mean	IPCA score
ATR	3.81	0.024	10.18	0.234	37.71	-0.566	0.37	-0.284	5.85	-0.129	59.24	-3.189
ATB	4.86	0.727	11.29	-0.956	42.61	-1.114	0.43	0.063	5.40	-0.119	59.09	-5.709
MNR	4.59	0.194	11.22	-1.214	35.83	-1.974	0.41	0.162	5.99	0.096	78.77	0.967
MNB	3.78	0.003	10.39	-0.222	34.77	-1.671	0.37	0.138	6.15	1.989	76.43	-0.143
DZR	8.40	-0.684	19.89	0.574	35.05	-2.172	0.43	0.195	6.83	0.462	86.74	1.685
DZB	9.73	-2.862	22.01	3.802	37.49	-1.725	0.43	0.240	7.17	0.226	86.14	-0.498
AKR	5.47	0.229	12.26	-0.466	48.53	1.224	0.45	0.076	6.65	-0.460	87.03	1.822
AKB	6.60	0.967	12.84	-0.381	46.75	1.259	0.50	-0.102	6.78	-0.312	82.35	1.199
CDR	6.74	0.541	15.25	0.136	47.36	2.078	0.44	-0.195	6.79	-0.285	82.75	0.908
CDB	7.93	-0.099	16.57	0.051	47.44	1.702	0.48	-0.056	7.31	-0.396	80.68	0.411
SER	4.20	0.764	11.56	-1.497	48.61	1.579	0.39	-0.135	6.09	-0.682	84.49	0.367
SEB	4.05	0.196	8.76	-0.063	50.48	1.431	0.46	-0.102	5.95	-0.391	81.23	2.180

Appendix 4. Contd.

Environments	No. of kernels/spike		No. of effective tillers/plant		Days to 50% heading		Days to 75% maturity		Grain filling duration		Grain protein (%)	
	Mean	IPCA score	Mean	IPCA score	Mean	IPCA score	Mean	IPCA score	Mean	IPCA score	Mean	IPCA score
ATR	35.23	-1.194	3.84	0.358	58.68	1.891	92.03	2.502	33.35	-0.725	17.20	1.817
ATB	38.19	-0.574	3.95	-0.716	58.24	1.195	93.12	1.979	34.88	-0.610		
MNR	45.49	0.551	3.67	-0.323	62.11	1.039	95.00	1.160	34.80	1.506	13.72	-0.908
MNB	45.40	-1.054	3.04	0.233	62.00	0.621	95.39	1.185	34.24	1.972		
DZR	58.67	2.827	4.84	-0.654	61.83	1.356	105.48	1.083	43.65	0.731	14.50	-0.832
DZB	57.33	0.746	5.01	1.674	62.87	1.467	107.28	1.102	44.41	0.339		
AKR	45.95	-1.432	2.93	0.465	60.29	-0.786	112.56	-0.906	50.44	-0.639	9.48	-0.123
AKB	50.12	3.054	3.13	0.131	80.15	-0.718	112.08	-1.186	50.08	-0.717		
CDR	48.52	-0.788	3.51	-0.432	69.37	-1.646	118.75	-1.561	49.37	0.923	10.60	-0.092
CDB	56.20	1.943	3.43	-0.456	69.92	-2.198	119.09	-1.962	49.17	0.549		
SER	39.31	-1.625	2.49	-0.453	81.80	-2.503	134.00	-1.554	52.20	-0.606	9.02	0.137
SEB	38.95	-2.150	2.27	0.136	62.99	0.280	134.89	-1.841	72.04	-3.122		

Appendix 5. IPCA scores from biplot analysis of genotypes for different traits in durum wheat

Code	Genotypes	IPCA scores										
		Grain yield/plant (gm)	Biol. Yield/ plant (gm)	No. of effective tillers/plant	No. of kernels per spike	1000 kernel weight (gm)	Spike length (cm)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling duration (days)	Grain protein content (%)
01	CDSS92B1467	-1.909	2.558	0.984	1.260	0.644	-0.291	3.673	-1.390	-1.030	0.305	0.278
02	CD91Y7	-0.244	0.711	0.398	0.845	0.018	-0.155	-1.106	0.628	-0.272	0.927	0.655
03	CD94523	0.190	0.150	-0.328	-0.749	1.025	-0.395	-0.587	-0.200	0.042	0.057	-0.380
04	CDSS93Y33	0.076	-1.199	-0.913	-0.861	0.030	0.595	-0.888	1.207	0.365	0.351	-0.182
05	CD91989	0.388	-0.671	-0.129	0.065	0.396	-0.542	-0.930	1.984	2.385	1.682	-0.422
06	CDSS92B193	-0.417	0.592	0.432	1.708	0.439	0.018	-0.586	-0.032	-0.568	-0.727	-0.410
07	CD 97383	0.017	-0.563	-0.935	-0.300	-0.903	-0.249	-1.158	-1.840	-1.400	-0.012	-0.531
08	CD 98206	-0.104	-0.091	0.457	0.079	-0.024	-0.715	-1.280	-0.592	-0.159	-01879	-0.292
09	CIGM91-349	-0.048	-0.085	0.016	-0.939	0.421	-0.245	-1.332	-0.631	-0.289	-0.701	-0.340
10	CIGM91-347-	0.959	-0.476	-0.406	0.405	0.149	-0.375	-0.222	-1.164	-0.803	-1.321	0.128
11	CD 94545-A-	0.742	-0.405	0.004	-0.608	-1.239	0.020	0.485	0.677	0.049	0.736	0.506
12	DZ 2234	0.307	-0.962	-0.497	-0.081	2.238	0.094	0.186	-0.436	-1.202	0.388	-0.304
13	CD 9S294-1Y	0.527	-0.846	-0.432	3.035	-0.379	-0.106	-0.981	0.866	2.195	1.020	0.021
14	DZ 2212-1BS	0.546	-0.514	-0.225	0.088	0.176	0.184	-0.815	0.383	0.965	-0.404	0.273
15	DZ293-2DZR	-0.561	0.541	-0.140	-0.179	-1.310	0.164	2.159	0.462	0.369	-0.392	0.403
16	DZ1675-1AK	-0.147	0.187	0.234	-1.968	-1.563	0.093	2.532	0.499	-0.532	-0.825	0.089
17	DZ1669-1AK	-0.873	1.126	0.207	-1.035	-1.670	0.065	2.481	0.750	-0.163	-0.025	0.234
18	CD91313	0.992	-0.436	0.109	-1.529	2.141	0.024	-2.102	-1.432	-1.337	1.003	-0.854
19	DUKEM/3/RUF	-0.380	1.196	0.094	0.545	0.518	0.103	-1.168	1.477	1.639	0.409	0.483
20	DZ 3117	0.015	-0.326	-0.021	-1.549	-1.286	0.056	2.018	-0.861	-1.409	0.742	0.769
21	Yerer	0.527	-0.623	-0.303	1.205	0.573	1.685	-0.780	0.490	1.534	0.620	0.299
22	CDSS93Y545	-0.578	0.811	0.616	2.296	-0.256	-0.010	-0.950	-0.322	-0.290	-0.829	-0.361
23	Gerardo	-0.216	0.633	0.395	-0.032	1.292	-0.604	-1.006	1.612	1.401	0.678	-0.183
24	DZ-04-118 (local check)	1.100	-1.737	0.064	-0.780	-2.213	0.645	1.982	-0.702	-0.860	-0.263	-0.598
25	Ude (standard check)	-0.904	0.430	0.319	-0.920	0.783	-0.087	0.379	-0.433	-0.631	0.462	0.719

Table 4. Pooled Analysis of variance over 12 environments for different traits in durum wheat (Eberhart and Russell, 1966 model)

Source	df	Mean sum of squares											
		Grain yield/ plant (gm)	Biol. yield/ plant (gm)	Harvest index	No. of effective tillers/plant	No. of kernels /spike	1000 kernel weight (gm)	Spike length (cm)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling duration	Grain protein content (%)
Genotypes	24	2.06**	5.47	0.006**	0.84**	498.03**	162.25**	4.20**	1054.03**	143.60**	69.98**	52.82**	1.49** (24)
Env. in linear	1	1109.0**	4623.7**	0.455**	191.4**	17101.2**	10266.9**	143.5**	25779.1**	11947.5**	60932.5**	33225.8**	1308.50** (1)
Env. + in Gen. X Env.	275	5.27**	21.13**	0.003	0.97**	78.97**	45.90**	0.86**	126.42**	47.32**	227.73**	125.70**	10.86** (125)
Gen. X Env. (linear)	24	3.15**	10.47**	0.002	0.53**	39.30**	35.18**	0.66**	116.90**	19.17**	30.36**	13.66**	0.59* (24)
Pooled deviation	250	1.06*	3.74	0.001	0.25	14.69*	6.04**	0.31*	24.72**	2.42**	3.86**	4.06**	0.38 (100)
Residual	600	0.85	3.94	0.002	0.24	11.93	3.57	0.26	17.01	1.19	1.95	2.16	0.38 (300)

*, ** **Significant at P ≤ 0.05, and 0.01 respectively,** in parenthesis are degrees of freedom

Abbrv.

Env. = Environment
Gen. = Genotype
Biol. = Biological

Table 5.1 Stability parameters for yield and its components of durum wheat genotypes tested in 12 environments

Code	Genotypes	Grain yield per plant (gm)				Biological yield per plant (gm)				Thousand kernel weight (gm)				Number of grains/spike			
		μ	b_i	S^2d_i	Ran	μ	b_i	S^2d_i	Ran	μ	b_i	S^2d_i	Ran	μ	b_i	S^2d_i	Ran
01	CDSS92B1467	6.02	1.77**	1.16**	9	13.76	1.74**	4.43*	11	45.11	1.10	9.70**	7	40.78	1.24	2.23	21
02	CD91Y7	5.56	1.03	-0.44	20	12.94	1.08	-1.20	19	42.97	0.97	-0.56	14	41.75	1.18	-9.69	18
03	CD94523	6.13	0.99	0.26	7	13.80	1.17	-0.95	10	40.50	1.26	0.36	18	53.97	0.94	2.93	6
04	CDSS93Y33	5.36	0.75	0.36	24	12.92	0.67*	4.12*	20	45.72	1.02	6.38**	5	42.33	0.94	8.99	17
05	CD91989	5.74	0.83	-0.14	15	13.66	0.84	-0.97	12	41.11	1.12	6.17**	16	50.83	1.06	21.98**	7
06	CDSS92B193	6.23	1.16	-0.04	5	14.33	1.19	0.48	4	36.36	1.19	5.82**	24	57.08	1.02	30.93**	2
07	CD97383	6.26	0.94	0.01	3	14.00	0.90	-0.38	7	45.50	0.78	1.54	6	43.36	0.79	-3.94	14
08	CD98206	5.57	0.99	-0.14	19	13.01	0.88	-1.35	18	44.03	0.97	-1.96	12	46.78	0.82	3.45	12
09	CIGM91-349	6.48	0.89	0.11	1	14.48	0.88	-2.40	3	40.25	1.10	0.69	19	56.64	0.99	-1.10	3
10	CIGM91-347	6.41	0.82	1.14**	2	14.54	0.92	0.55	2	42.44	1.12	3.89*	15	56.25	1.04	3.83	4
11	CD94545-A	5.62	0.90	0.85*	18	12.58	0.95	0.40	23	39.75	0.63*	0.44	21	41.47	0.82	-6.76	19
12	DZ2234	5.92	1.05	0.54	11	13.54	0.86	-0.76	16	49.47	1.57**	8.74**	1	40.31	0.90	-4.09	23
13	CD95294-1Y	5.48	0.97	-0.05	22	12.20	0.86	-0.53	25	37.03	0.93	-1.37	23	57.25	1.59**	9.70*	1
14	DZ2212-1BS	5.63	0.89	-0.01	17	13.50	0.90	-0.51	13	39.84	0.99	2.19	20	50.83	1.16	3.44	8
15	DZ2293-2DZR	6.26	1.16	0.61	4	14.59	1.23	-2.04	1	43.03	0.71*	2.43	13	49.36	0.99	-6.17	9
16	DZ1675-1AK	5.82	1.03	-0.16	14	13.33	0.98	-0.97	17	47.64	0.65*	3.30*	3	40.39	0.58*	-1.15	22
17	DZ1669-1AK	5.67	1.28	0.19	16	13.87	1.30	-1.20	9	41.08	0.57**	2.26	10	42.39	0.78	-1.74	16
18	CD91313	5.92	0.62*	0.14	12	13.44	0.77	-2.84	14	41.11	1.53**	1.52	17	40.86	0.54**	-2.18	20
19	DUKEM/3/RUF	6.21	1.31	-0.45	6	14.24	1.30	-0.01	5	48.03	1.14	-1.70	2	44.78	1.18	3.28	13
20	DZ3117	5.93	0.76	0.02	10	14.01	0.90	-0.93	6	44.06	0.67*	3.26*	11	47.61	0.82	10.88*	10
21	Yerer	5.82	1.14	0.46	13	13.90	1.01	1.91	8	44.22	1.17	1.25	9	46.89	1.28	-3.19	11
22	CDSS93Y545	6.03	1.23	0.84*	8	12.84	1.07	0.38	21	36.25	0.93	2.79	25	53.83	1.43*	1.33	5
23	Gerardo	5.55	1.02	-0.30	21	12.71	1.06	-1.58	22	46.83	1.33*	0.55	4	42.69	1.09	-3.34	15
24	DZ-04-118 (L. check)	4.59	0.35**	-0.39	25	13.41	0.54**	1.64	15	37.61	0.36**	1.84	22	38.11	0.86	-0.80	25
25	Ude (S. check)	5.42	1.10	0.62	23	12.53	1.03	-0.38	24	45.03	1.26	2.11	8	38.25	0.99	9.97*	24
	Grand mean	**5.83**				**13.52**				**42.72**				**46.61**			
	Standard error		0.154				0.142				0.121				0.147		

***, ** Significant at P ≤ 0.05, and 0.01 respectively ;** Where, μ - Mean value, b_i - Regression value and S^2d - Deviation from regression

Table 5.2 Stability parameters for morphological traits of durum wheat genotypes tested in 12 environments

Code	Genotypes	Spike length (cm)				Plant height (cm)				Number of effective tillers/plant			
		μ	b_i	S^2d_i	Ran	μ	b_i	S^2d_i	Ran	μ	b_i	S^2d_i	Ran
01	CDSS92B1467	5.53	1.36	-0.09	24	78.85	1.62**	65.49**	8	3.58	1.39	0.27*	9
02	CD91Y7	5.63	1.02	-0.12	23	76.03	0.67	0.86	18	3.72	1.12	-0.07	7
03	CD94523	6.39	0.87	-0.15	11	76.42	0.78	-10.91	14	3.36	1.14	-0.04	16
04	CDSS93Y33	7.16	1.40	-0.57**	5	76.95	0.78	-12.36	12	3.50	0.81	0.42**	12
05	CD91989	6.80	1.01	-0.04	7	74.67	0.87	-0.77	15	3.47	0.82	0.07	14
06	CDSS92B193	6.40	0.63	-0.08	10	71.03	0.83	-6.18	21	3.78	1.50*	-0.03	4
07	CD97383	6.33	0.54	-0.11	14	79.64	1.04	222.30**	7	4.03	1.45*	0.88**	1
08	CD98206	6.02	0.82	0.24*	19	73.20	0.71	-5.33	17	3.36	1.11	-0.04	17
09	CIGM91-349	6.37	0.42*	-0.13	12	65.92	0.69	-14.12	25	3.33	0.85	-0.17	19
10	CIGM91-347-	6.43	0.48*	-0.03	9	70.58	0.97	-9.85	23	3.19	0.81	-0.09	24
11	CD94545-A-	5.85	0.65	-0.01	21	85.95	1.15	-4.97	6	3.75	0.90	-0.14	5
12	DZ2234	6.88	1.39	-0.19	6	77.29	1.07	-13.10	11	3.58	0.94	-0.04	10
13	CD95294-1Y	6.07	0.95	-0.18	17	74.28	0.79	-8.40	16	3.03	0.66	-0.03	25
14	DZ2212-1BS	7.39	1.17	0.09	3	78.45	0.83	-10.04	9	3.22	0.78	-0.04	22
15	DZ2293-2DZR	6.57	1.19	-0.16	8	90.20	1.31	61.11**	4	3.64	1.21	0.05	8
16	DZ1675-1AK	6.14	0.74	-0.06	15	100.33	1.59**	-7.01	2	3.36	0.88	-0.13	18
17	DZ1669-1AK	5.70	1.00	-0.12	22	101.69	1.68**	6.10	1	3.47	1.03	-0.06	13
18	CD91313	5.99	0.69	-0.05	20	70.33	0.47**	-11.12	24	4.03	1.43*	-0.11	2
19	DUKEM/3/RUF	7.90	1.73*	0.03	1	78.01	0.76	-5.21	10	3.44	0.91	-0.14	15
20	DZ3117	6.04	0.98	-0.08	15	91.72	1.47*	-7.26	3	3.25	0.77	-0.12	21
21	Yerer	7.60	1.41	1.70**	2	70.74	0.83	-12.86	22	3.17	0.75	-0.13	24
22	CDSS93Y545	6.10	0.93	-0.21	16	72.23	0.80	-5.33	19	3.50	1.24	-0.03	11
23	Gerardo	7.19	1.46	0.23*	4	76.70	0.82	-4.16	13	3.28	0.82	-0.05	20
24	DZ-04-118 (L. check)	6.35	1.20	0.38**	13	89.95	1.48*	-5.48	5	3.86	0.52*	0.12	3
25	Ude (S. check)	5.51	0.97	-0.08	25	71.51	1.04	-8.44	20	3.75	1.17	-0.06	6
	Grand mean	**6.25**				**78.75**				**3.51**			
	Standard error		0.234				0.155				0.182		

*, ** **Significant at P ≤ 0.05, and 0.01 respectively;** Where, μ - Mean value, b_i - Regression value and S^2d - Deviation from regression

Table 5.3 Stability parameters for phenological traits and grain protein content of durum wheat genotypes tested in 12 environments

Code	Genotypes	Days to 50% heading (days)				Days to 75% maturity (days)				Grain filling period (days)				Protein content (%)			
		μ	b_i	S^2d_i	Ran	μ	b_i	S^2d_i	Ran	μ	b_i	S^2d_i	Ran	μ	b_i	S^2d_i	Rank
01	CDSS92B1467	63.75	1.26**	1.88**	14	109.11	1.09*	0.81	16	45.36	0.94	-0.05	12	12.57	0.99	-0.22	9
02	CD91Y7	68.42	0.87	-0.29	4	110.17	1.00	1.88*	11	41.75	1.06	4.78**	24	12.31	1.18	0.25	16
03	CD94523	64.22	1.05	-1.05**	12	109.44	0.98	-0.00	14	45.22	0.99	0.39	14	11.78	0.94	-0.17	22
04	CDSS93Y33	65.42	0.76**	1.969**	10	110.44	0.96	4.97**	10	45.03	1.03	2.53**	17	12.22	0.95	-0.31	18
05	CD91989	70.39	0.64**	4.73**	1	114.19	0.73**	1.28	2	43.81	0.80**	0.79	23	11.63	0.92	-0.13	24
06	CDSS92B193	63.69	1.22*	1.08*	15	108.68	1.04	-0.25	19	44.97	1.05	0.37	18	12.07	1.00	0.04	20
07	CD97383	63.00	1.48**	1.74**	18	109.00	1.13**	1.44	17	46.00	1.00	3.97**	11	11.86	0.77*	-0.15	21
08	CD98206	63.08	1.08	0.72	17	109.83	1.02	-0.65	12	46.75	1.05	0.89	7	13.12	0.96	-0.18	3
09	CIGM91-349	66.67	1.13	1.31*	8	111.58	106	0.01	7	44.92	1.12*	2.75**	19	11.61	1.02	-0.16	25
10	CIGM91-347-	64.44	1.21*	1.02*	11	109.61	1.08	1.99*	13	45.17	1.08	1.39	16	12.49	1.02	-0.17	10
11	CD94545-A-	61.89	0.81*	-0.78	22	108.03	0.97	-0.72	20	46.14	0.98	1.29	10	12.77	0.99	0.14	7
12	DZ2234	59.64	1.04	0.26	2	106.72	1.11*	-0.30	23	47.08	1.06	0.37	6	12.26	0.89	-0.29	17
13	CD95294-1Y	67.22	0.85	3.10**	9	114.31	0.79**	2.17*	1	44.69	0.72**	-0.18	20	11.75	1.02	-0.11	23
14	DZ2212-1BS	66.61	0.97	1.00*	21	111.81	0.90*	1.02	6	45.19	0.97	1.09	15	12.90	1.20*	-0.30	4
15	DZ2293-2DZR	60.81	0.93	-0.15	19	110.64	0.98	1.42	8	49.83	0.98	0.39	2	12.36	0.94	0.19	13
16	DZ1675-1AK	62.86	0.94	0.20	23	110.61	1.10*	6.13**	9	47.75	1.21**	2.20*	5	12.31	0.87	-0.16	15
17	DZ1669-1AK	59.17	0.80*	-0.66	24	109.14	1.02	2.60**	15	49.97	1.10	5.73**	1	12.77	1.03	-0.22	8
18	CD91313	58.22	1.23**	2.70**	7	106.03	1.11*	5.46**	24	47.81	1.00	3.62**	4	12.42	1.00	1.45**	11
19	DUKEM/3/RUF	66.75	0.74**	2.05**	25	113.50	0.86**	2.22*	3	46.75	0.90	-0.31	8	12.40	0.95	1.10	12
20	DZ3117	57.78	1.10	5.60**	3	105.61	1.17**	2.65**	25	48.11	1.07	12.22**	3	13.52	1.18	0.15	1
21	Yerer	68.50	0.95	1.26*	16	112.94	0.85**	2.19*	5	44.44	0.89	-0.09	21	12.81	0.96	-0.16	6
22	CDSS93Y545	63.61	1.05	-0.74	5	108.86	1.04	1.56*	18	45.25	1.05	0.19	13	12.17	1.01	-0.10	19
23	Gerardo	67.22	0.71**	1.93**	6	113.42	0.88*	2.39**	4	46.19	0.94	0.74	9	12.35	0.89	0.47**	14
24	DZ-04-118 (L. check)	67.19	1.12	1.83**	13	108.00	1.09*	2.03*	21	40.81	1.05	0.46	25	13.26	1.13	0.82**	2
25	Ude (S. check)	63.81	1.06	-0.01	20	107.83	1.02	5.56**	22	44.03	0.99	2.02*	22	12.81	1.18	0.04	5
	Grand mean	**60.87**				**109.98**				**45.72**				**12.42**			
	Standard error		0.071				0.040				0.055				0.164		

*, ** **Significant at P ≤ 0.05, and 0.01 respectively;** Where, μ - Mean value, b_i - Regression value and S^2d - Deviation from regression

Table 6. Additive Main Effects and Multiplicative Interaction (AMMI) for different traits of durum wheat analyzed over 12 environments

Source of variation	DF	Grain yield per plant (gm)	Biol. yield per plant (gm)	Harvest index	No. of effective tillers/plant	No. of kernels per spike	1000 kernel weight (gm)	Spike length (cm)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Grain filling duration (days)	Grain protein content (%)
Genotype	24	6.19*	16.26	0.017**	2.53**	1494.80**	486.76**	14.91**	3162.09**	430.81**	209.94**	158.47**	4.48** (24)
Environments	11	302.45**	1260.49**	0.124**	52.06**	4663.91**	2800.05**	25.86**	7030.67**	3258.41**	16617.95**	9061.57**	785.10** (5)
Reps. within Env.	24	6.60	89.26	0.034	1.06	87.80	14.09	1.71	117.12	5.58	8.05	11.03	3.59 (12)
Gen. X Env.	264	3.86**	13.50**	0.005*	0.86*	52.44**	26.76**	0.78	102.12**	12.11**	19.25**	15.25**	1.30** (120)
IPCA 1	34	10.94**	34.96**	0.009**	2.10**	110.92**	82.49**	2.60**	291.06**	57.27**	77.47**	34.645**	2.53** (28)
IPCA 2	32	4.95**	18.00**	0.007**	1.97**	86.61**	45.81**	1.10**	267.58**	13.09**	32.10**	31.02**	1.70** (26)
IPCA 3	30	4.46**	16.42**	0.006*	1.04	77.01**	27.58**	0.81	98.22**	9.03**	14.04**	22.42**	1.17 (24)
IPCA 4	28	4.15**	12.94	0.005	0.67	51.32*	20.76**	0.55	76.51**	8.36**	13.16**	18.41**	0.46 (22)
IPCA 5	26	2.64	9.90	0.004	0.51	37.81	15.19	0.49	39.16	5.01	6.38	7.27	0.16 (20)
IPCA 6	24	2.58	8.85	0.004	0.46	35.11	13.25	0.33	33.51	2.77	5.60	6.78	-
IPCA 7	22	1.70	7.75	0.002	0.31	32.88	10.06	0.31	23.80	2.72	4.99	4.83	-
IPCA 8	20	1.52	6.71	0.002	0.25	20.88	10.13	0.28	19.45	1.40	4.60	4.53	-
IPCA 9	18	1.09	4.28	0.002	0.27	16.08	7.06	0.24	16.87	1.17	3.63	3.89	-
IPCA 10	16	0.98	4.18	0.002	0.18	11.62	4.67	0.20	13.30	0.75	2.12	2.15	-
IPCA 11	14	0.62	1.91	0.001	0.09	9.63	3.38	0.19	11.45	0.51	2.14	1.08	-
Residual	576	2.38	9.46	0.004	0.72	33.64	10.56	0.67	48.26	3.50	5.75	6.28	0.94 (288)

*, ** **Significant at P ≤ 0.05, and 0.01 respectively;** in parenthesis are degrees of freedom

Table 7. Heritability (%) estimates of different traits of durum wheat studied over 12 environments

Traits	Environments												Combined
	ATR	ATB	MNR	MNB	DZR	DZB	AKR	AKB	CDR	CDB	SER	SEB	
Grain yield	32	58	26	22	68	63	41	24	39	27	11	20	39
Biological yield	23	33	31	20	22	50	25	32	46	41	42	46	28
Harvest index	47	36	32	41	60	48	30	34	27	55	58	69	67
1000-kernel weight	62	58	86	93	92	93	94	90	83	84	89	73	95
No. of kernels per spike	78	84	83	77	89	87	85	76	73	84	81	82	97
No. of effective tillers/ plant	41	38	43	19	20	54	43	38	34	44	22	15	66
Spike length	62	80	78	32	79	91	76	73	76	76	75	78	95
Plant height	54	58	92	89	96	65	96	96	97	92	92	73	97
Days to 50% heading	94	92	99	96	99	97	90	89	92	98	84	65	97
Days to 75% maturity	89	90	95	89	92	84	44	86	30	72	44	64	91
Grain filling period	55	76	93	74	80	69	63	77	78	90	76	82	90
Grain protein content	58		42		68		54		46		75		71

Where, ATB – Alem Tena Broadcast, ATR – Alem Tena Row, MNB – Minjar Broadcast, MNR – Minjar Row, DZB – Debre Zeit Broadcast, DZR – Debre Zeit Row, AKB – Akaki Broadcast, AKR – Akaki Row, CDB – Chefe Donsa Broadcast, CDR – Chefe Donsa Row, SEB – Selale Broadcast and SER – Selale Row.

Table 8. Genotypic (CV_G) and Phenotypic (CV_P) coefficient of variability and range of different traits of durum wheat studied over 12 environments

Traits	Environments																	
	ATR			ATB			MNR			MNB			DZR			DZB		
	CV_G	**CV_P**	**Range**	**CV_G**	**CV_P**	**Range**	**CV_G**	**CV_P**	**Range**	**CV_G**	**CV_P**	**Range**	**CV_G**	**CV_P**	**Range**	**CV_G**	**CV_P**	**Range**
Grain yield (GY)	6.3	46.7	2.2-5.1	9.3	29.4	3.6-6.5	-1.1	32.5	3.6-6.7	2.9	33.9	2.5-5.2	15.0	36.1	5.9-11.8	22.0	82.9	4.6-15.4
Biol. Yield (BY)	-1.6	67.1	8-12	8.7	62.7	9-15	13.1	111.9	9-18	5.8	73.8	8-15	6.3	62.5	18-25	31.6	127.3	16-30
HI	1.4	2.7	0.30-0.45	0.2	1.8	0.33-0.53	0.2	1.2	0.33-0.50	0.3	1.08	0.30-0.44	0.2	0.7	0.30-0.50	0.2	1.0	0.30-0.49
TKW	22.5	63.9	31-44	22.9	71.7	37-50	51.9	72.2	27-46	53.6	86.4	25-46	52.6	67.2	26-42	60.8	75.3	29-46
No. Kernels	95.9	178.4	27-51	94.6	147.4	26-48	90.9	145.9	37-65	46.5	87.4	40-56	105.3	143.3	44-77	102.9	151.2	43-73
No. Tillers	0.2	16.3	3-5	3.5	20.9	3-6	5.8	155.7	3-5	1.3	19.4	2-3	3.5	44.6	4-8	10.4	37.1	3-7
Spike length	4.4	12.7	5-7	5.9	10.6	5-7	6.3	11.7	5-7	8.9	67.3	4-11	11.4	20.4	5-9	13.8	13.0	6-10
Plant ht.	35.2	125.7	48-75	25.6	65.6	34-70	138.6	174.9	60-101	164.1	77.7	64-100	176.4	82.8	69-119	108.1	287.0	73-122
DTH	38.6	45.5	50-68	28.4	36.0	50-66	37.0	37.7	51-69	25.8	29.3	52-68	27.4	44.2	54-73	32.6	35.7	55-73
DTM	29.9	41.5	81-101	24.6	33.3	84-101	14.1	16.3	91-103	14.3	19.8	92-105	12.1	15.1	100-113	11.9	117.4	103-115
GFD	15.6	53.4	25-39	26.9	52.1	25-42	24.7	30.3	26-43	13.7	28.2	30-10	9.6	15.8	40-48	7.4	17.4	40-48
Protein cont.	4.9	15.6	15.12-19.97				-0.2	13.5	12.63-16.51				3.1	7.9	13.07-16.69			

Table 8. Contd.

Traits	Environments																			
	AKR			AKB			CDR			CDB			SER			SEB		COMBINED		
	CV_G	**CV_P**	**Range**	**CV_G**	**CV_P**	**Range**	**CV_G**	**CV_P**	**Range**	**CV_G**	**CV_P**	**Range**	**CV_G**	**CV_P**	**Range**	**CV_G**	**CV_P**	**Range**	**CV_G**	**CV_P**
GY	7.1	37.8	4.0-7.5	7.4	78.6	3.7-9.0	8.5	48.1	4.8-9.9	5.0	45.8	5.8-10.5	1.7	40.1	2.3-6.3	2.5	31.6	3.0-5.7	21.0	60.9
BY	7.3	73.7	9-15	13.2	98.9	8-16	15.9	72.3	12-20	0.2	78.0	12-20	12.9	66.2	5-15	-2.9	52.0	7-11	17.2	87.0
HI	0.7	74.9	0.36-0.47	0.4	2.8	0.41-0.66	0.2	0.91	0.36-0.51	0.2	0.63	0.39-0.56	-0.3	1.15	0.30-0.52	0.2	0.4	0.37-0.53	1.1	2.1
TKW	51.8	52.5	38-61	40.2	54.1	39-58	47.7	77.0	37-58	45.0	70.2	37-60	38.6	299.9	39-58	29.6	61.8	42-60	371.1	396.3
No. Ker.	116.5	179.3	32-59	145.3	280.7	31-70	104.0	222	35-66	131	206.5	44-76	71.4	123.4	28-51	66.1	110.9	31-51	105.2	1119.5
No. Tills.	3.1	15.0	2-4	-1.6	15.4	2-4	0.2	11.6	3-4	2.6	13.4	3-4	-2.8	21.9	2-3	0.0	13.7	2-3	17.2	37.3
Spk. Len.	4.7	9.0	6-8	5.2	10.9	6-8	5.3	10.6	6-8	0.7	10.5	7-9	-7.1	14.3	4-8	0.5	22.4	5-7	74.1	84.6
Plant ht.	173.3	192.5	72-13	151.2	15.0	70-108	160.4	138	69-109	115	146.4	65-105	134	170.9	70-112	123.5	260.1	62-106	131.7	137.5
DTH	9.1	12.3	58-68	13.5	18.5	57-68	14.8	18.8	63-74	17.4	18.3	63-65	14.4	22.7	57-71	13.2	34.3	74-85	221.6	227.1
DTM	1.2	5.7	107-115	2.6	3.8	106-114	0.7	5.3	115-123	1.4	3.0	118-123	2.0	9.5	128-138	3.8	10.4	130-144	61.9	67.1
GFD	7.9	21.6	45-56	9.3	17.6	46-55	10.4	19.1	43-54	14.1	19.3	43-55	22.9	44.7	50-62	22.7	37.4	64-82	11.1	124.7
Prot. cont.	1.2	4.0	8.62-10.10				2.2	9.7	9.09-11.74				2.2	4.5	7.89-9.94				9.3	17.1

Where: HI = Harvest index, TKW = Thousand-kernel weight, DTH = days to 50% heading, DTM = Days to 75% maturity and GFD = Grain filling duration
ATB – Alem Tena Broadcast, ATR – Alem Tena Row, MNB – Minjar Broadcast, MNR – Minjar Row, DZB – Debre Zeit Broadcast, DZR – Debre Zeit Row, AKB – Akaki Broadcast, AKR – Akaki Row, CDB – Chefe Donsa Broadcast, CDR – Chefe Donsa Row, SEB – Selale Broadcast and SER – Selale Row.

LIST OF APPENDICES

The grain of durum wheat is mainly required for the manufacturing of pasta products (macaroni, spaghetti and semolina) because of its kernel size, hardness, and golden amber color (Efrem *et al.,* 2000a). In Ethiopia, it is also traditionally consumed in a variety of ways. The most common Ethiopian traditional recipes are '*dabo*' (Ethiopian bread), '*injera'* (thin bread), '*nifro'* (boiled whole grain sometimes mixed with pulses), '*dabo kolo'* (ground and seasoned dough shaped and deep fried) and '*kinche'* (crushed kernels, cooked with milk or water and mixed with spiced butter) (Tesfaye and Getachew 1991). Recently, however, with the current privatization policy of the government of Ethiopia, the number of food processing industries is increasing. As a result, there is a rising demand of durum wheat for the production of pasta and macaroni products, which are becoming an important part of daily diet in the urban areas of Ethiopia.

Many of the cultivars of this tetraploid wheat (2n=4x=28) grown in Ethiopia are landraces, and hence, they are mixtures of different types, which have evolved through hybridization and selection over thousands of years under various environmental conditions. Thus, they have low yield potential and poor performance (Getachew *et al.,* 1993; Tesfaye *et al.,* 1998). Research efforts made at Debre Zeit Agricultural Research Center (National Durum Wheat Research Project) led to the development of superior varieties and improved landraces from land race collections and introductions through hybridization and selection yet, these are not enough to substitute to the import made by the food processing agro-industries. Besides, durum wheat generally lack stability of performance and depict inconsistent behavior when grown over wide range of environments. To make it competitive to *Triticum aestivum*, it is essential to develop a variety possessing stable performance, since stability in performance is one of the most desirable properties of a genotype to be identified/released as a cultivar for wide cultivation (Kumar and Chowdhury, 1991).

Therefore, it is important to develop adaptable and stable genotypes with good processing quality to fulfill the current spotlight of the government *i.e.* replace import and make Ethiopian farmers competitors in the world market. Stable performance is a desirable attribute of varieties, for countries such as Ethiopia, where environmental variations are very high and unpredictable (Tesfaye *et al.,* 1998; Adugna and Labuschahne, 2002), which leads to significant genotype-environment interactions

even within a small geographic area, making cultivar development and recommendation more difficult. These difficulties arise mainly from the masking effects of variable environments (Pham and Kang, 1988). Under such circumstances, evaluation of genotypic performance at a number of locations provides useful information to determine their adaptation and stability (Crossa, 1990). Eberhart and Russell (1966) recommended growing of varieties in adequate number of environments, covering a full range of possible environmental conditions, so that useful information is available regarding stability.

Stability refers to non-erratic performance with respect to agronomic traits and stable cultivars show minimal or low interactions (Allard and Bradshaw, 1964). Stability also denotes consistency in rank relative to other cultivars in a given set of environments (Yue *et al.,* 1997). Romagosa and Fox (1993) described yield stability as the ability of genotype to avoid substantial fluctuations in yield over a range of environments. A variety can be considered superior if it has potential for high yield under favorable environment, and at the same time a great deal of phenotypic stability.

The differential performance of genotypes tested across different locations and over different years is due to genotype and environment interaction, and also it influences the selection and recommendations of cultivars (Annicchairico 1997; Tesfaye *et al.,* 1998; Joshi *et al.,* 2002; Adugna and Labuschahne, 2002). It is a major concern to the breeders in the process of evaluation of genotypes when they are grown at several locations for testing their relative rankings, which usually do not remain same. This causes difficulty in demonstrating significant superiority of any variety. Genotype-environment (G x E) interaction is present whether varieties are pure lines, single-crosses, double-crosses, S_1 lines or any other material with which breeders is working (Eberhart and Russell, 1969; Tesfaye *et al*., 1998).

An understanding of environmental and genotypic causes of genotype-environment interaction is important at all stages of plant breeding, including ideotype design, parent selection, selection based on traits and selection based on yield (Katunzi *et al*., 1991; Yan and Hunt, 2001). New varieties are proposed for commercial release, information on genotype-environment interaction and stability, clearly indicating their

specific and/or general adaptations, need to be available for the user (Kumar and Chowdhury, 1991; Adugna and Labuschagne, 2002).

Grain yield, the major concern of most crop breeders, is a complex character and it's the result of interaction of direct and indirect components, influenced by environmental fluctuations (Dabholkar, 1999). It is difficult to manipulate through recording yield alone. Several experimental findings clearly indicated that major yield components in wheat include: fertile tillers per plant, number of grains per spike and 1000 grain weight (Sharma and Kaul, 1986). Thus, by improving these direct and some other indirect components, grain yield can be improved. However, to study this single environment may not provide precise information since environmental effects play an important role (Menon and Sharma, 1995).

Although the performance of a genotype mainly depends on the environmental interactions, yet in many cases a linear relationship is found between performance of genotype and the environmental condition. Several methods have been proposed to analyze genotype-environment interactions or phenotypic stability (Westcott, 1986; Becker and Leon, 1988; Annicchairico, 2002; Adugna and Labuschagne, 2002). Joint regression analysis is the most popular among the univariate methods because of its simplicity of calculation and application, where as Additive Main Effects Multiplicative Interaction (AMMI) is gaining popularity and is currently the main alternative approach to the joint regression analysis in many breeding programs (Westcott, 1986; Annicchairico, 1997; Adugna and Labuschagne, 2002). This model is considered appropriate; if one is interested in predicting genotypic yield in specific environments and it is proved that it is valuable in genotype by environment interaction studies (Zobel *et al.,* 1988; Annicchairico, 1997).

Estimate of phenotypic stability, which involves regression analysis, has proved to be a valuable technique in the assessment of the relationship between the response of genotype and environmental changes. The present investigation, therefore, was carried out with the following objectives:

1.1 Objectives:

i. To estimate adaptability and phenotypic stability parameters for grain yield, its components and protein content.

ii. To classify environments and identify stable genotypes performing well under high, medium and low yielding environments.

iii. To assess genetic variability and estimate heritability of important agronomic and quality traits.

2. LITERATURE REVIEW

2.1 Durum wheat

2.1.1 Origin and characteristics

Tetraploid wheat (*Triticum turgidum L. var. durum)* is the most important wheat species cultivated in Ethiopia. Taxonomically wheat belongs to the genus *Triticum*, subfamily *Pooideae* of the grass family *Gramineae (Poaceae)* (Briggle and Reitz 1963). The Mediterranean region and Ethiopia are the most important centers of diversity for the species and North Africa and West Asia account for the large part of its production in developing countries (Tesfaye *et al.,* 1998; Abebe and Giorgis, 1991).

2.1.2 Climatic and soil requirements

Altitude plays an important role in the distribution of wheat production through its influence on rainfall, temperature, and diseases and insect-pests. In Ethiopia they are distributed mainly in the altitudinal range of 1800-2800 meters above sea level. In Shoa regions, the soil, moisture and disease condition in the 1900-2300m a. s. l. altitude zone are favorable for the production of early and intermediate maturing varieties of wheat. This is estimated to comprise 25% of the total wheat area, while the remaining 75% falls in the 2300-2700m a. s. l. altitude zone. There, early, intermediate and late varieties are grown. Soil types used for wheat production vary from well-drained fertile soils to water logged heavy vertisols (Tesfaye *et al.,* 1998).

2.1.3 Uses of Durum wheat

Wheat constituents a large portion of the daily diet of the population and contributes significantly to the calories and protein intake. The average per capita wheat consumption is 0.9% per year (CIMMYT, 2000). This trend will increase especially in the urban areas in the future.

European and American countries almost totally use durum wheat for pasta products, whereas in the Middle East and North Africa, local bread-making accounts for about half of the consumption and about equal shares, are used for pasta, couscous and various other uses (Efrem *et al.,* 2000b).

The grain of durum wheat in Ethiopia is consumed in different forms such as leavened bread, pancakes, macaroni and spaghetti, biscuits and pastries. The most common

Ethiopian recipes are: Dfo-Dabo (Ethiopian loaf or bread) which is usually prepared during holidays and festive occasions, hambasha (bread from Northern Ethiopia), Kitta (unleavened bread), injera (thin bread), nifro (boiled whole grain sometimes mixed with pulses), kolo (roasted grain), dabo-kolo (ground and seasoned dough, shaped and deep fried), kinche (crushed kernels, cooked with milk or water and mixed with spiced butter, and chechebsa (thin flat bread broken in to small pieces and rubbed with spiced butter) (Tesfaye and Getachew 1991; Efrem *et al.,* 2000b).

Straw is mainly used as livestock feed and fuel at times of scarcity. Ethiopia used to export durum wheat grain and flour until the late fifties (Pinto, 1971 cited from Efrem *et al*., 2000b). Today, however, the country is importing about 0.7 million tons of wheat grain and flour per year through foreign purchases and food aid (Efrem *et al*., 2000 b).

2.1.4 Grain protein

Durum wheat is a good source of protein. The average protein content is higher for durum wheat than bread wheat and may vary from 9-18% (Simmonds, 1989). He also compared the protein content in durum wheat and other cereals and found 13 and 12% (dry basis) for durum and bread wheats, respectively. As in most grain quality traits in wheat, protein content is known to be affected by genetic and environment mainly location (Bemnet *et al*., 2003).

Grain protein concentration is the most important index of semolina quality for pastification, which depends on the interactions among genotype and environmental and agronomic factors. Nitrogen availability in the soil (Banziger *et al*., 1992), air temperature (Craffi *et al*., 1996) and soil water content (Fares *et al*., 1993) during grain filling are particularly important.

Applications of nitrogen fertilizers increase the quantity of yield, with a subsequent increase in grain protein. The agronomic management of nitrogen fertilization and the utilization patterns by the plant are, therefore, of major concern for the improvement of durum wheat grain quality. With this background, the National Durum wheat Research Project tested some genotypes in Debre Zeit and Akaki for the improvement of grain protein quantity and quality by application of different levels of nitrogen fertilizers (Bemnet *et al*., 2003). But the ideal environment for better grain protein durum wheat production is not yet clearly identified. Thus the present work may give some information.

Pasta products made from durum wheat semolina require adequate level of protein for proper processing characteristics nutritional value and overall quality (Efrem *et al.,* 2000a). A grain protein content of 13% for durum is a standard in quality throughout the grain industry (Riley *et al.,* 1998).

2.1.5 Factors affecting durum wheat production and quality

The increase in population and the subsequent rise in the demand for agricultural produce are expected to be greater in many developing countries where production is already insufficient in particular regions with unfavorable conditions. Breeding widely adapted genotypes with stable and high yield across environments is important for these countries since yield-stabilizing inputs are often limited or not available. Limitations in yield-stabilizing inputs in developing countries increase the need for widely adapted genotypes to cope with environments require different trait combination (Braun *et al*., 1992). Due to the masking effect of these variable environments breeders encounter difficulties in selecting new varieties for release (Tesfaye *et al.,* 1998). Romagosa and Fox (1993) indicated that the common breeding strategy for variable environments is generally to develop widely adapted varieties by testing over a range of diverse conditions covering representative samples of spatial and temporal variations.

Among the major bottlenecks, genotype by environment (G x E) interactions are challenging for breeder recommendation of genotype across environments. This is because; G x E interaction reduces the association between phenotypic and genotypic values and may causes selections from one environment to perform poorly in other, forcing breeders to examine genotypic adaptation (Romagosa and Fox, 1993). Interaction of genotype and environment occurs when a specific difference of environment many have greater effect on some genotypes than on others; or there may be a change in the orders of merit of a series of genotypes when measured under different environments (Hernandez *et al*., 1993; Yan *et al*., 2000).

But in the case of developing countries, and particularly in unfavorable conditions, a very different picture is offered, because of complex problems. Resource-poor farmers in many region of the world practicing agriculture in these situations have adopted a strategy based on both interspecific and intraspecific diversity to overcome the risk (Ceccarelli, 1997). The theoretical framework of this issue developed by Falconer in (1989) that if a breeder wants to improve performance in environment A, he should select in environment A. That is to say that the top yielding lines a breeder select in high yielding environment would not be selected in low yielding environment and a wheat breeder select in high yield environment would not be selected in a low yielding environment and vice versa. The reason for this is G x E crossover interaction (Ceccarelli and Grando, 1991). Plant breeding strategies should, therefore, be different in stress and non-stress environments because of the intensity of crossover interaction.

2.2 Genotype by environment (G x E) interaction

To a geneticist, environment is the sum total of physical, chemical and biological factors that influence the development of an organism (Dabholkar, 1999). Basford and Cooper (1993) described the environment as ‘a complex assemblage of interacting physical, chemical and biological systems with considerable uncertainty about both their nature and their interconnections’. In other words, the term environment relates to the set of climatic, soil, biotic (pests and diseases) and management conditions in an individual trial carried out at a given location in one year (in the case of annual crops) or over several years (in the case of perennial crops). In particular, an

environment identifies a given location-year (annuals) or location-crop cycle (perennials) combination in the analysis of trials repeated over time (Romagosa and Fox, 1993).

G x E interaction is differential genotypic expression across environments and largely arises from the diverse response of genotypes to climatic variables (mainly temperature and rainfall) and soil characteristics during plant growth and development. Yan *et al.,* (2000) stated that, any measured yield at a given location in a given year is a mixture of the year, location and genotype main effects plus various interaction effects. Reliable selection for the genotype main effect requires removal of other unfixable variations, that is, the various year and location related effects. The only way to achieve this is to conduct multiple-location trials in multiple years (Rea and Vieira, 2002). Multilocation variety trials play a decisive role in the effort to identify and develop promising genotypes on the basis of phenotypic stability in different environments (Vargas *et al.,* 1999; Tiruneh, 2000). However, this depends on the level of accuracy of yield estimates and magnitude of G x E interactions (Gauch, 1988).

G x E interaction is studied in order to answer a number of questions related to varietal adaptation and stability. Understanding G x E is useful, amongst others for developing different cultivars in different agro-ecologies, effective allocation of resources and for the characterization of genotype responses to variable productivity levels (Yau, 1995).

Researchers usually ignore G x E interaction encountered and base genotype selection solely on mean performance across environments. Plant breeders and agronomists need a practical selection that would use or exploit G x E interaction. Despite availability of and comparisons among several methods designed to combine yield and stability in to a single selection criterion (Kang and Pham, 1991), practical integration of stability of performance with yield has not been achieved.

Ignoring G x E interaction is problematic when interaction is larger than the genotype main effect, which is a common scenario in yield trials (Gauch and Zobel, 1997). In wheat variety trials large G x E interaction complicates agronomist's and breeder's research because durum wheat performance is less predictive and cannot be interpreted on the basis of only genotype means and environment means. Furthermore, interaction complicates cultivar recommendations because genotypes must be targeted to specific locations (Rea and Vieira, 2002).

The emphasis on Genotype by location (G x L) interaction effects is justified even when analysis of adaptation relates directly to genotype response to environmental factors. Specifically adapted genotypes can be targeted to respond well under environmental conditions prevailing in a given area, provided that these conditions are not highly variable from year-to-year (Girma *et al.,* 2000).

Very often breeders encounter situations where the relative rankings of varieties change from location to location and/or from year to year. The interplay in the effect of genetic and non-genetic on development is termed as 'genotype by environment (G x E) interaction' (Comstock and Moll, 1963; Prabhakaran and Jain, 1992).

2.2.1 Component of G x E interaction

G x E interaction is composed of genotype by location (G x L), genotype by year (G x Y) and genotype by location by year (G x L x Y) constituents (Gauch and Zobel, 1996). If G x L is the important portion of G x E, then specific adaptation is exploitable by subdividing target areas in to homogeneous regions that minimize G x E interaction within regions (Yan *et al.,* 2000). Generally, testing over a representative range of conditions is the common strategy. Such wide testing necessitates description of genotypic response across environments. Breeders aim to cover a representative sample of spatial and temporal variation. Some times a breeder’s selection of environments in one year may have little relation to those experienced in the next (Tiruneh, 2000). The sampling problem associated with yearly variation would suggest testing for many crop cycles. However, to save time breeders opt to substitute temporal variation with spatial variation, assuming that testing over a wide geographic range can ensure parallel degree of temporal buffering capacity in their germplasm (Becker and Leon, 1988).

Significance of mean square for genotypes by locations suggests that the region for which genotypes are being breed comprises of a number of special environments. In such circumstances geographic region could be subdivided in to sub-regions that are relatively homogeneous.

2.2.2 Causes of G x E interaction

The G x E interaction is as much a function of the environmental variables and a function of the genotypic, morphological, phenological and physiological traits of the varieties. Identification of causal factors of the G x E effect and quantification of the unexplained variation are of prime importance for selecting for stability or to recommend environmentally superior varieties (Signor *et al*., 2001).

Reasons for the occurrence of G x E interactions can be expected when there is wide variation between genotypes for morphophysiological characters conferring resistance to (or avoidance of) one or more stress (es) (as determined by climatic, soil, biotic and management factors) (Annicchiarico, 2002).

Understanding of the causes of G x E interaction can be used to establish breeding objectives, identify ideal test conditions, and formulate recommendations for areas of optimal cultivar adaptation. Understanding of the cause of G x E interaction is also used to identify traits that contribute to better genotype performances and environments that facilitate genotype evaluation (Yan and Hunt, 2001).

Most of the characters of living organisms are determined by nuclear borne genes. The genetic material in higher organisms is Deoxy-ribo Nueclic Acids (DNA), which is composed of nucleotides of four kinds. Metabolic processes in living organisms are catalyzed by enzymes, which are mainly composed of proteins. Structure and function of proteins is determined by genetic material-the genes. It is now well known that the sequence of nucleotides on DNA strands determines the sequence of amino acids on polypeptides. Any change in the sequence of nucleotides leads to a corresponding change in the sequence of amino acids in polypeptides and ultimately change in genetic function. Environmental agencies, both internal and external, can lead to altered nucleotide sequence, which is recognized as mutations. Mutation is reflected

in altered gene function and subsequently changed phenotype. We know that biosynthesis takes place in stepwise fashion such that each step governed by an enzyme whose structure/function is determined by a particular gene. Thus, there are many opportunities for environmental fluctuations to induce G x E interactions at various levels of metabolism. While this provides an insight in to the complex causes of G x E interactions and offers more opportunities by which they could be investigated (Hulmel *et al.,* 1999).

2.2.3 Significance and Implication of G x E interaction for plant breeding

G x E interaction is an important concern to all plant breeders. A given cultivar performs differently in different environments due to G x E interactions. In any breeding program, it is necessary to screen and identify phenotypically stable genotypes that could perform uniformly under different environmental conditions. Such a breeding effort requires basic information of G x E interaction (Kumar and Chowdhury, 1991). The interaction can hinder progress from selection by masking genotypic effect (Comstock and Moll, 1963). The presence of G x E interaction reduces the correlation between phenotype and genotype making it difficult to assess the genetic potential of a particular genotype whose relative ranking will be altered in different environments (Prabhakaran and Jain, 1992).

Evaluation of genotypic performance at a number of locations provides useful information to determine their adaptation and stability (Crossa, 1990). Measuring G x E interactions helps to determine an optimum breeding strategy of either to breed for specific or wide adaptation, which depends on the expression of stability under a limited or wide range (Yue *et al.,* 1997). Moreover, G x L interaction allows the grouping of relatively similar sites in relation to genotypic performance within which the interacting is minimum (Eberhart and Russell, 1966; Romagosa and Fox, 1993; Annicchiarico, 1997).

When G x E interaction is due to variation in predictable environmental factors (location), breeders can have the alternatives of either developing specific varieties for different environments (locations, soil types, management systems, etc.), or broadly adapted varieties that can perform well under variable conditions (Adugna and Labuschagne, 2002).

If there were no G x E interactions selection would be greatly simplified because the 'best' genotype in one environment would also be the 'best' genotype for all target environments. Experience suggests that this scenario is the exception rather than the rule (Basford and Cooper, 1993). Therefore, G x E effects should not be ignored, rather analyzed using appropriate techniques, in order to explore the potential opportunities and disadvantages (Annicchiarico, 2002).

An understanding of environmental and genotypic causes G x E interaction is important at all stages of plant breeding, including ideotype design, parent selection, selection based on traits and selection based on yield. G x E interaction is present whether varieties are pure-lines, single crosses, double-crosses, top-crosses, S_1 lines or any other materials with which breeder is working (Romagosa and Fox, 1993). The magnitude and nature of G x E interactions often dictate the features of breeders' selection and testing procedure (Mussa and Yohannes, 2003).

2.3 Adaptability and phenotypic stability

Adaptability is the ability of a genotype to show good adaptedness or adjust in a wide range of environments. In breeding for wide adaptation (*i.e.* adaptability), the aim is to obtain a variety that performs well in a definite subset of environments within a target region. Genotypic adaptation implies the shaping of population and species gene pool in response to environmental changes. A genotype will be considered adapted from the breeding point of view to a given type of conditions when it is able to give an economic production, and not necessarily only survive in that set of conditions. The adaptive response of a variety is assessed with respect to other genotypes and tends to undergo modification when better performing germplasm becomes available (Annicchiarico, 2002).

The adaptability of a variety over diverse environments is usually tested by the degree of its interaction with different environments under which it is planted. A variety or genotype is considered to be more adaptive or stable one if it has a high mean yield but a low degree of fluctuation in yielding ability when grown over diverse environments (Becker and Leon, 1998).

The success of crop improvement activities largely depends on the identification of superior varieties. A variety can be considered superior if it has potential for high yield under favorable environment, and at the same time a great deal of phenotypic stability. Stability refers to non-erratic performance with respect to agronomic traits and stable cultivars show minimal or low interactions (Allard and Bradshaw, 1964). Stability also denotes consistency in rank relative to other cultivars in a given set of environments (Yue *et al.,* 1997; Ali *et al.,* 2003).

Tesfaye *et al.,* (1998) suggested the selection of materials that maintain productivity in poor environments or that are superior in favorable environments rather than those with regression coefficients equal to 1. Genotypes with b=1 are less productive in poor environment than those with low regressions and also yield less in favorable environments as compared to these with high regressions. Limitations in the availability of inputs in developing countries increase the need for stable cultivators that cope with environmental variation. In situations where the availability of inputs are not ensured, cultivars with good performance and stability should be recommended. There are two ways by which a variety can achieve stability in performance. Firstly, the variety can be made up of a number of genotypes each of which is adapted to a somewhat different range of environments. Secondly, individuals themselves may be well buffered so that each member of the population is well adapted to a range of environments (Dabholkar, 1999).

2.3.1 Stability of yield and related components

Yield stability is complex because it involves genetic, physiological, morphological and phenological traits (McVetty and Evans, 1980). Yield improvement can be achieved by selecting for yield per se or their components, through improvement of morphological and physiological trait, and by factors that reduce yield losses.

High yield stability may be associated with low mean yield (or low stability with high mean yield), which complicates genotype selection or recommendation (Bekele *et al*., 1992). As an extreme example of high stability associated with low yield, consider a hypothetic genotype that yields just above zero in all environments (greatest stability according to its static concept), or that is consistently the least yielding (greatest stability according to the dynamic concept (Annicchiarico, 2002).

Many of the characters that plant breeders seek to improve are morphologically, physiologicaly and genetically complex. Subdivision of the complex character into components represents chronological steps in the developmental processes. Grain yield in wheat can be analyzed in terms of yield components (for *e,g*. number of kernels per spike and kernel weight) (Garcia del Moral *et al.,* 2003) that appear sequentially with later developing components under control of earlier developing ones.

Sultana *et al.,* (2002) emphasized that the study of individual yield component can lead to simplification in genetic explanation of yield stability and hence is valuable to breeders in prediction and determination of the effect of environment. Although we may be able to increase yield using one component, in most cases, it will be very slow because of the compensation in other yield components (Romagosa and Fox 1993).

Developing crop cultivars with high grain yield has been the principal aim of durum wheat breeding programs worldwide. In Ethiopia, it is of special interest because of the low and erratic distribution of rainfall. This is specially severe in the lowlands, resulting in a moderate stress around anthesis, which increase in severity throughout grain filling (Gebeyehou *et al.,* 1982). Understanding the effect of environmental variations on yield and its component formation becomes an essential step in the development of higher-yielding and more stable cultivars.

Belay *et al.* (1993), found that kernels per spike was the yield component most sensitive to drought while kernel weight remains relatively stable due to high remobilization of stored parenthesis assimilates. Kernel weight may suffer a terminal stress caused by high temperatures that increase evaporation from the soil, particularly in the warmer regions, *i.e*. in the lowlands.

Mather and Jinks (1971) observed the plants that perform well in dry areas must integrate many characteristics that contribute to efficient use of moisture. Stand establishment and successful early tiller production have also been shown to contribute to high yields under drought conditions.

Plants produce their maximum biomass under adequate water supply, whereas moisture stress causes a marked decrease in plant biomass production (Saleem, 2003). Harvest index has been amongst the most commonly advocated physiological parameters to be used as estimator of yield potential in small grains (McVetty and Evans, 1980). Kernel weight was the unique yield component that was moderately sensitive to moisture regime variations and appeared to be relatively stable to temperature changes (Garcia del Moral *et al.,* 2003). But it is known to be affected to a significant extent, by degree of genetic make-up as well as the growing environment and weather conditions at harvest (Bemnet *et al*., 2003).

Heading date plays an important role in the determination of biomass. The change in growing environment and plants heredity influences all yield, yield components, biomass and heading date. Soil moisture, soil fertility and atmospheric temperature affect the growth processes; development and expression of yield components (Sultana *et al.,* 2002).

Grain filling period is the period between flowering and physiological maturity. Physiological maturity is the point after which there is no significant increases in the amount of grain dry matter. The variation in grain filling period can be used to design durum wheat variety suitable to a particular environment. Grain weight is the product of the rate and duration of the grain filling period. Grain filing involves the translocation of photosynthetic products from the source to the sink. 80-90% of wheat grain carbohydrates are synthesized after flowering, while the remaining 10-

20% are translocated from the plant's reserves (Przulj and Madenov, 1999; Gebeyehou *et al.,* 1982).

Grain filing is maintained by a high contribution from assimilation before and immediately after anthesis and remobilization of vegetative revenues during kernel growth. In the same way, water deficit around anthesis may lead to a loss in yield by reducing spikelets per spike and the fertility of surviving spikelets (Sultana *et al.,* 2002). In addition, drought stress from anthesis to maturity, especially if accompanied by high temperatures, hastens leaf senescence, reduces the duration and rate of grain filling, and hence reduce mean kernel weight under different environments.

The duration of the sowing-to-heading phase is determined by the genotype's photoperiodic and temperature responses (Gebeyehou *et al.,* 1982). This phase includes tillering and organogenesis processes, during which the formation of two important yield components takes place: spikelets per spike and grains per spike. Similarly, medium maturity and dwarfness in durum are also preferable to harvest higher grain yield under high input management conditions (Sharma and Sain, 2004).

Days-to-heading was believed to affect the duration of grain filling period, and kernels per spike. Differences between genotypes in time to maturity can have a pronounced yield effect on yield per crop where selection has focused on earlier maturity, there may be no increase in yield per crop but a marked increase in yield per day (Evans and Fischer, 1999).

Tiller production is known to be the 1st developmental process in cereals, and then it may exercise a direct influence on all other traits that are developed later. The duration of grain filling period could modify kernels per spike by reducing abortion of pollinated florets after anthesis (Garcia del Moral *et al,* 1991; Belay *et al.*, 1993).

2.3.2 G x E interaction and Stability analysis

Various methods have been proposed for the statistical analysis of interaction in general, and G x E in particular. All are attempted to discover more by assuming that "data = pattern + noise", and most want to get pattern while eliminating the maximum noise (Freeman, 1973). These methods can be divided in to two major groups, *i.e.* univariate and multivariate stability statistics. Joint regression is the most popular among the univariate methods because of its simplicity of calculation and application, where as AMMI is gaining popularity and is currently the main alternative multivariate approach to the joint regression analysis in many breeding programs (Annicchiarico, 1997).

2.3.2.1 Stability analysis using Eberhart and Russell (1966) model

Different stability estimates have been proposed to measure the consistent performance of genotypes tested across a wide range of environments. Pooled analysis of variance combined with joint regression analysis proposed by Yates and Cochran (1938) cited from Frnacis and Kannenberg (1978), modified by Finlay and Wilkinson (1963) and made popular by Eberhart and Russell (1966) has been, and still is, a popular technique for studying G x E effects and stability. They used two parameters (b_i and S^2d_i) to define stability. S^2d_i is largely used to rank the relative stability of cultivars (Becker and Leon, 1988). The indication is that b_i could be used to describe the general response to the goodness of environmental conditions where as S^2d_i actually measures the yield stability (Adugna and Labuschagne, 2002). According to this model a stable variety is one that has high mean (X_i), unit repression coefficient (β_i=1) and the deviation from regression as small as possible (S^2d=0).

2.3.2.2 Stability analysis using Additive Main effects and Multiplicative Interaction (AMMI) model

The model was developed in 1952 (Williams, 1952 cited from Yau, 1995). It has been called biplot analysis, or considered simply as principal component (PC) analysis, and was used before the introduction of the term AMMI analysis. Lately, AMMI analysis has been applied to different crops by different scientists (Zobel *et al.*, 1988; Crossa *et al*., 1990).

AMMI analysis is inherently more versatile than joint regression analysis (JRA), because it can use one, two, or more axes as needed to represent the interactions for a given data set. Thus, AMMI analysis is less prone to the problem commonly encountered with JRA (i.e., the low amount of G x E explained). Usually only PC1 is used in biplot, because PC1 is the most informative and usually the only component shown in biplot (defined here as graphs containing two kinds of points or entities, rather than a kind of analysis). But PC1 and PC2 can be plotted together (Kempton, 1984).

Biplot is a powerful way of detecting important sources of G x E effects (Zobel *et al*., 1988), besides being statistically more effective. On a biplot, genotypes and sites having PC1 values close to zero have small interaction effects, while those having large positive or negative PC1 values are largely responsible for the G x E interaction. Entries yield relatively better in sites having PC1 values of the same sign, but not in sites with PC1 values of opposite sign. Plant breeders can easily select from a biplot those entries that are high yielding and stable (little interaction with sites). This model is considered appropriate if one is interested in predicting genotypic yields in specific environments (Annicchiarico, 1997). The IPCA scores of a genotype in the AMMI analysis is an indication of the stability of a genotype across environments (Yau, 1995; Guach and Zobel, 1996).

However, the general replacement of JRA with AMMI is not supported. Which analysis to use depends on a study's objectives. If the aim is to study the G x E interaction in detail, then AMMI is definitely preferable for many breeders, however, if simple knowledge of the responsiveness of entries to growing conditions is important, then this information cannot be provided by AMMI analysis. The AMMI model combines the additive analysis of variance for main effects with the multiplicative PC analysis for the interaction (i.e the residual from the ANOVA). The effectiveness of AMMI analysis is due to its capturing a large portion of the G x E sum of square, clearly separating main and interaction effects, providing agricultural researcher with different kind of opportunities and the model often provides agronomically meaningful interpretation of the data. Addition results from AMMI are useful for performing environment classification for easy cultivar recommendation (Gauch and Zobel, 1997).

2.3.3 Genotype and environment classification using AMMI Biplot

As peculiar feature, AMMI can concentrate on genotype main effects that are relevant for environment classification while ignoring environment main effects and most of the interaction noise that are irrelevant. AMMI environment classification is important for the main question to answer 'what wins where'. It is powerful to answer this question and important for grouping locations with identical winner in to mega-environment and for targeting suitable genotypes for each mega-environment. Most of the time AMMI-1, *i.e*. a biplot using the first IPCA axis, is used for environment classification since for most of the traits the variation absorbed by the first IPCA score is much larger than any other axis (Ebdon and Gauch, 2002).

The National Durum Wheat Breeding Program of Ethiopia aims at developing widely adapted, stabile and high yield genotypes with resistance to biotic and abiotic stresses. On the other hand Ethiopian farmers repeatedly experienced crop failure or fluctuations in crop production due to erratic and inadequate rainfall almost in alternating years. This combined with diverse agro climatic condition of the country which vary even within small locations (Getachew *et al*., 1993) and greatly affect yield stability estimates. Therefore, it is necessary to form homogenous sub grouping of environments and genotypes and to identify stable and high yielding cultivars.

Although AMMI analysis of yield data does not use environmental data but environmental factors such as rainfall, temperature, attitude, latitude, nitrogen fertilization, irrigation and clay content have often been found to be correlated with AMMI environmental interaction statistics (singular vector). The results of AMMI analysis are useful in supporting breeding program decisions such as specific adaptation to target and selection of environments or test site locations (Gauch and Zobel, 1997).

2.4 Heritability

The ratio V_G/V_P (where V_G and V_P are genotypic and phenotypic variances, respectively) expresses the extent to which individual phenotypes are determined by the genotypes. This is called heritability in broad sense, or the degree of genetic determination (Amin *et al.,* 1992). The extent of heritability determines transmissibility of polygenic traits like plant height, thousand-kernel weight, grain yield per plant, etc. (Firouzian, 2003).

The magnitude of heritability in different environment varies more as function of the genetic variability of the material; included in a given trial, and adaptive or constitutive nature of the genotypic difference than as function of environment. Adaptive character, which will be expressed only when exposed to a given environment, may actually show a large heritability under non-stress condition (Ceccarelli, 1989). To strength this observation (Falconer and Mackay, 1996; Ceccarelli, 1997) yield in low and high yielding environment can be considered as separate traits, which are not necessarily maximized buy identical sets of alleles.

G x E interaction hinders the expression of single plant heritability and prevents early generation selection for final characters (yield, quality and stability). One of the necessary preconditions to optimize and exploit single plant heritability is exploitation of G x E interactions (Askew *et al*., 1997). Both its genotype and environmental variance determine the individual genotype. The proportion of the observed variation in a progeny that is inherited determines coefficient of heritability.

Earlier studies pertaining to heritability in wheat have indicated variable results. High estimates of heritability for plant height and grain yield was recorded by Saleem, *et al*. (2003) while Gupta and Verma (2000) cited from Firouzian (2003) found medium to low and Chowdhry *et al*. (1997) found moderate to high heritability estimates for plant height and grain yield in wheat. Firouzian (2003) found 75% to 93.31% for plant height, 85% to 96.37% for thousand-kernel weight and fairly high heritability estimates for grain yield.

Saleem, *et al*. (2003) observed 63.31% to 90% heritability for thousand-kernel weight. Chowdhry *et al.* (1997) also observed moderate to high estimates of heritability for thousand-kernel weight.

2.5 Genetic variability

Combination of traits in a plant, which minimize the deleterious effects and maximize the advantageous effects results in the real success of a plant (Ceccarelli *et al.,* 1991). Hybridization is one of the main tools to produce genetic variability. Genetic variability is the basis of selection and further improvement in any crop species. Broader the range of heritable variation more effective will be the selection and vice versa (Firouzian, 2003). The practical knowledge of mechanisms of inheritance of the genetic traits involved, occupies key post in the process of progress forwards desired end (Chandra *et al.,* 2004).

3.MATERIALS AND METHODS

3.1 Description of experimental sites

The experiment was conducted in twelve environments comprising of six locations namely; Alem Tena, Minjar, Debre Zeit, Akaki, Chefe Donsa and Selale (in the farmer's field) with two planting patterns (Row and Broadcasting). These locations are the main multi-location variety testing sites for the National Durum Wheat Research Project and are representative to the different wheat growing agro-ecologies in the region. Accordingly Chefe Donsa, Akaki and Selale represent the highland zones (2200-2750 meters above mean sea level) and are characterized by high annual rainfall (>1000mm) and poorly drained black (vertisol) soils. Debre Zeit and Minjar (1900-2300 meters above mean sea level) represent the mid-altitude areas and are characterized by moderate annual rainfall (700-900mm) and well drained black (vertisol) soils. Alem Tena is a representative site (1575 meters above mean sea level) for moisture stress area in the rift valley having a well-drained sandy soil, and mostly erratic type of annual rainfall (500mm).

In general, the experimental sites vary considerably in their edaphic and climatic conditions. Maximum and minimum monthly temperature (^{0}C) and monthly rainfall (mm) for the year 2004 given in Appendix 1 whereas altitude, soil type and recommended dates of sowing for the test sites are given in Table 1.

3.2 Genetic materials used in the study

The experimental materials consisted of 25 genotypes among which 14 were introduced from CIMMYT, seven advanced from the National Durum Wheat Research Project crossing program, two released varieties (Yerer and Gerardo), one landrace local check (DZ-04-118) and one recently released high yielding standard check (Ude). List of the genotypes along with their pedigree, sources of origin and sta tus are given in Table 2.

Table 1. Altitude, soil type and recommended dates of sowing for the test sites

No.	Location	Altitude (Meters above mean sea level)	Soil type	Recommended dates of sowing
1	Alem Tena	1200m	Light soil	July 10
2	Minjar	1800m	Vertisol	July 15
3	Debre Zeit	1900m	Pellic vertisol	July 13
4	Akaki	2200m	Pellic vertisol	July 21
5	Chefe Donsa	2450m	Pellic vertisol	July 23
6	Selale	2750m	Pellic vertisol	July 30

Remark:. *The soil in Alem Tena is sandy in addition to being light soil.*

3.3 Description of the Experiment

The field trials were conducted under rainfed condition in the 2004 growing season at six locations. The experimental materials at each location were sown with two methods of sowing (row and broadcasting) using a randomized complete block design (RCBD) with three replications. The plot size was 2.0 m^2 with four rows of 2.5m length and 0.20m width. The seeds were sown by hand at a rate of 150 kg/ha (30gm/plot) and the planting depth was kept at 5cm. Sowing date and fertilizer application were done according to the specific recommendations given to each location (Table 1). The recommended full rate of phosphorus, in the form Diammonium Phosphate (DAP) was applied at planting while nitrogen, in the form of Urea was applied half at planting and the half at tillering stage of the crop development. Weeds were controlled twice at tillering and boot stages by hand weeding.

Table 2. Pedigree and source of durum wheat genotypes used in the study

Code	Genotypes	Pedigree	Source	Status
01	CDSS92B1467	NEHAMA-15/BRZINA-2//PLATA-8	CIMMYT	Advanced line
02	CD91Y7	AUK/GUIL//GREEN	CIMMYT	Advanced line
03	CD94523	DACK/KIWI//OSTE/3/CHEN 841/4/MEX175/5/	CIMMYT	Advanced line
04	CDSS93Y33	HC/3/GUIL//CIT71/C11	CIMMYT	Advanced line
05	CD91989	HIPER-1/PLATA-16	CIMMYT	Advanced line
06	CDSS92B193	NEKAT-1/LOTUS-4	CIMMYT	Advanced line
07	CD97383	LABUD/SRN2	CIMMYT	Advanced line
08	CD98206	LABUD/INGRIS 3//GAN	CIMMYT	Advanced line
09	CIGM91-349	ALTAR 84//ALTAR 84/SERI/3/6*ALTAR 84	CIMMYT	Advanced line
10	CIGM91-347	ALTAR 84//ALTAR 84/SERI/3/6*ALTAR 84	CIMMYT	Advanced line
11	CD94545-A	ALGA/HUI//YAV 79/3/FILLO 14/GODIN	CIMMYT	Advanced line
12	DZ2234	IMLO/Ranum/A4#72/3/GERARDO -4BS-1DZO-KBS-4KBS	CIIMYT/ ETHIOPIA	Advanced line
13	CD95294-1Y	CHEN/ALTAR 84//JO 69	CIMMYT	Advanced line
14	DZ2212-1BS	Yemen/cit"s'//Pie's'/3/Taganroy/4/Hui 's'//cit 71/GII	CIMMYT	Advanced line
15	DZ2293-2DZR	BHA"s"//cit 71/CII/BOY's'/4/3* Shenkora 29	Ethiopia	Advanced line
16	DZ1675-1AK	Yemen cit's'/pic's'/Taganroy B. B/4/Hora Lraspirgro//cm9908/3/Rahum	CIMMYT	Advanced line
17	DZ1669-1AK	Yemen cit's'/pic's'/Taganroy B. B/4/Boohai/Hora//Gerardo/Boohai	CIIMYT/ ETHIOPIA	Advanced line
18	CD91313	KARA-CAYLAK-2-1A	CIMMYT	Advanced line
19	DUKEM/3/RUF	DUKEM/3/RUFF/FGO//YAV 79	CIMMYT	Advanced line
20	DZ3117	GONDAR 22/DZ 04-118//DZ 1052	ETHIOPIA	Advanced line
21	Yerer	Chen/Tez/3/Guil//CII	CIIMYT	Released variety in 2002
22	CDSS93Y545	PLATA 10/TRNLET-2	CIMMYT	Advanced line
23	Gerardo	VZ 466/61-130xGII''s'', CM9605	CIMMYT/ ETHIOPIA	Released variety in 1976
24	DZ- 04-118 (Local check.)*	–	ETHIOPIA	Improved landrace released in 1976
25	Ude (S. check)	Chen/ALTAR 84//Aid	CIMMYT	Released variety in 2002

**** = Local check developed through mass selection***

3.4 Data recorded

The data were recorded on five randomly selected plants per genotype per replication for the following traits.

3.4.1 Grain yield and its components

i) Grain yield per plant (GYP): Grain yield per plant in grams was taken after harvesting, threshing, cleaning and drying the produce at about 12.50% moisture content.

***ii) Biological yield per plant (BYP)*:** The plants harvested for the analysis of grain yield per plant were weighed in grams at about 12.50% moisture content before threshing to obtain biological yield per plant.

iii) Harvest index (HI): It was calculated as ratio of grain yield per plant to total biological yield.

HI = Grain yield /Total biological yield

***iv) Number of grains per spike (NGS)*:** NGS were counted from the main tiller of each of the spike of five randomly selected plants and expressed as average.

v) 1000-kernel weight (TKW): One thousand kernels were counted from a random sample drawn from bulk produce and weight in grams was recorded.

3.4.2 Morphological traits

***i) Plant height (PH)*:** Plant height was measured from the ground level of the plant to the tip of the spike, excluding the awn in centimeters (cm).

***ii) Number of effective tillers per plant (NTP)*:** The tillers with effective spikes on each of the sampled plants were counted and averaged to represent the number of effective tillers/per plant.

***iii) Spike length (SL)*:** The average length was measured from base to tip of the main spike.

3.4.3 Phenological traits

i) Days to 50% heading (DTH): Days to 50% heading were counted as the number of days from planting to full emergence of spikes appeared in 50% of the plants in the plot.

***ii) Days to 75% maturity* (DTM):** The days to 75% maturity were counted from date of sowing to 75% of the plants in the plot physiological maturated *i.e*. when the peduncle turned to yellow.

***iii) Grain filling period (GFD)*:** Grain filling period was computed by subtracting the number of days to heading from the number of days to maturity.

GFD = Days to 75% maturity - *D*ays to 50% heading

3.4.4 Quality traits

i) Grain protein content

Grain protein content was estimated from a random sample of 100 gm of hand-threshed seeds of each genotype per replication taken from the produce of Row planted plots at each location. The seeds were milled and total Nitrogen percent (N%) was determined by Kjeldahl method as described in the manual by Sahlemedhin and Taye, 2000. The total N% was converted into grain protein content (%) by the formula:

Grain Protein Content (%) = N (%) x 6.25

3.5 Statistical analyses

The data were subjected to statistical analysis using AGROBASE 20 (Agrobase 20, 1999) computer software. Simple analysis of variance for each test environment for differences among genotypes, and pooled analysis of variance for G x E interaction was made according to Eberhart and Russell (1966) model and multivariate AMMI effects were computed for classification of genotypes and environments. Variance components were estimated from expected mean squares.

3.5.1 Stability analysis using Eberhart and Russell (1966) model

The stability analysis was carried out following Eberhart and Russell (1966) model. The general model is:

$$Y_{ij} = \mu_i + b_i I_j + \delta_{ij}$$

Where: Y_{ij} - is the mean performance of ith genotype in the jth environment

(i = 1, 2, ... , 25; j = 1, 2, ...,12)

μ_i - is the mean performance of ith genotype over all the environments

b_i - is the regression coefficient – a measure of response of ith genotype to varying environments.

I_j - is the environmental index of the jth environment

δ_{ij} - is the deviation from regression of ith genotype in jth environment

This approach for the measurement of phenotypic stability is based on regression analysis. An appropriate structure for ANOVA for stability is presented in Table 3.

Table. 3. Structure of pooled analysis of variance for stability (Eberhart and Russell, 1966) model

Source	df	Mean sum of squares	F test
Genotypes Environment + (Genotype x Environment) Environment)	g – 1 g (n – 1)	MS_1	$\frac{MS_1}{MS_3}$
Environment (linear) Genotype x Environment (linear) Pooled deviations	1 g – 1 g (n – 2)	MS_2 MS_3	$\frac{MS_2}{MS_3}$ $\frac{MS_3}{MS_4}$
Genotype 1 Genotype 2 - - Genotype n	n – 2 n – 2 - - n - 2		
Pooled error	n(r - 1) (g - 1)	MS_4	
Total	ng - 1		

The environmental index I_j is calculated as:

$$I_j = \left(\sum_{i-1}^{25} \frac{Y_{ij}}{g}\right) - \left(\sum_{i-1}^{25} \sum_{j-1}^{12} \frac{Y_{ij}}{gn}\right) \qquad \text{(j = 1, 2, ...,12)}$$

Note that the sum of environmental index should be zero.

$$\sum_j I_j = 0$$

The environmental index is the deviation of all the genotypes at a given location from the overall mean.

This model has two parameters; i) Regression coefficient (b_i) which is calculated as:

$$b_i = \sum_{j-1}^{12} Y_{ij} I_j \Big/ \sum_{i-1}^{25} I_j^2 \qquad \text{(i = 1, 2, ... , 25)}$$

ii) The mean squared deviation from regression ($\bar{S}^2 d_i$) which is obtained as:

$$\bar{S}^2 d_i = [\sum_j \delta_{ij}^2 \Big/ (n-2)] - Se^2/r \qquad \text{(i = 1, 2, ... , 25)}$$

Where $\sum_j \delta^j ij = \left[\sum_j Y^2 ij - \frac{Yi.^2}{L}\right] - \frac{\left(\sum_{j-1}^{12} Yij\, I_j\right)^2}{\sum_j I_j^2}$

(i = 1, 2, ... , 25; j = 1, 2, ...,12)

Where, Se^2 – Pooled error variance

r - Replication

It is also called a parameter of predictability.

According to the model, a stable variety is defined if it meets the following requirements/conditions:

i) High mean yield ($\bar{y}$) *i e.* $\bar{y} > \mu$

ii) $b_i = 1$ and

iii) $\bar{S}^2 d_i$ approaching zero.

The difference between expected and observed values summed over locations for a genotype is called pooled deviation. A genotype with low-pooled deviation is more stable. The individual pooled deviation is tested against pooled error. When pooled deviation is significant, it is used to test environment (linear) and G x E interaction (linear). Environment (linear) and G x E interaction (linear) (predictable components) are normally greater than pooled deviation (unpredictable component) and tested by F-test (Singh and Chaudhary, 1985).

Individual deviation from linear regression is tested as follows:

$$F = \left[\left(\sum_j \delta_{ij}^2 \right) \Big/ (n-2) \right] \Big/ Poold\ error$$

Test of b_i values is done as follows:

$$t = \frac{bi - 1}{SE_{(b)}}, \quad \text{at } n-2\ df$$

$$\text{SE of (b)} = \sqrt{\frac{MS\ due\ to\ pooled\ deviation}{\sum_j I_j^2}}$$

Similarly, $SE\ of\ (b_i) = \sqrt{\frac{MS\ due\ to\ pooled\ deviation\ of\ ith\ \text{variety}}{I_j^2}}$

$$MS \;\; Pooled\ deviation\ of\ i^{th}\ \text{var}iety = \frac{\delta_{ij}^{2}}{n-2} \text{ with } n-2 \text{ df.}$$

Where, SE - Standard error
b - Regression coefficient
MS - Mean sum of square, and
I_j^2 - Environmental index

3.5.2 Classification of genotypes and environments using Additive Main effects and Multiplicative Interaction (AMMI) model

AMMI model first applies the additive analysis of variance model to two-way data, and then applies the multiplicative principal component analysis (PCA) model to the residual from the additive model, that is, to the interaction (Yau, 1995). AMMI analysis is done with MATMODEL software, developed by Gauch (1986) cited from Gauch and Zobel (1997). In this model the first component is main effect and the additive part of the model. Grand mean, genotype means and environmental means are analyzed by the ordinary ANOVA. The second component, the non-additive interaction in the multiplicative part of the model, is analyzed by PCA. For any G x E combination, the additive part (main effects) of the AMMI model equals the genotype mean plus the environment mean minus the grand mean, and the interaction (multiplicative part) is the genotype scores times the environment scores (Zobel *et al*., 1988).

The AMMI model for average yield, Y_{ij}, over replicates of the i^{th} genotype in the j^{th} environment is:

$$Y_{ij} = \mu + G_i + E_j + \sum_{n=1}^{N} \lambda_n Y_{in} \delta_{in} + E_{ij}$$

Where (i = 1, 2, ... , 25; j = 1, 2, ...,12)

Where: Y_{ij} - is the performance of i^{th} genotype in the j^{th} environment

μ - is the overall mean

G_i - is genotypic main effects

E_j - is environmental main effects

N - is the number of PCA axes

λ_n - is the singular value of the n^{th} PCA axis

Y_{in} and δ_{in} - are scores for the i^{th} genotype and j^{th} environment on the n^{th} PCA axis

E_{ij} - is the residual term distributed N (0, σ^2)

The result of AMMI analysis can be presented graphically in the form of biplot (Gabriel, 1971) cited from Gauch and Zobel (1997). When a genotype and an environment have the same sign on the PCA axis, their interaction is positive; if different, their interaction is negative. If a genotype or an environment has a PCA score nearly zero it has small interaction effects and hence can be fitted into additive model (Zobel *et al*., 1988; Gauch and Zobel, 1997). In particular, the closeness between pairs of locations or pairs of genotypes in the biplot is proportional to their similarity for G x E effects. Genotypes represented by a point near the origin of axes reveal limited G x E interaction on the contrary, material that is far from the origin and for which the angle formed between the genotype point, the origin and the environment is small. Locations far from the origin show rather peculiar responses of genotypes (Gauch and Zobel, 1997). The abscissas of the AMMI biplot are the main effects while the genotype interaction scores and environment scores are on the ordinate.

3.5.3 Heritability & Genetic variability estimates

Heritability (broadsense) of the traits studied was estimated as a ratio of genetic variance to phenotypic variance (Fehr, 1983).

Heritability (%) = [(σ_g^2 **/** σ_p^2 **) x100]**; where σ_g^2 and σ_p^2 are genotypic and phenotypic variance, respectively.

To calculate variability among the traits, the mean range of the traits over the environments, genotypic coefficient of variability (CV_G) and phenotypic coefficient of variability (CV_P) at each location were estimated according to the method suggested by Burton and De Vane (1953) cited from Chandra *et al*., (2004) as follows:

$$V_G = \frac{MSg - MSe}{r}$$

Where, V_G – is genotypic variance

MSg – Mean square due to genotypes

MSe – Environmental variance (error mean square)

$$CV_G = \left(\frac{V_G}{x} \right) x100$$

r – Number of replications

x – Grand mean

$$V_P = GV + MSe$$

V_P – Phenotypic variance

$$CV_P = \left(\frac{V_P}{x} \right) x100$$

4. RESULTS

4.1 Analysis of variance (ANOVA) for individual environments:

Analysis of variance revealed significant differences among the genotypes for most of the traits in each environment. Grain yield per plant showed significant differences among the genotypes only in Alem Tena Broadcasting (ATB), Akaki Row planted (AKR), Debre Zeit Row planted (DZR) and Debre Zeit Broadcasted (DZB) environments. Significant differences among genotypes were observed for biological yield per plant in DZB, Chefe Donsa row planted (CDR) and Selale row planted (SER) environments. Harvest index showed significant differences among genotypes in environment Alem Tena Row planted (ATR), Minjar Broadcasted (MNB), DZR, DZB, Chefe Donsa Broadcasted (CDB) and Selale Broadcasted (SEB) environments. Number of effective tillers per plant was significant in MNR, DZB, AKR and CDB while genotypes showed significance differences among themselves for spike length in all environments except in MNB and CDB. Number of kernels per spike exhibited significant differences for the genotype source of variation in all environments. Protein content revealed significant difference for genotypes in all environments except in Minjar. Significant differences among the genotypes were also observed for 1000-kernel weight, plant height, days to 50% heading, days to 75% maturity and grain filling duration in all environments (Appendices 2a-2l).

4.2 Pooled Analysis of variance:

Pooled analysis of variance (Table 4) showed highly significant ($P \leq 0.01$) differences among the testing environments (locations and planting methods), genotypes and G x E interaction. The mean difference amongst the genotypes and environments were highly significant for all the traits except genotypes for biological yield per plant when tested against genotype and environment interaction component. The results therefore suffice the basic condition for G x E interaction since they revealed that average performance of genotypes for different traits studied varied significantly so far as their average performance over all the environments was concerned.

Table 4

The partitioning of G x E interaction into linear and non-linear component exhibited that both were important. G x E interaction (linear) component was highly significant ($P \leq 0.01$) for all the traits except for harvest index when tested against residual indicating that genotypes performed differently across environments. Pooled deviation was highly significant ($P \leq 0.01$) for 1000-kernel weight, plant height, days to 50% heading, days 75% maturity and grain filling period; and significant ($P \leq 0.05$) for grain yield per plant, number of kernels per spike, and spike length; except non-significant for biological yield per plant, harvest index, number of effective tillers per plant and protein content indicating non-linear components also accounted for G x E interaction.

The relative magnitude of environment, genotype and G x E interaction components for all the traits was significantly different. The variance due to environment was larger than due to genotypes and G x E interaction for all the traits. The non-significant G x E interaction for harvest index indicated that the genotypes did not interact with the environments. As this trait could not satisfy the basic requirement for stability studies, hence further analysis for stability parameters was not carried out.

4.3 Estimates of stability parameters

The estimates of three parameters of stability *viz*, μ , b_i and S^2d were obtained for individual genotype. The results for grain yield and its components (Table 5.1); morphological traits (Table 5.2), phenological traits and protein content (Table 5.3) are presented below.

Yield and yield components

Grain yield per plant

The phenotypic stability of the genotypes as measured by mean performance over environments (μ), the linear regression (b_i) and the deviation from regression function (S^2d) indicated that 19 out of 25 genotypes did not reveal significant G x E interaction as both regression mean square and deviation from regression mean square were non- significant. Of these 19 genotypes, 13 performed greater than the grand mean (Table 5.1). Mean performance of genotypes over environments ranged from

4.59 gm in DZ-04-118 (local check) to 6.48 gm in CIGM91-349 (CIMMYT introduction).

Genotype CDSS92B1467 showed high mean (μ), regression coefficient (b_i) greater than unity and non-predictable behavior (S^2d significantly different from zero). Genotypes CD91313 and DZ-04-118 (local check) showed regression value significantly less than unity and non-significant deviation from regression mean square, indicating more dominance of linear and predictable G x E interaction.

Genotypes CIGM91-347, CD94545-A and CDSS93Y545 exhibited significant deviation from regression mean square indicating more prevalence of non-linear component of variance hence, were unpredictable.

Eight genotypes namely; CD94523, CDSS92B193, CD97383, CIGM91-349, DZ2234, DZ2293-2DZR, DUKEM/3/RUF and DZ3117 had mean grain yield above the average, regression coefficient equal to unity and deviation from regression approaching zero, thus found to be stable.

The genotype CD91313 exhibited regression slope significantly less than unity with mean performance greater than the grand mean (5.92 gm) was found to be least responsive. This tend to more adaptable under poor growing environments.

All genotypes with the exception of CDSS93Y33 outyielded both the local and standard checks. Rank order of CIMMYT genotypes from one to nine except fourth in terms of grain yield performance showed that introduction from CIMMYT performed better than Debre Zeit cross materials (Table 5.1).

Biological yield per plant (gm)

For biological yield per plant all genotypes except two-exhibited non-significant S^2d, thus found to be predictable. Genotypes CDSS92B1467 and CDSS93Y33 had S^2d is significantly different from zero and regression coefficient significantly greater than and less than unity, respectively. Genotype DZ-04-118 (local check) exhibited non-significant S^2d and regression (b_i) value significantly less than unity.

Table 5.1

Biological yield per plant was maximum (14.59gm) recorded by genotype DZ2293-2DZR followed by genotype CIGM91-347 (14.54gm), CIGM91-349 (14.48gm) and DUKEM/3/RUF (14.24gm). The minimum biological yield per plant was recorded by genotype CD 95294-1Y (12.20 gm). Genotypes CD94523, CD91989, CDSS92B193, CD97383, CIGM91-349, CIGM91-347, DZ2234, DZ2293-2DZR, DZ1669-1AK, DUKEM/3/RUF, DZ3117 and Yerer had mean greater than the grand mean, unit regression coefficient and non-significant S^2d, hence these were identified to be stable (Table 5.1).

Number of grains per spike

The mean performance of the tested genotypes varied from 38.11 in DZ-04-118 (local check) to 57.25 in CD95294-1Y. Twelve genotypes had mean number of grains per spike greater than the overall average while all the genotypes were superior in performance than the local and standard check.

Five genotypes, namely CD91989, CDSS92B193, CD95294-1Y, DZ3117 and Ude did not fit to the regression model since they had S^2d significantly different from zero. Of the twenty predictable genotypes, genotype CDSS93Y545 had high mean (μ), regression coefficient significantly greater than one, thus found to be suitable for better environments. Genotype CD95294-1Y produced number of grains better than the grand mean, had above average linear regression ($b_i>1$) but its S^2d significantly different from zero. Genotypes DZ1675-1AK and CD91313 had regression coefficient significantly less than unity and $S^2d = 0$, but with less number of grains per spike than the average. Genotypes CD94523, CD98206, CIGM91-349, CIGM91-347, DZ 2212-1BS, DZ2293-2DZR and Yerer had higher number of grains per spike than the average, b equal to one and non-significant deviation from regression, hence were identified to be stable (Table 5.1).

1000-kernel weight (TKW)(gm)

Genotype DZ2234 had the highest thousand-kernel weight (49.47 gm) while CDSS93Y545 had the lowest (36.25 gm). Genotypes CDSS92B1467, CD91Y7, CDSS93Y33, CD97383, CD98206, DZ2234, DZ2293-2DZR, DZ1675-1AK, DUKEM/3/RUF, DZ3117, Yerer, Gerardo and Ude (standard check) exhibited higher

thousand-kernel weight than the grand mean (42.72 gm) and the local check. Furthermore, six of the genotypes namely; CDSS92B1467, CDSS93Y33, CD97383, DZ2234, DZ1675-1AK and DUKEM/3/RUF were found much better than the standard check (Ude).

Thirteen genotypes exhibited significant regression and deviation from regression mean square for 1000-kernel weight. Of these four genotypes *viz;* CDSS92B1467, CDSS93Y33, DZ2234 and DZ3117 did not fit to the linear regression model due to their significant deviation from regression. Gerardo was the only genotype that had regression coefficient significantly greater than unity mean thousand-kernel weight greater than the grand mean and non-significant S^2d and hence, found suitable for favorable environments. Inversely, genotype DZ2293-2DZR was more suitable for unfavorable environments because of its high mean, b significantly less than one and non-significant value of S^2d. Genotypes CD 94545-A, DZ1669-1AK, CD91313 and DZ-04-118 (local check) had regression coefficient significantly less than unity and non-significant values of S^2d, but with poor performance.

Genotypes CD91Y7, CD97383, CD98206, DUKEM/3/RUF, Yerer and Ude (standard check) had average grain weight higher than grand mean, regression coefficient equal to one and non significant S^2d, thus identified to be stable genotypes for this trait (Table 5.1).

Morphological traits

Number of effective tillers per plant

The maximum number of effective tillers per plant (4.03) was obtained from genotypes CD97383 and CD91313 whereas the lowest (2.03) was from genotype CD95294-1Y. Only five genotypes outperformed the standard check while two were superior than the local check. Genotypes CDSS92B1467, CD91Y7, CDSS92B193, CD97383, CD94545-A, DZ2234, DZ2293-2DZR, CD91313, DZ-04-118 (local check) and Ude (standard check) recorded higher number of effective tillers per plant than the grand mean (Table 5.2).

Table 5.2

Six genotypes revealed significant regression and deviation from regression mean square for this trait. Genotypes CD91313 and CDSS92B193 with maximum number of effective tillers per plant, regression significantly greater than unity and non-significant deviation from regression, were found to be suitable for better environments. Where as DZ-04-118 (local check) with regression coefficient significantly lower than unity and non-significant deviation from regression identified to be suitable for poor environments.

Genotypes CD91Y7, CD94545-A, DZ2234, DZ2293-2DZR, and Ude (standard check) had higher number of effective tillers per plant and unit b_i value and S^2d equal to zero found to be stable. Hence, they may be recommended for cultivation in different environments.

Spike length (cm)

The longest spike length (7.90 cm) was obtained from genotype DUKEM/3/RUF while the shortest (5.51 cm) was from standard check (Ude). Thirteen genotypes showed longer spike length than the grand mean (6.25 cm).

Three genotypes showed significant regression mean square and five had significant deviation from regression mean square indicating non-prevalence of linear and non-linear G x E interaction, respectively. Genotypes CDSS93Y33, Yerer, Gerardo and DZ-04-118 (local check) had S^2d value significantly different from zero, hence, were unpredictable.

Genotypes CIGM91-349 and CIGM91-347, with regression value significantly less than unity and non significant S^2d identified to be suitable for unfavorable environments while genotype DUKEM/3/RUF with b_i value significantly greater than unity and non significant S^2d for favorable environments. Genotypes CD94523, CD91989, CDSS92B193, CD97383, DZ2234, DZ2212-1BS and DZ2293-2DZR had average spike length larger than the population mean with regression coefficient equal to one and non-significant S^2d, hence were identified as stable (Table 5.2).

Plant height

The average plant height ranged from 65.92 cm recorded by genotype CIGM91-349 to 101.69 cm by genotype DZ1669-1AK. Five genotypes exhibited significant regression mean squares; two had significant deviation from regression mean squares while one showed significance for both.

Genotype CD91313 exhibited b_i value significantly less than unity, plant height less than the population mean and non-significant deviation from regression, thus found suitable for unfavorable environments. Genotypes DZ1675-1AK, DZ1669-1AK, DZ3117 and DZ-04-118 exhibited long height, had regression coefficient significantly greater than unity and non-significant S^2d. Thus, they were found to be suitable tall genotypes for favorable environments. Sixteen genotypes had average plant height less than the population mean, unit regression coefficient and non-significant deviation from regression, hence considered as stable for this trait (Table 5.2).

Phenological traits

Days to 50% heading (days)

Genotype DZ3117 was the earliest with 57.78 days for heading while genotype CD91989 with 70.39 days found to be the latest. Five genotypes namely; DZ3117, DZ2234, DZ2293-2DZR, DZ1669-1AK and CD91313 headed earlier while all the remaining 20 genotypes headed later than the grand mean (60.87 days). Eight genotypes, *viz*; CDSS97B1467, CDSS93Y33, CD91989, CDSS92B193, CD97383, CIGM91-347, CD91313 and DUKEM/3/RUF showed significance for both the parameters, three for regression mean squares while seven for deviation from regression mean squares.

Genotype DZ1669-1AK showed b_i significantly less than unity and non-significant S^2d, thus found suitable for unfavorable environments. Genotypes CD91Y7, CD98206, DZ1675-1AK, CDSS93Y545 and Ude (standard check) took number of days for heading more than the overall mean, had unit regression coefficient and S^2d approaching zero, could be considered stable for late heading (Table 5.3).

Table 5.3

Due to their earlier heading time, unit b_i and S^2d approaching zero, genotypes DZ2234 and DZ2293-2DZR (Debre Zeit crosses) were found to be stable for earliness.

Days to 75% maturity (days)

Majority of the genotypes took lesser number of days to mature than the mean days of population. Genotype DZ3117 with 105.61 days was the earliest to mature where as genotype CD95294-1Y with 114.31 days was the latest.

Genotypes CD91Y7, CDSS93Y33, CD91989, CIGM91-349, CD95294-1Y, DZ 2212-1BS, DZ2293-2DZR, DZ1675-1AK, DUKEM/3/RUF, Yerer, and Gerardo took longer days to mature than the population mean (109.98 days). Eight genotypes, *viz*; CD95294-1Y, DZ1675-1AK, CD91313, DUKEM/3/RUF, DZ3117, Yerer, Gerardo and DZ-04-118 (local check) showed significance for both the parameters while five for regression and six for deviation from regression mean squares.

Genotypes CDSS92B1467, CD97383 and DZ2234 had above average linear regression (b_i>1) and non-significant S^2d, hence, were found suitable for better environments. Genotypes CD91989 and DZ2212-1BS due to below average linear regression coefficient than unity and non-significant S^2d found suitable for poor environments but with late maturity (Table 5.3).

Three genotypes *viz*; CD94523, CDSS92B193, CD98206 were identified to be stable for early maturing while two namely, CIGM91-349, and DZ2293-2DZR for late maturity due to their unit regression and deviation from regression and non-significant deviation from regression values.

Grain filling period (days)

The number of days for grain filling from heading to maturity varied from 40.81 recorded by genotype DZ-04-118 (local check) to 49.97 recorded by genotype DZ1669-1AK. The mean grain-filling period of the population was observed to be 45.72 days.

Genotypes CD97383, CD98206, CD94545-A, DZ2234, DZ2293-2DZR, DZ1675-1AK, DZ1669-1AK, CD91313, DUKEM/3/RUF, DZ3117 and Gerardo took longer

grain filling period than the population. Genotypes CIGM91-349 and DZ1675-1AK showed significance for both parameters while genotypes CD91Y7, CDSS93Y33, CD97383, DZ1669-1AK, CD91313, DZ3117 and Ude (standard check) showed significance for S^2d and CD91989 and CD9S294-1Y for b_i. Genotypes CD91989 and CD95294-1Y exhibited below average stability with regression coefficient significantly less than unity, shorter grain filling period than the population mean and non-significant S^2d, thus found suitable for unfavorable environments.

None of the genotypes had predictable above average stability. Eight genotypes namely CDSS92B1467, CD94523, CDSS92B193, CIGM91-347, DZ2212-1BS, Yerer, CDSS93Y545 and DZ-04-118 had short grain filling period with unit regression value and non-significant S^2d, identified to be stable. Among the longer duration genotypes six found to be stable (Table 5.3).

Quality traits

Grain protein content (%)

The maximum protein content (13.52%) was found in genotype DZ3117 at Alem Tena location while the lowest (11.61%) was recorded in genotype CIGM91-349. Ten genotypes *viz*; CDSS92B1467, CD98206, CIGM91-347, CD 94545-A, DZ 2212-1BS, DZ1669-1AK, DZ3117, Yerer, DZ-04-118 (local check) and Ude (standard check) showed higher grain protein content than the population mean (12.42 %), while more than half of the genotypes had low grain protein content (Table 5.3). Only three genotypes, namely; CD98206, DZ3117 and DZ-04-118 attained higher grain protein content than standard (13.00%) recommended for durum wheat for industrial purpose

All but three genotypes observed to be predictable with non-significant S^2d. DZ 2212-1BS had protein content more than population mean, regression coefficient significantly greater than unity and non-significant S^2d, found suitable for favorable environments. Genotype CD97383 showed below average stability but with poor performance indicating that this genotype is sensitive to changes of environment. But the remaining eight genotypes, *viz*; CDSS92B1467, CD98206, CIGM91-347, CD94545-A, Yerer, DZ1669-1AK, DZ3117 and Ude (standard check) with mean protein content more than grand mean, unit b_i value non-significant S^2d implying that they were more stable genotypes (Table 5.3). Among the stable genotypes DZ3117

was identified to be the best since it had protein content higher than the standard (13.00%) and was also high yielder with stable performance across environments.

4.4 Classification of environments and genotypes based on their adaptability using AMMI Biplot

Results of AMMI analysis using the same data showed that there were highly significant differences ($P \leq 0.01$) among the genotypes, the environments and G x E interaction for all the traits studied except for biological yield per plant and spike length where genotypic main effects and G x E interaction were observed non-significant, respectively (Table 6).

The G x E interaction component of variation was partitioned into 12 possible interaction principal component axes (IPCA), equal to the number of environments. The interaction variance was explained in 11 IPCA to capture the entire total pattern contained in the G x E interaction. The 12^{th} IPCA was pooled into the residual. However, for most of the traits studied, including grain yield, only the first four axes explained a statistically significant portion of the G x E interaction variance. For harvest index, the first three while for number of effective tillers per plant and grain protein content the first two IPCA axes were found to be significant. In general, for all traits the first IPCA explained much of the interaction variance followed by the subsequent IPCA axes. The first four IPCA together explained 76.68% of the total interaction variance for grain yield, 74.32% for number of kernels per spike, 80.38% for thousand kernel weight, 87.35% for plant height, 89.83% for days to 50% heading, 87.58% for days to 75% maturity and 83.41% for grain filling period. In case of harvest index and biological yield per plant the first three significant IPCA scores together explained 56.64% and 63.32% of the total interaction variance, respectively. For number of effective tillers per plant, spike length and protein content the first two significant IPCA scores together explained 59.02%, 59.78% and 73.55% of the total interaction variance, respectively (Table 6).

Table 6

The AMMI analysis provides a graphical representation of summary information on main effects, and the first interaction axis in the form of a biplot of IPCA1 and G x E interaction to classify genotypes and environments.

Grain yield per plant

The biplot analysis (Fig 1 and Appendix 5) revealed that genotypes CD97383, CIGM91-349 (CIMMYT introductions) and DZ3117 (DZ-cross) exhibited IPCA scores closer to zero and high mean yield, thus found to be stable. DZ-04-118 (local check) is entirely different from other genotypes both in yield (lowest) response and interaction (high positive IPCA score). Genotype CDSS92B1467 was high yielding but with negative IPCA score. All genotypes with negative IPCA score were not adapted to any of the environments. Genotypes CIGM91-347, CD91313, CD94523 and DZ2234 were high yielders since their mean greater than the grand mean and with positive IPCA scores thus were adapted to AKB, SER, SEB, MNR, ATB and AKR. No genotype showed adaptability to DZR, DZB and CDB environments.

Biplot also showed Debre Zeit Row and Broadcast as high yielding environments but with negative IPCA scores and Chefe Donsa Broadcast as high yielding environment with IPCA score near zero. The Akaki Broadcast environment was identified as high yielding with positive IPCA values. Selale Row and Selale Broadcast, Minjar Row, Akaki Row and Alem Tena Broadcast were identified as low yielding but with positive IPCA scores (Fig 1 and Appendix 4).

Biological yield per plant

According to biplot of biological yield per plant genotypes DZ-04-118 possessed the highest positive IPCA score while genotype CDSS92B1467 exhibited the highest negative IPCA score but with low yield. Genotypes CD94523, CIGM91-349, CD98206 (high yielders) and DZ1675-1AK (low yielder) had IPCA scores near zero (Fig 2 and Appendix 5) indicating that these genotypes showed stable performance for this trait.

Among environments DZB and DZR were identified as high yielding environment but with negative interactions while CDR was found to be high yielding with IPCA

score near to zero. AKR, MNR, SEB, ATB, AKB and MNB were identified as low yielding with positive IPCA scores (Fig 2 and Appendix 4).

Genotypes CD91989, CIGM91-347, Yerer, CIGM91-349, CD91313 and DZ3117 had high mean performance and with positive interaction and were adapted to AK (for both methods of sowing), ATB, MNR, MNB and SER. Genotypes DZ2293-2DZR, CDSS92B193, DZ1669-1AK and DUKEM/3/RUF with high mean performance exhibited negative interactions and were adapted to ATR and CDR environments

Harvest index

Biplot analysis (Fig 3 and Appendix 5) identified genotypes DZ2293-2DZR, DZ1675-1AK, CD95294-1Y, CDSS92B1467, DUKEM/3/RUF, CD91Y7, CD97383 and Gerardo with higher harvest index and positive IPCA scores. DZ 2234 was the only high performing genotype with IPCA zero and hence, found to be stable. Genotypes CDSS93Y33, DZ3117, CD91989, DZ2212-1BS, DZ1669-1AK and Yerer had low harvest index and showed positive IPCA scores while CDSS92B193, CDSS93Y545, CIGM91-349, CD94523, CIGM91-347 and CD91313 had high harvest index and exhibited negative IPCA scores.

Accordingly, AKR and DZB were identified as high performing environments with positive interaction while CD (B and R) and SEB with negative interaction. MN (B and R) was found to be low performing environments with positive interaction (Fig 3 and Appendix 4).

Due to similar interaction, genotypes DZ2293-2DZR, DZ1675-1AK, CDSS92B1467, CD91Y7, DUKEM/3/RUF, DZ1669-1AK and Gerardo were adapted to AKR and DZB environments whereas CDSS93Y33, CD91989, CDSS92B193, DZ2212-1BS, Yerer and DZ2212-1BS to MN (for both methods of sowing) environment.

Figure 1

Figure 2

Figure 3

Number of grains per spike

Genotype CD95294-1Y exhibited the highest positive IPCA score for number of grains per spike followed by CDSS92B193, CDSS93Y545, CIGM91-347, DZ2212-1BS and CD91989 whereas genotype DZ1675-1AK exhibited the highest negative IPCA score followed by CD94523, DZ2293-2DZR and CDSS92B193 and all with higher number of grains than the population mean. Genotypes DZ2234 and Gerardo had IPCA score zero, identified to be stable but they performed lower than the grand mean, however, genotypes CD91989, CD98206, DZ2212-1BS, and DZ2293-2DZR had IPCA score near zero and performed better than the grand mean, thus identified to be stable high performing genotypes (Fig 4 and Appendix 5).

Likewise environments DZR, CDB, DZB and AKB identified to be high yielding with positive IPCA score and grouped as similar. CDR found to be high yielding but with negative IPCA score while MNR as low yielding with positive scores (Fig 4 and Appendix 4).

Genotypes CD95294-1Y, CDSS93Y545, CDSS92B193 and CIGM91-347 were adapted to DZ (for both methods of sowing), CDB and AKB environments, CD94523, CIGM91-349 and DZ3117 to CDR whereas CDSS92B1467, CD91Y7 and DUKEM/3/RUF to MNR environment due to similar interactions.

Thousand-kernel weight

For 1000-kernel weight genotype DZ2234 and CD91313 possessed the highest positive IPCA score and were high and low performing, respectively. Among the high performing genotypes DUKEM/3/RUF, Gerardo, CDSS92B1467, Ude and Yerer were positively interactive while DZ2293-2DZR, DZ1675-1AK, DZ1669-1AK, CD97383 and DZ3117 were found to be negatively interactive. Genotype CD98206 had zero IPCA score while CD91Y7 and CDSS93Y33 were close to zero, hence were identified to be stable with high performance. Genotypes CD94523, CD91989, CDSS 92B193, CIGM91-349, CIGM91-347 and DZ2212-1BS though possessed positive IPCA scores but they were had low performance (Fig 5 and Appendix 5).

Figure 4

Figure 5

Similarly environments AK (B an R), CD (B an R) and SE (B an R) exhibited positive IPCA scores with better performance and were classified to be in one group (Fig 5 and Appendix 4). All high performing genotypes found to be adapted to this high yielding environment group.

Number of effective tillers per plant

Genotype CDSS92B1467 showed highest positive IPCA score while genotypes CDSS93Y33 and CD97383 showed higher negative IPCA scores for this trait. Genotypes CIGM91-349 with low and CD94545-A with high performance showed IPCA score very close to zero thus, classified as stable genotypes. Genotypes CD91313 and DZ-04-118 (Local check) exhibited IPCA scores near to zero and a higher number of tillers than population mean, could also be considered as stable (Fig 6 and Appendix 5)

DZB was identified as best performing environment with positive IPCA score followed by DZR but with negative IPCA score. Other better performing environments were ATR with positive while ATB and MNR with negative IPCA scores. AK (B and R) were found to be poor performing, positively interacting environment (Fig 6 and Appendix 4). Genotypes CD91Y7, CDSS92B193 and Ude were adapted to ATR environment while genotypes CDSS93Y545, CD98206, Gerardo, DZ1675-1AK, DZ1669-1AK and DUKEM/3/RUF to AK (B and R) environment because of their similar interactions (Fig 6).

Plant height

Genotype CDSS92B1467 exhibited the highest positive IPCA score while genotype CD91313 exhibited the highest negative IPCA score for this trait. Majority of the genotypes were from short height group and showed negative IPCA scores while three genotypes had positive IPCA score. Genotypes CIGM91-347- and DZ2234 with short plant height showed IPCA scores near zero indicating these to be stable across the tested environments. Genotypes DZ1675-1AK and DZ1669-1AK were similar in their interaction and main effects, were far displaced from the rest of the genotypes (Fig 7 and Appendix 5).

Figure 6

Figure 7

AK (B and R), SE (B and R), DZR and CDR observed to better performing with positive IPCA score and were classified as similar. DZB was identified as better performing with negative IPCA scores, while MNR as poor performing with positive IPCA score. ATR and ATB also revealed highest negative IPCA scores for this trait. MNB and CDB showed IPCA scores near to zero when compared to the rest of the environments (Fig 7 and Appendix 4). Genotypes DZ1675-1AK, DZ1669-1AK, CD91313, DZ3117 and CD94545-A were adapted to AKR, DZR, AKB and SE (B and R) environments while CDSS92B1467, DZ2234 and Ude to MNR environment due to similar IPCA scores (Fig 7).

Days to 50% heading

Genotype CD91989 took comparatively longest time to flower and possessed highest positive IPCA score followed by Gerardo, DUKEM/3/RUF and CDSS93Y33. The maximum negative IPCA scores were revealed by genotypes CD97383, CDSS92B1467, CIGM91-347 and CDSS92B193, hence were found to be better for poor environments. None of the genotypes was adapted to all environments (Fig 8 and Appendix 5).

Highest positive IPCA score was revealed by ATR while highest negative IPCA score was revealed by SER. AT (B and R), MNR, DZR, DZB and SER environments recorded positive while AK (R and B) negative IPCA scores and favored earlier flowering (Fig 8 and Appendix 4). In general, there were two groups of genotypes one adaptive to positive interactive while second to negatively interactive environments. Genotypes CD91313 and DZ3117 headed earliest than the other and specifically adapted to AK (R and B) environments (Fig. 8).

Days to 75% maturity

Genotypes CD91989 and CD95294-1Y exhibited highest positive IPCA score while genotypes CD97383 and DZ3117 showed highest negative. Genotypes CD94523, CD 98206, CD94545-A and DZ1669-1AK showed IPCA scores near zero and identified to be average stable (Fig 9 and Appendix 5). All genotypes except six showed negative IPCA scores and were found to be adapted to AKR and ATB environments.

Figure 8

Figure 9

AT (R and B) favored earlier maturity followed by MN (R and B) while SE (R and B) favored later maturity compared to the other testing environments. ATR exhibited highest positive IPCA score while CDB and SER exhibited highest negative IPCA scores for this trait. No specific environment showed IPCA score near zero.

Environments AT (B and R), MN (R and B) and DZ (R and B) with similar positive IPCA score was categorized in one group while AK (B and R) with similar negative IPCA score in another. Only three genotypes *viz*; DZ2293-2DZR, DZ2212-1BS and Yerer were adapted to first group of environment. None of the genotypes adapted to CD (B and R) and SE (B and R) environments (Fig 9 and Appendix 4).

Grain filling period

Majority of the genotypes showed similar means thus the AMMI biplot did not classify them. However, according to their IPCA scores, genotypes CD91989, CD95294-1Y and CD91313 showed high positive IPCA scores while genotype CIGM91-347 showed high negative in comparison to rest of the genotypes (Fig 10 and Appendix 5).

MN (R and B) showed highest positive IPCA score while SEB showed highest negative for grain filling period. None of the environments showed IPCA score near zero. Environments MN (R and B), DZ (B and R) and CD (B and R) with positive interaction were classified as similar in one group while AK (B and R) and AT (B and R) with negative interaction as another similar group (Fig 10 and Appendix 4).

Protein content

In case of protein content, genotype DZ3117 showed the highest positive IPCA score and maximum protein content followed by DZ2212-1BS, Yerer, Ude, CD98206 and DZ1669-1AK. Genotype CIGM91-349 had the lowest protein content with negative IPCA scores (Fig 11 and Appendix 5).

The highest protein content (17.20%) was recorded at Alem Tena followed by Debre Zeit (14.5%) and Minjar (13.74%) where as the lowest (9.03%) was observed at Selale.

Figure 10

Figure 11

Alem Tena showed the highest positive while MN showed the highest negative IPCA score followed by Debre Zeit. Akaki, Selale and Chefe Donsa showed IPCA scores near zero compared to the other locations. Genotype CD95294-1Y was adapted to all locations since its IPCA score equaled to zero. Genotype DZ-04-118 was adapted to Debre Zeit and Minjar while large numbers of genotypes with negative IPCA score were adapted to Akaki and Chefe Donsa locations. Genotype DZ3117 was specifically adapted genotype to Alem Tena, which exhibited similar highest positive IPCA score and highest grain protein content (Fig 11 and Appendix 4).

4.5 Estimates of heritability and Coefficient of variability

4.5.1 Heritability estimates

Heritability estimates based on analysis of variance of individual and pooled over environments are given in Table 7.

The heritability estimates for grain yield per plant varied from 11 percent in SER environment to 68 percent in DZR while pooled estimates were 39 percent. In general heritability was medium in Debre Zeit location and low in Selale. In Debre Zeit, Selale and Minjar location method of sowing did not affect heritability.

In case of biological yield per plant, heritability varied from 20 percent in MNB to 50 percent in DZB with an average of 28 percent. Selale and Chefe Donsa locations showed similar but moderate heritability estimates in row as well as broadcasting method of sowing while in Debre Zeit broadcasting, estimates were double than row method of sowing.

Harvest index recorded highest heritability (69%) in SEB followed by DZR (50%). In Chefe Donsa row method of sowing exhibited lowest estimates (27%) while almost double (55%) in broadcasting method of planting. The pooled estimates were recorded 67 percent and in general, heritability was medium in all locations.

Table 7

`High heritability was observed in all locations and in both the methods of sowing for 1000-kernel weight except Alem Tena (medium) and number of kernels per spike. The pooled estimates were highest 97 percent for number of kernels per spike and 95 percent for 1000-kernel weight. Method of sowing in all locations also did not show differences in heritability for these traits.

For number of effective tillers per plant, heritability estimates were observed to be highest (66%) when pooled over environments. In Debre Zeit broadcasting environment heritability was maximum (54%) while in Selale broadcasting it was minimum (15%). In general, heritability was low in Selale location, DZR and MNB while medium in other environments.

Spike length recorded highest heritability estimates (95%) when pooled over locations and method of sowing. In general, heritability was observed to be high in all locations and method of sowing except at MNB and ATR environments where it was medium and method of sowing also showed differences. The estimates were almost identical in all environments except ATR, MNB and DZB.

Heritability estimates for plant height was observed to be highest (97%) in CDR environment as well as when pooled over environments. In general, it revealed high heritability in all environments except at Alem Tena (medium) in both the methods of planting. Method of sowing in each location did not show differences in heritability except at Debre Zeit, where, it was medium in broadcasting and high in row method of sowing.

For days to 50% heading, heritability estimates were the highest (99%) in DZR and MNR environments. The lowest estimates (65%) were recorded at Selale in broadcasting situation. Selale is the only location showing differential heritability otherwise in all locations and methods of sowing it was found to be high and estimates were almost equal.

Incase of days to 75% maturity the highest heritability (91%) was recorded in pooled estimates. High heritability and equal estimates were observed at Alem Tena, Minjar, and Debre Zeit locations in both the methods of planting. Akaki, Chefe Donsa and Selale recorded differential estimates and medium heritability except AKB and CDB, which showed high heritability.

High heritability was observed for grain filling period in all environments except for ATR and AKR where it was found to be medium. The highest estimates (95%) were recorded in MNR environment followed by pooled estimates (90%). Method of sowing revealed difference only at Akaki and Alem Tena locations where row method exhibited medium while broadcasting showed high heritability.

Heritability estimates of grain protein content were computed for row method of planting over all the six locations. The estimates ranged from 42 percent at Minjar to 75 percent at Selale location. The pooled estimates were observed to be 71 percent. Selale followed by Debre Zeit exhibited high heritability while all other locations showed medium heritability.

4.5.2 Estimates of coefficient of variability

Genotypic coefficient and phenotypic coefficient of variability (CV_G and CV_P) ***e***stimates and range different traits of durum wheat are given in Table 8.

The CV_G estimates for grain yield varied from -1.1 at MNR to 22.0 at DZB. The CV_P estimates were higher than CV_G and varied from 29.4 in ATB to 82.9 in DZB. CV_G estimates for biological yield varied from -1.6 to 31.6 at ATR and DZB respectively; while the CV_P estimates were highest (127.3) in DZB while lowest (52.0) were in SEB. Pooled estimates revealed CV_P almost three times more than CV_G (210). More variation (4.6-15.4 gm) for grain yield per plant was observed in Debre Zeit location under Broadcast method of sowing while Alem Tena location showed the lowest range (2.2-5.1 gm) for variability. DZB also showed wider range (16-30 gm) while ATR lowest (8-12 gm) for biological yield per plant.

Table 8

Harvest index recorded highest CV_G (1.4) in ATR while lowest (-0.3) in SER. AKR exhibited highest (74.9) CV_P estimates while almost zero (0.4) in SEB. High CV_G estimates were observed in all environments for number of kernels per spike. The lowest was 46.48 in MNB whereas the highest was 145.29 in AKB. Similarly, the CV_P estimates for this trait varied from 87.4 in MNB to 280.7 in AKB. But it was 1119.5 when pooled over environments. In general harvest index varied from 0.30 to 0.66 over different environments.

The CV_G estimates for grain yield, biological yield, harvest index and number of kernels per spike were lower than CV_P estimates across all environments.

For 1000-kernel weight, CV_G and CV_P estimates were observed to be highest (371.1 and 396.3, respectively) when pooled over environments. The difference between CV_G and CV_P was very small for this trait. Wider range (27-46 gm) of thousand-kernel weight was observed at MNR environment.

CV_G estimates for number of effective tillers per plant varied from 0.0 to 10.0 at environments SEB and DZB respectively. The highest CV_P estimates (155.7) for number of effective tillers per plant were observed in MNR while the lowest (11.6) in CDR. The CV_G estimates for this trait were also lower than CV_P estimates across all environments. In many of the environments tiller number obtained were 3-5.

Plant height and spike length recorded highest CV_G (131.7 and 74.1, respectively) and CV_P (137.5 and 84.6, respectively) estimates when pooled over environments while lowest CV_G (25.6) and CV_P (65.6) estimates for plant height were observed in ATB. Low difference between CV_G and CV_P was also observed for these traits.

In case of days 50% heading the highest CV_G (221.6) and CV_P (227.1) for this trait was recorded in pooled estimates while the lowest estimates (9.1 and 12.3, respectively) were found in AKR. Little differences between these two genetic parameters was observed across environments

For days to 75% maturity, CV_G were the highest (67.1) in pooled estimates while the lowest (0.7) in CDR environment. The CV_P (117.4) was highest in DZB while the lowest (3.0) in CDB. In general, CV_P estimates were lower across environments except in DZB.

CV_G for grain filling period was estimated from 7.4 to 26.9 in DZB and ATB environments, respectively. The highest CV_P estimates for grain filling period were recorded in pooled environments while the lowest (15.8) were observed in DZR. The CV_P estimate was higher than the CV_G for this trait.

The CV_G estimates for grain protein content were varied from -0.2 to 4.9, where the highest was obtained at Alem Tena and the lowest at Minjar. Lowest CV_P (4.0) was recorded in AKR while highest (17.1) was obtained when pooled over environments. The CV_P estimate was higher than the CV_G estimate.

Genotypes showed high variability for plant height while low for spike length across environments (Table 8).

5. DISCUSSION

5.1 Simple and pooled analysis of variance (ANOVA)

Considering individual environment ANOVA results, the component of variance due to genotype was highly significant ($P \leq 0.01$) for most the traits studied in all environments except for number of effective tillers per plant, which showed significant differences in MNR, DZB, CDB and AKR environments (Appendices 2a to 2l). This indicated that genotypes differed significantly amongst each other for most of the traits studied. Tesfaye *et al.,* (1998) found the same results for a data set of durum wheat landrace genotypes tested during 1988-1990 in Akaki, Debre Zeit, Chefe Donsa and Bichena locations.

The genotypes tested also showed inconsistent performance for most of the traits, which was reflected in their variable ranks at the testing locations. This showed the differential performance of the genotypes and the existence of qualitative type of interaction and that superiority depends on the environment. Replication variance found significant for most of the traits in Alem Tena and Selale (Appendices 2a, 2b, 2k and 2l). There was termite problem in some plots in Alem Tena and drainage problem in some plots in Selale resulting into differences among blocks. .

Pooled analysis of variance for stability was carried out following Eberhart and Russell (1966) model (Table 4). There were highly significant ($P \leq 0.01$) differences among genotypes for all the traits studied except biological yield per plant. Environments (locations and planting methods) also showed highly significant ($P \leq 0.01$) differences amongst each other. This indicated that differences existed among environments and highly significant variances due to genotypes, revealed the presence of genetic variability in the material included in this study for all the traits except for biological yield. The mean squares due to G x E interaction effects also showed significant differences for all the traits studied except for harvest index, indicating that the genotypes responded differently relative to each other to change in environment.

The variation due to environment was larger than that due to genotypes for most of the traits, which was larger than the G x E interaction. This variability was mainly due to the distribution of rainfall, which differed greatly across the locations during the

experimental year (Appendix 1). Adugna and Labuschagne (2002) working on phenotypic stability of linseed also reported very high fluctuations in the growing environments of Ethiopia.

Significance of G x E source of variation permitted the partition of environment and G x E sources of variation into environment (linear), G x E (linear) interaction effects (sum of squares due to regression, b_i) and unexplainable deviation from linear regression (pooled deviation mean squares, S^2d). It indicated that the stability parameter b estimated by linear response to change in environment was not the same for all the genotypes.

The significance of environmental effects and their interactions warrants further analyses of the stability and adaptation of the genotypes. Stability analysis using the Eberhart and Russell regression model was performed in order to identify adaptable and stable varieties to the testing environments. According to their model, a stable genotype is characterized by average response (unit regression) and least deviation accompanied by high mean. Stability differences were assessed on the basis of mean performance, linear regression coefficient and deviation from regression. Rooted in this analysis, the deviations were low for most of the traits, except for days to heading and days to maturity that were higher, showing the good fit of the regression model

The non-linear response as measured by pooled deviations from regression were significant for most of the traits, indicating that the differences in linear response among genotypes across environments did not only account for all the G x E interaction effects, and therefore, the fluctuation in performance of genotypes grown in various environments was not fully predictable. Thus, S^2d parameter becomes important. These results are in agreement with earlier findings of Eberhart and Russell (1966) and Kenga, *et al*., (2003).

Kumar and Chowdhury (1991) observed linear proportion of G x E interaction for grain yield in durum wheat. Solomon *et al.,* (1995) observed the same for grain yield in bread wheat, number of kernels per spike, thousand kernel weight, spike length, plant height and number of effective tillers per plant in durum wheat. Therefore, it was inappropriate to select genotypes on the basis of mean yield alone; both genotype

characteristics (trait) and stability of performance would be needed to evaluate genotype performance (Kang, 1993).

5.2 Estimates of stability parameters

The deviations were low for majority of the genotypes for most of the traits studied showing the good fit of the regression model (Tables 5.1–5.3). Based on the regression coefficient b, the genotypes tested could be categorized as those having more than average stability, average stability and below average stability for all the traits in the range of environments they encountered. Many belonged to the average stability group for all the traits studied. Stability of yield and related components were variable, the most unstable, non-predictable being days to heading and days to maturity, according to this study.

Yield and yield components

Grain yield per plant

Finlay and Wilkinson (1963) and Perkins and Jinks (1968) found that linear response is positively associated with mean performance. Eberhart and Russell (1966) and Paroda and Hayes (1971), however, emphasized that both linear (b_i) and non-linear (S^2d_i) components of G x E interaction should be considered in judging the phenotypic stability of a particular genotype and their responses were independent from each other. Muhammad *et al.,* (2003) suggested that the linear regression could simply be regarded as a measure of response of a particular genotype which depends largely upon a number of environments, whereas the deviation from regression line was considered as a measure of stability, genotype with the lowest or non significant standard deviation being the most stable and vice versa.

Genotypes may be grouped together, depending on the magnitude of their regression greater than, equal to, or less than unity. The regression coefficient reflects the response, or adaptation of a cultivar in various environments, rather than indicating stability. Based on linear (b_i) and non-linear (S^2d) components of G x E interaction and high mean values eight genotypes *viz.,* CD94523, CDSS92B193, CD97383, CIGM91-349, DZ2234, DZ2293-2DZR, DUKEM/3/RUF and DZ3117 with high grain yield, b_i value equal to unity and S^2d non significant were identified to be stable and recommended for cultivation in all environments (Table 5.1). Tesfaye *et al.*

(1998) in similar studies also reported that many of the landraces belonged to the average stability group.

The cultivars with a regression coefficient greater than unity are more adapted to favorable growing conditions and those with a regression coefficient less than unity are specifically adapted to poor growing environments. Accordingly genotype CD91313 showed regression value significantly less than unity and non-significant deviation from regression mean square, indicating its adaptability to poor environments. None of the genotypes found suitable for favorable environments except CDSS92B1467 but with unpredictable behavior. Romagosa and Fox (1993), have given emphasis for breeding widely adapted genotypes with stable and high yielding ability across environments which is particularly important for developing countries like Ethiopia where yield stabilizing inputs are often limited or not available.

All genotypes had outyielded the local and standard checks. Rank order of CIMMYT genotypes from one to nine except fourth in terms of grain yield performance showed that introduction from CIMMYT performed better than Debre Zeit cross materials and four out of eight stable genotypes belonged to the high yielding (6.13 to 6.48 gm/plant) introduction group.

Biological yield per plant (gm)

Pooled analysis revealed that (Table 4), there were no significant differences among the genotypes for this trait, thus most of the genotypes had almost similar mean biological yield. But conversely, Kumar and Chowdhury (1991) obtained highly significant differences among genotypes for biological yield. Genotype DZ-04-118 (local check) found to have below average stability thus, recommended for cultivation in poor environments. Genotypes CDSS92B1467 and CDSS93Y33 revealed significant regression value but due to their significant S^2d indicated that both linear and non-linear contributed to G x E interaction hence, their stability cannot be predicted. Half of the genotypes including all the eight those were stable for grain yield had showed average stability for biological yield per plant since their linear response was equal to unity and non-linear as zero. It showed that the genotypes were well buffered and could adjust their response to the changing environment. The stable genotype *viz.,* DZ2293-2DZR recorded the maximum (14.59 gm) biological yield per

plant followed by CIGM91-349 (14.48 gm) and DUKEM/3/RUF (14.24 gm) (Table 5.1).

Harvest index

In the present study, harvest index was not affected by environmental changes (Table 4), appearing a very stable trait, possibly due to high proportion of translocated pre-anthesis reserves for grain filling when photosynthetic source is limited by stress Saleem (2003). However, Kumar and Chowdhury (1991) obtained highly significant differences for the G x E source of variation for this trait. Since stability refers to non-erratic performance with respect to agronomic traits and stable cultivars show minimal or low interactions (Allard and Bradshaw, 1964).

Number of grains per spike

More than half of the genotypes showed higher number of grains than the population mean (Table 5.1). Genotype CDSS93Y545 exhibited above average stability thus, found suitable for better environment while genotypes DZ1675-1AK and CD91313 showed below average stability but with poor performance, recommended for poor environments. Genotypes CD94523, CIGM91-349 and DZ2293-2DZR (high yielder and stable in terms of grain yield), CD98206, CIGM91-347, DZ2212-1BS and Yerer found to be stable concerning this trait hence, were suitable for growing in all environments. Kinyua and Kirigwi (1993) reported that most of the tested wheat genotypes did not significantly deviate from linear regression thus, performing stable for this trait. The high yielder and stable genotypes CIGM91-349 and CD94523 had also higher number of grains per spike *i.e*., 56.25 and 53.97, respectively compared to the highest 57.25 observed in CD95294-1Y, an unpredictable genotype.

1000-kernel weight (TKW)(gm)

The significance of regression and deviation from regression mean square for more than half of the total genotypes revealed that both linear and non-linear components contributed to G x E interaction. Eight out of 14 among the better performing genotypes were the DZ-crosses and checks. Genotype DZ2234 was identified to be the best but its performance could not be predicted over environments due to highly significant S^2d (Table 5.1). Gerardo was found to be suitable for cultivation under favorable environment while genotype DZ2293-2DZR for unfavorable environments. Genotypes CD91Y7, CD97383, CD98206, DUKEM/3/RUF, Yerer and Ude (standard check) were identified to be stable, hence suitable for growing under all environments. Genotypes CD97383 and DUKEM/3/RUF were also stable for grain yield while CD98206 and Yerer for number of grains per spike. According to Garcia del Moral *et al.* (2003), kernel weight was the unique yield component that appeared to be relatively stable to environmental changes.

Morphological traits

Number of effective tillers per plant

Tiller production is known to be the 1st developmental process in cereals and it may exercise a direct influence on all other traits that are developed later. Mather and Jinks (1971) observed that plants that perform well in dry areas must integrate many characteristics that contribute to efficient use of moisture. Stand establishment and successful early tiller production have also been shown to contribute to high yields under drought conditions.

Ten genotypes including the local and the standard checks had higher number of effective tillers per plant than the grand mean. Genotypes CDSS92B193 and CD91313 with maximum number of effective tillers per plant, regression significantly greater than unity and non significant deviation from regression, showed above average stability, thus recommended for better environments, where as DZ-04-118 (local check) was recommended for poor environment due to significantly less regression value than unity. Genotypes CD91Y7, CD94545-A, DZ2234, DZ2293-2DZR, and Ude (standard check) (Table 5.2) were found to be stable for this trait, hence recommended for cultivation in all environments.

Spike length (cm)

In some of the genotypes significance of regression and deviation from regression mean squares indicated the presence of both linear and non-linear components of variance for G x E interaction. Kinyua and Kirigwi (1993) also observed contribution of linear regression in all the cultivars studied for this trait. More than half of the genotypes showed longer spike length than the grand mean (Table 5.2). Genotypes CIGM91-349 (high yielder and stable for grain yield) and CIGM91-347 possessed below average stability were recommended for low yielding environments while genotype DUKEM/3/RUF (high yielder and stable for yield besides, the longest spike length) with above average stability found to be suitable for better environments. Genotypes CD94523, CD91989, CDSS92B193, CD97383, DZ2234, DZ2212-1BS and DZ2293-2DZR identified as stable and recommended for all environments.

Plant height

The introduction of dwarf wheat varieties led to the striking increase in wheat yields all over the world. The dwarf durum wheat varieties are more responsive to high level of inputs. However, in developing countries limited input conditions put considerable constraints on the full exploitation of genetic potential of the new wheat varieties. In developing countries like Ethiopia there is large area of rainfed wheat where annual fertilizer consumption per unit area is also very low. In general, all genotypes, except DZ2293-2DZR, DZ1675-1AK, DZ1669-1AK and DZ3117, in this study were classified as semi-dwarf following the classification of the National Durum Wheat Research Project (*i.e.* genotypes less than 90cm in height are classified as semi-dwarf, 90–100cm are medium and greater than 100 cm as tall genotypes). The CIMMYT introduction were shortest in height compared to DZ-cross genotypes. Sixteen genotypes of semi-dwarf height were identified as average stable and recommended for general cultivation. Genotype CIGM91-349 was the shortest (65.92 cm) and highest yielder (6.48 gm/plant) among all genotypes. Its high yield advantage could be attributed due to dwarf plant height (Table 5.2).

The tall genotypes DZ1675-1AK and DZ1669-1AK with maximum (100.33 and 101.69 cm, respectively) height exhibited above average stability. Thus, they were considered suitable for favorable environments. Likewise, medium tall genotypes DZ3117 and DZ-04-118 (local check) were also identified suitable for favorable environments. But they could not be recommended for high input agriculture since

lodging was one of the problems for these long genotypes. Genotype CD91313 was suitable for poor environments.

Phenological traits

Days to 50% heading (days)

Eight of the twenty-five genotypes revealed the presence of both linear and non-linear components of G x E interaction while three showed predominance of linear and seven non-linear components. All but six genotypes headed later than the grand mean. Early heading genotypes were from DZ-crosses. Genotype DZ1669-1AK was suitable for unfavorable environments. Genotypes CD91Y7, CD98206, DZ1675-1AK, CDSS93Y545 and Ude (standard check) were identified as stable with longer heading days while DZ2234 and DZ2293-2DZR were found stable with shorter heading days thus these were good for lowland (moisture stress) environments (Table 5.3).

Earlier genotypes generally perform better than later ones in low yielding environments because of high water availability at the end of the crop season, but this advantage tends to disappear under favorable environments. The cooler conditions of the highlands compared with the lowland delayed heading date for about 20 days (Appendix 1), causing a more intense effect of temperature on phenological development under water shortage conditions.

Genotype DZ3117 took the shortest time (57.78 days) for heading hence, it is one of the reasons that make this genotype high yielder and stable though unpredictable for days to heading in all environments including Alem Tena (moisture stress environment).

Days to 75% maturity (days)

The duration of the sowing-to-heading phase is determined by the genotypic photoperiodic and temperature responses (Gebeyehou *et al.,* 1982). This phase includes tillering and organogenesis processes, during which the formation of two important yield components *viz;* spikelets per spike and grains per spike takes place. Similarly, medium maturity and dwarfness in durum are also preferable to harvest higher grain yield under high input management conditions (Sharma and Sain, 2004).

Most of the DZ-cross genotypes took longer time to mature than the population mean except genotype DZ3117 which took minimum number of days (105.61) to mature. Eight genotypes revealed the presence of both linear and non-linear, while five showed the predominance of linear and six non-linear components of G x E interaction.

Genotypes CDSS92B1467, CD97383 and DZ2234 had above average stability and were suitable for better environments while CD91989 and DZ2212-1BS possessed below average stability thus recommended for poor environments. Genotypes DZ2234 and DZ3117 (stable and high yielder in terms of grain yield), due to their shortest maturity period than the rest of the genotypes, may be recommended for those environments affected by terminal moisture stress. Genotype CD94523, CDSS92B193 and CD98206 among the early maturing and CIGM91-349 and DZ2293-2DZR among the late maturity were identified as average stable for all environments (Table 5.3).

Grain filling period (days)

Eleven genotypes had a longer grain filling period than the population mean (Table 5.3). Seven genotypes, exhibited the preponderance of non-linear component hence did not fit to the regression model. Two genotypes showed the presence of both linear and non-linear components of G x E interaction while two only the linear. Genotypes CD91989 and CD9S294-1Y were recommended for poor environments. Eight genotypes with shorter grain filling period and six with longer were classified as stable. The high yield advantage (Table 5.1) of genotype DZ2293-2DZR (with longest grain filling period and high yield) may be attributed due to extended grain filling period, which leads to heavier kernels. The advantage of long grain filling period was also reported by Signor *et al*. (2001).

Grain filling is maintained by a high contribution from assimilation before and immediately after anthesis and remobilization of vegetative revenues during kernel growth. Grain filling period has a positive effect on grain yield in areas where there is optimum rainfall and reduced grain production under moisture stress environments (Garcia del Moral *et al.,* 2003). Budak (2000) stated that kernel shriveling due to

drought stress during grain filling period of wheat resulted in decrease grain yield. The duration of grain filling period could modify kernels per spike by reducing abortion of pollinated florets after anthesis (Garcia del Moral *et al.,* 1991). Nevertheless, longer GFP should increase grain yield, provided that later stages of grain filling do not occur under terminal drought stress (Gebeyehou *et al.,* 1982).

The biological complexity underlying G x E interaction in almost all phenotypic effects are not related to the gene in any simple way. Rather they result from a chain of physico-chemical reaction and interactions initiated by genes but leading through complex chains of events, controlled and modified by other genes and the extents explained the effect of G x E interaction on important traits (Baker, 1988; Zobel *et al*., 1988; Gauch and Zobel, 1996; Yan and Hunt, 2001).

Quality traits

Grain protein content (%)

Grain protein concentration, the most important index of semolina quality for pastification, depends on the interactions among genotype and environmental and agronomic factors. Nitrogen availability in the soil (Banziger *et al*., 1992), air temperature (Craffi *et al*., 1996) and soil water content (Fares *et al*., 1993) during grain filling are particularly important. Producing durum wheat genotypes with high and stable grain protein content is one the main goals of breeding programs.

The stability analysis in this study revealed that genotypes CDSS92B1467, CD98206, CIGM91-347, CD94545-A, DZ2212-1BS, DZ1669-1AK, DZ3117, Yerer, DZ-04-118 (local check) and Ude (standard check) showed higher grain protein content than the population mean. However, only three genotypes namely; CD98206 (13.12%), DZ3117 (13.52%) and DZ-04-118 (local check) (13.26%) attained higher than the standard (13.00) (Riley *et al.,* 1998) grain protein content. The genotype DZ3117 was the best in this respect since it was also high yielder with stable performance, hence recommended for cultivation in all environments. Besides, genotypes CDSS92B1467, CD98206, CIGM91-347, CD94545-A, DZ2212-1BS, DZ1669-1AK, DZ3117 and Ude (standard check) exhibited average stability for protein content (Table 5.3) and thus, recommended for all environments. Yerer is recommended for favorable while

CD91313 for unfavorable environments due to their above average and below average stability.

Results of the present work clearly showed the differences between locations due to climatic conditions in determining yield, yield components, related traits (days to heading, days to maturity, grain filling period and plant height) and grain protein content. Lower temperature and longer grain filling period, allowing more accumulation of assimilates into the grain, which resulted in heavier kernels, and higher grain yields. The positive effect of lengthening days to maturity and grain filling period on grain yield had been previously reported by (Belay *et al.,* 1993). The effect of grain-filling period on kernel weight probably resulted from increased photosynthesis.

The regression estimates for most of the traits' stability of the genotypes tested were not significantly different from 1.0. This indicated that there was flexibility for component compensation for these traits so that yield was stable. It also showed that the genotypes were well buffered and could adjust their response to the changing environment. According to Eberhart and Russell (1966), a stable variety is one with unit regression (b=1), and a deviation from regression as small as possible ($S^2d=0$). Lin *et al*. (1986) considered a stable variety, as one with small variation in its performance in different environments or if its response to environments is parallel to the mean response of all genotypes in the trial or to the residual mean square from the regression model on the environmental index is small.

In general, the results listed in Table 5.1 to 5.3 further suggested that the stability of grain yield was contributed by the stability of different characters in different genotypes. For example, five characters contributed the yield stability of genotype CIGM91-349 while for that of CD97383 and DZ3117 were by four and three characters, respectively. Similar results have been reported by Efrem *et al.* (2000b).

5.3 Classification of environments and genotypes according to IPCA scores

G x E interaction by definition involves both genotypes and environments. To effectively understand and interpret G x E interactions, the interaction axis and associated environment and genotype scores need to be explained in biologically meaningful terms.

The abscissa shows the main effects and the ordinate shows the interaction 1 scores that capture interaction effects. In all AMMI plots, a horizontal dashed line shows the interaction score of zero, and the grand mean is indicated as a vertical, dashed line. The ordinates are the interaction scores for genotype parameters and the abscissa are the means for genotypes (averaged over environments).

Results of AMMI analysis using the same data showed that there were highly significant differences ($P \leq 0.01$) among the genotypes, the environments and G x E interaction, except for biological yield per plant and spike length where genotypic main effects and G x E interaction were non-significant, respectively (Table 6). The significant differences among the environments indicated that the locations can be used as testing stations for different environments while significance differences among genotypes revealed the differential responses of genotypes to different environments. The G x E interaction was composed of 11 components (IPCA) along with their contribution of sum of squares (SS) with decreasing importance. F tests used to measure significance of the components at $p \leq 0.01$ level recommended inclusions of the 1st four interaction PCA axes in the model in most of the traits studied.

For any G x E combination, Fig 1-11, the additive part (main effects) of the AMMI model equals the genotype mean plus the environment mean minus the grand mean, and the interaction (multiplicative part) is the genotype score times the environment score (Zobel *et al.,* 1988).

Like the results obtained from AMMI model used in international wheat yield trial (Crossa *et al.*, 1991), the AMMI model used in this study exhibited simple interaction which required one IPCA axis to account for considerable amount of variation in the

G x E interaction. This could be associated with the nature of the crop, environmental characteristics or diverse genetic background obtained from different sources.

The proportion of variance explained by the first two IPCA axes was greater than 50% in majority of the traits. Eigenvalues for the first two axes were greater than the mean of all eigenvalues; hence, much of the variability was accounted by the first two or three components. The IPCA axes after the fourth had no real contribution representing G x E interaction, rather, most of it was attributable to noise caused by different situations. Therefore, the sum of squares due to fourth to eleventh IPCA axis could be summed and classified as a noise, because they had no real predictive power.

The environments showed a high variability in both main effects and interaction effects (Table 6). Therefore it was necessary to classify the environments to recommend target genotypes according to adaptation. Tiruneh (2000); in tef, Romagosa and Fox (1993); in Triticale, Ghadri *et al*. (1980) in wheat and Eberhart and Russell (1966) in maize have also reported grouping of environments and genotypes based on the G x E pattern. Similarly, a recent study (Adugna and Labuschagne, 2002) undertaken on the phenotypic stability of linseed in Ethiopia also revealed very high fluctuations in growing environments of Ethiopia.

Grain yield per plant

CDB found to be average environment for grain yield since its IPCA score close to zero. But DZB was negatively interactive with the genotypes since it showed high negative IPCA score while AKB revealed high positive IPCA score demonstrating it to be positively interactive with the tested genotypes (Fig 1). Tiruneh (2000) reported the same results for G x E interaction of 18 tef genotypes tested in seven environments.

The yield potential of the testing sites and the level of discrimination they pose on the genotypes was identified. The highest mean yield was observed at Debre Zeit (9.73 gm) while the lowest was recorded in Alem Tena (3.81gm) followed by Selale (4.05gm). Debre Zeit and Akaki, areas with relatively good rainfall (amount and distribution) showed the positive IPCA 1 scores (Fig 1 and Appendix 4). The low

yielding environments, Alem Tena and Selale, represented areas where crop failure is common, showed negative environment IPCA 1 scores. These may be different from the rest of the environments in the group because of very short growing period (Alem Tena) and drainage problem (Selale). The differences observed in the pattern of discrimination among locations necessitated the development of different lots of germplasm for each group of locations. Therefore, the identification of genotypes that can favorably grow over these variable environments is necessary to attain increased grain yield in these areas. Accordingly, three genotypes have been identified as stable and four found adapted to positively interactive environments.

Grain yield was greater in the locations where the altitude range was from 1900-2400 m a.s.l. than areas with below 1800m a.s.l., a consequence of heavier kernels and a longer plant cycle (vegetative period and grain filling period).

Biological yield per plant

DZB exhibited the highest positive IPCA score for biological yield per plant while SER showed the highest negative IPCA score demonstrating DZB was favorable while SER as poor environment for the tested genotypes. CDB showed IPCA score near to zero indicating it as average environment for most of the genotypes. Four genotypes with IPCA score zero showed no interaction identified as stable, while six positively interactive were identified as adapted to positively interactive group of environments (Fig 2 and Appendix 4)

Harvest index per plant

The highest harvest index (0.50) was found at AKB while the lowest (0.37) was at ATR and MNB. The highest positive IPCA score for this trait was exhibited by DZB while the highest negative was by ATR indicating these to be favorable and unfavorable environments, respectively. Lack of specific environment showing IPCA score near zero indicated that the genotypes and the environments were highly interacted for this trait. Only one genotype DZ2234 was identified as stable with IPCA score zero. Seven genotypes were adapted to positively interactive high yielding

environment DZB and AKR while six to positively interactive low performing MN (R and B) environments (Fig 3 and Appendix 4)

Number of kernels per spike

Number of kernels per spike decreased significantly under water stress (Saleem, 2003). The reduction of these traits at Alem Tena may be due to this reason. AKB revealed the highest positive IPCA score followed by DZR, representing favorable environments while SEB and SER showed highest negative IPCA scores representing poor environments for this particular trait ((Fig 1 and Appendix 4) Variations in grain yield between environments were predominantly associated with variations in kernels per spike. This result agrees with (Belay *et. al.,* 1993) in durum wheat.

Four non-interactive better performing genotypes were identified as stable while four positive interactive were adapted to positive interactive environments DZ (R and B), CDB and AKB.

Thousand-kernel weight

SER and SEB gave higher mean thousand-kernel weight (50.48 and 48.61, respectively) while MNB gave lower mean kernel weight (34.77). This indicated that environments with high amount of rainfall were favorable for production of durum wheat genotypes with heavier kernels. The decrease in grain weight in Minjar may be due to disturbed uptake efficiency and photosynthetic translocation within the plant (Iqbal, *et al*., 1999) that produced shriveled kernels could be due to hast end maturity and windy weather.

CD (R and B) and SE (R and B) showed highest positive IPCA scores for this trait and considered as favorable environments while DZ (R and B) and MN (R and B) showed highest negative IPCA scores, rated as unfavorable environments. ATR showed IPCA score near zero (Fig 5 and Appendix 4), indicating it to be average environment. Three stable genotypes were adapted to all environments. Five better performing genotypes were positive interactive and adapted to positive interactive high performing environments *viz;* AK, CD, and SE (for both methods of sowing).

Number of effective tillers per plant

The highest number of effective tillers per plant (5.01) was obtained in DZB environment while the lowest (2.27) in SEB. DZB also possessed the highest positive IPCA score while ATB showed the highest negative IPCA score, indicating DZB and ATB to be favorable and unfavorable environments, respectively. Tiller production is known to be the 1st developmental process in cereals and then it may exercise a direct influence on all other traits that are developed later (Schmid, 1992). Thus it may be one of the reasons that made Alem Tena unfavorable environments for most of the traits that are developed later. AKB showed IPCA score near zero suggesting it to be average environment (Fig 6, Appendices 4 and 5). The genotypes including a local check DZ-04-118 found to be non-interactive with zero IPCA score, hence were adapted to ATR environment while six to AK (B and R) due to their similar interaction.

Spike length

The G x E source of variation for this trait was not significant (Table 6) suggesting that all the genotypes showed similar response for the testing environments thus, the environments were not be classified.

Plant height

A decrease in plant height was observed in all genotypes at Alem Tena followed by Minjar environments. The longest mean height was recorded at Akaki while other locations did not show much difference for it. Since Alem Tena is found in the rift valley, this may be because of insufficient and erratic rainfall. Stress conditions made plants to complete their life cycle within short period resulting into smaller vegetative parts.

Similarly, ATR and ATB also revealed highest negative IPCA scores for this trait, indicating these environments negatively interacted with genotypes while SEB, DZR and AKR showed highest positive IPCA scores suggesting the reverse condition. MNB and CDB showed IPCA scores near zero, hence classified as average environments for most of the genotypes. Five genotypes were found adapted to

positive interacting better performing environments due to similar interaction while the non-interactive identified as stable (Fig 7, Appendices 4 and 5).

Days to 50% heading

In general, genotypes revealed lesser number of days to heading and were earlier in maturity at Alem Tena followed by Minjar, Debre Zeit, Akaki and Chefe Donsa. AT (B and R), MNR, DZ (B and R) and SER were positively interactive environments while AK (R and B) negatively interactive and favored early heading. Two genotypes CD91313 and DZ3117 with early heading found adapted to AK (R and B) environments in this group due to similar interaction. No genotype was identified to be stable and adapted to for all environments (Fig 8)

Days to 75% maturity

AT (R and B) favored earlier maturity of 92.03 and 93.12 days, respectively while SE (R and B) late maturity of 134 days compared to the other testing environments. ATR exhibited highest positive IPCA score, indicating it was positively interacted with the genotypes while CDB and SER exhibited highest negative IPCA scores for this trait. No specific environment was identified that showed IPCA score near zero for this trait. This indicated that none of the environments was found to be non-interactive with the genotypes.

Environments AT (B and R), MN (R and B) and DZ (R and B) had positive interaction and were grouped as similar and only three genotypes DZ2293-2DZR, DZ2212-1BS and Yerer with similar positive interaction were adapted to MN group of environments (Fig 9).

Grain filling period

The longest grain filling period (72.04 days) was recorded in SEB while the shortest period (33.35 days) was recorded in ATR. This is may be due to the high temperature and forced maturity in Alem Tena since Alem Tena is a lowland environment while the low temperature in Selale made the grain filling period to be extended. MN (R and B) showed highest positive IPCA score, indicating that they interacted positively and were better environments for most of the genotypes while SEB showed higher negative IPCA score and consequently negatively interactive. No specific

environment showed IPCA score near zero *i.e.* all environments are highly interacted with the genotypes for this trait. The similar means of genotypes observed for grain filling period is not suffice condition for AMMI biplot for classification (Fig 10 and Appendix 5).

Protein content

The IPCA score for protein content was near zero at Akaki, Chefe Donsa and Selale, indicating these to be stable, highest positive at Alem Tena indicating to be positively interactive while higher negative was recorded at Debre Zeit and Minjar indicating these to be negatively interactive locations. In terms of average protein content of genotypes Alem Tena was the best location followed by Debre Zeit and Minjar.

The increase of grain protein concentration that occurred in Alem Tena having restricted water supply could be related to the relationship between N uptake and translocation, which are partly affected by the environment. . High protein but low grain yield at Alem Tena, according to Budak (2000), may be due to the drought occurrence during grain filling period. Improvement of grain yield and protein content through direct selection is difficult because of the well-documented negative association (Metho *et al*., 1997). In dry environments, when yield response to available nitrogen (N) is low, the nitrogen goes to increased protein production in grain. In wet areas, nitrogen goes to increase wheat yields.

Areas with low amount of rainfall are good for good pasta quality durum wheat production. One of the reasons for the low grain protein content in the highlands may be N leaching due to the high amount of rainfall and aeration problem due to the water logging problem that made mineral uptake by the roots from the soil complicated. The higher location mean protein content advantage at Alem Tena than that of the highlands could be due to the severe water logging at Akaki at the early growth stages of the crop. Under waterlogged conditions, N availability is critical for cereal yield. In similar studies, it was reported that a higher level of N was required to obtain the highest grain protein content than at Debre Zeit (Bemnet *et al.,* 2003).

In wet environments with high yields, large additions of N fertilizer are often required to maintain or increase protein. The problem is that it is not possible to predict growing season moisture or temperature. Therefore, a high application of nitrogen at

or prior to seeding to increase protein carries a high level of investment risk under dry land farming.

Therefore, in general, Alem Tena is considered as low yielding location in terms of grain yield and its components whereas best for realizing grain protein content. Debre Zeit showed positive IPCA score while SE and Alem Tena negative for most of the traits. Therefore, Debre Zeit is classified as high yielding environment while Alem Tena and Selale as low yielding environments. However, Akaki and Chefe Donsa were average environments for yield, its components and other traits.

Genotype CD95294-1Y with IPCA score near to zero was found to be non-interactive and stable while DZ-04-118 with similar positive interaction was adapted to Akaki and Chefe Donsa locations. DZ3117 recorded the maximum protein content and highest positive IPCA score showing similar positive interaction and adaptation to Alem Tena location (Fig 11, Appendices 4 and 5).

5.4 Heritability

Study of statistical parameters like heritability is not only helpful to evaluate the genetic stability and performance of any particular genotype but it is also a measure to determine the effectiveness of selection for a particular trait in that genotype. High heritability further indicates the effectiveness of selection in early segregating generations. A low heritability on the contrary indicates that the selection must be delayed till later generations (Firouzian, 2003).

Thousand-kernel weight is useful yield related trait that affix to grain yield. High heritability for kernel weight and number of kernels per spike (Table 7) in all the testing environments except in Alem Tena indicated that selection for this trait would be more effective and successful in early segregating generations without going for further progeny testing. Therefore, kernel weight and number of kernels per spike can be considered as a promising yield selection criterion because of its acceptable heritability value. These results are in close conformity with the findings of Chowdhry *et al*. (1997) and Firouzian (2003). Chandra *et al*. (2004) also obtained high heritability for number of kernels per spike and moderately high to high heritability for thousand-kernel weight.

In most of the environments very high heritability was registered for spike length and grain filling period, suggesting that the characters were predominantly controlled by additive genes. Plant height revealed high heritability in all environments except at Alem Tena (medium) in both methods of planting. The results indicated that additive genes predominantly controlled the character. It also indicated that this trait was highly heritable and therefore, selection for this trait would give positive response toward the improvement of this trait. Earlier studies pertaining to heritability in wheat have indicated variable results. High estimates of heritability for plant height were recorded by Saleem *et al.* (2003), medium to low by Gupta and Verma (2000) cited from Firouzian (2003) and moderate to high by Chowdhry *et al.* (1997) and by Firouzian (2003) and Chandra *et al*. (2004) high to very high heritability estimates were reported for plant height in wheat.

High heritability and equal estimates were observed for days to 75%maturity at locations having altitude lower than 2000m a. s. l. in both the methods of planting while the highlands revealed medium heritability for this trait. Days to 50% heading showed highest heritability in most of the environments. These results indicated the effect of additive genes. Harvest index and grain protein content exhibited moderately high to high heritability in most of the environments. This implied that additive genes might be responsible to some extent for the control of these traits.

Grain yield is the prime objective of plant breeders. High estimates of heritability for this trait would be helpful for breeders to select for the best combinations and to reach at the desirable level of yield potential. Although selection for grain yield is difficult owing to its polygenic nature but according to our results, it showed low to moderately high heritability indicating the potential of effective selection for grain yield at early stages. Similarly, biological yield and number of effective tillers per plant exhibited low to moderately high heritability indicating the importance of both additive and non-additive genetic effects. But Firouzian (2003) obtained high heritability for grain yield and Chandra *et al*. (2004) for biological yield.

In general, the results indicated prevalence of fairly high estimates of heritability for most of the traits studied over environments, therefore, selection for these traits could

be practiced more effectively at early stages and does not need to go for further progeny testing. These traits can also be incorporated in future breeding strategies for the improvement of durum wheat. However, selection for polygenic traits like grain yield must be practiced with due care.

5.5 Coefficient of variability

Genetic variability is the basis of selection and further improvement in any crop species. Very high CV_G and CV_P and little differences between these two genetic parameters were observed in thousand-kernel weight, spike length, plant height and days to 50% heading (Table 8). These results indicated that the expression of these traits were mostly due to genetic effects and could be modified by selection. Chandra *et al*. (2004) obtained the same result for plant height but low CV_G and CV_P estimates for thousand-kernel weight.

Higher estimates of CV_G and CV_P were also obtained for number of kernels per spike. But the CV_P estimates were greater than the CV_G suggesting the variation for this trait is predominated by environmental factors.

Lower values of CV_G and CV_P were obtained for the traits, *viz*; grain yield, biological yield, harvest index and number of effective tillers per plant over the testing environments indicating the preponderance of non-additive genetic effects. Estimates of CV_P were greater than CV_G for these traits, which revealed that the variations for these traits were mainly due to environmental factors. However, Chandra *et al*. (2004) reported high CV_G and CV_P but little difference between the two estimates for biological yield and low CV_G and CV_P estimates for harvest index.

Similarly, the estimates of CV_P were greater than CV_G for days to 50% heading, grain filling period and protein content indicating the variation for these traits was mainly due to non-genetic factors.

For those environments where genotypic and phenotypic coefficient of variations did not show much difference in magnitude, the environmental effect was minimal and there was a good ground for the genotypes to express their genetic potential for the various traits.

To conclude, in this study, high CV_G, CV_P and heritability estimates were obtained for thousand-kernel weight, number of kernels per spike, plant height, spike length and days to 50% heading. This indicated the involvement of additive gene effects for these characters and could be exploited through selection for genetic improvement of the crop.

6. SUMMARY ABD RECOMMENDATIONS

Stability and wide adaptation are of vital importance in Ethiopia where fluctuations in growing conditions are very high. One of the limitations of durum wheat when compared to bread wheat is its low yield. Therefore, by exploiting the good adaptation and stability of yield and its components of durum wheat genotypes, it would be possible to develop/identify high yielding and well adapted varieties. For this, evaluation of genotypic performance at a number of locations provides useful information to determine their adaptation and stability.

This study first underlines the magnitude of the environment effect, which accounts for more than half of the total variance of durum wheat yield and related traits in Eastern Shoa region of Ethiopia. G x E interaction effect also appears important when compared with genotype effect.

Therefore, the results of this study generally indicated that G x E interaction cannot be ignored and hence, requires attention in durum wheat multi-location trials. Knowledge of G x E interaction facilitates the choice of an appropriate model in a stability analysis. Information on the relative contribution of environments and their interactions with genotypes is helpful in determining whether to increase the number of testing environments. It also allows the breeder to exploit widely adapted varieties within the homogenous set of environments and also enables a correct choice of testing sites for early germplasm screening that are introduced from abroad (mostly from CIMMYT) and also hybridized in the National Durum Wheat Research Project. But the dynamic nature of environment, that made G x E interaction random, it is difficult to transfer this result to other durum wheat G x E system. Thus, the trial should be repeated to made concrete conclusion.

The presence of G x E interaction and environmental sources of variation were highly significant, selection should be according to the merits of the environments and it also suggests to breeders that one of the goals in breeding programs is to produce high-yielding cultivars for a wide range of environments. Alternatively, classifying the environments may reduce the G x E interaction, particularly grouping homogeneous locations together and classifying the environments into favorable, medium and poor environment group reduces the effect of G x E interaction on selection. To capitalize

on the G x E interaction and to select breeding materials adapted to favorable and unfavorable growing conditions, selection of specific cultivars adapted to specific environments appears to be necessary. Conversely, enhancing genetic diversity and providing materials that perform well in poor and in favorable environments, are desirable to achieve sustainable agriculture.

Environment classification may be further improved by considering site-specific information on, *e.g.* soil characteristics (fertility or depth) had not been collected for the field trials involved in this study and deserve consideration in the future.

These results also confirm the importance of testing genotypes under representative environmental conditions to identify best, the most stable and highest yielding genotypes. Two years of testing over numerous environments, which is the current practice within the variety release program, increases the probability of reaching this goal more than do one-year trials. However, some pairs of years with similar climatic characteristics may not provide sufficiently representative conditions.

The deviations were low for most genotypes for most of the traits studied showing the good fit of the regression model. Genotypes CD94523, CDSS92B193, CD97383, CIGM91-349, DZ2234, DZ2293-2DZR, DUKEM/3/RUF and DZ3117 outperformed in grain yield and average stability as their regression values not different from unity. Where growing conditions are favorable or made so by the application of inputs, the responsive genotype CDSS92B1467, could be the better alternative. Those genotypes that showed average stability and good performance may not be as good as the responsive ones under favorable conditions. The genotypes used in this study can be described as having specific as well as wide adaptation for most of the traits in the conditions encountered

If we review the overall situation from Table 5.1 to 5.3, it becomes obvious that genotype DZ2293-2DZR appeared to have high mean and stable performance for eight traits including grain yield followed by genotype CD98206 and DZ2234, which were stable for seven traits. Genotypes CD94523, CDSS92B193, CIGM91-349, CD94545-A, DUKEM/3/RUF, Yerer and Ude (standard check) were stable for five parameters while genotypes CD91Y7, CD91989, CD97383 and CIGM91-347 for four

traits. Genotypes CD91989, DZ2212-1BS and DZ3117 became stable for three traits, Genotypes DZ1669-1AK, CDSS93Y545 and Gerardo stable and responsive for two traits, genotypes CDSS92B1467, CDSS93Y33 and CD9S294-1Y only for one trait and genotypes DZ1675-1AK, CD91313 and DZ-04-118 (local check) were not stable for any of the traits. Plant height and biological yield per plant appeared to be stable traits since half of the genotypes showed stable performance for these traits.

Yield is negatively correlated with protein content since Alem Tena is the lowest in grain yield but the highest for protein content. Wheat varieties differ slightly in their ability to convert soil N to grain protein. Some higher protein varieties tend to have lower yield potential. Care should be taken when selecting varieties to consider both yield and protein potential as well as overall agronomic characteristics

Areas with low amount of rainfall are good for good pasta quality durum wheat production. To improve the protein content in the highlands, time of N fertilization and the rates should also be modified. In general, the agronomic practices should have to be different across environments.

The introduction of durum wheat varieties is one of the most powerful tool and cost-efficient means of enhancing crop productivity and farmers' incomes. Efficiency in varietal itself and in the process of matching varieties to production areas implies an understanding of plant responses to diverse environments and cropping systems in a target production zone. Multi-location testing remains the main tool for understanding varietal responses to environments, but the process is both time-consuming and expensive.

The introduced durum wheat genotypes gave higher yield (show better performance for most of the traits), so, introduction and screening of germplasm is necessary where economic advantage due to their better yield and shortening the breeding procedure can out weigh those advantages obtainable from growing only landrace and local cross varieties. In almost all the cases introductions were stable and responsive for most of the traits. From the results it was possible to conclude that genotypes introduced from CIMMYT and screened by the National Durum Wheat Research Project had exhibited average response and were also stable. Most of the stable

materials for most of the traits studied were introductions. For instance, for grain yield per plant all the genotypes ranking from one to nine, except the fourth were CIMMYT introductions. However, since unequal numbers of genotypes from different sources were included in the study, and the experiment was conducted for one year this should not be considered as conclusive.

The results of heritability estimates indicated the prevalence of fairly high estimates of heritability for all traits except for grain yield 34% and biological yield 18%. Therefore, selection for these traits could be practiced more effectively at early stages of evaluation. However, selection for polygenic traits like grain yield must be practiced with due care.

For those traits that showed high CV_G estimates and small difference between CV_P and CV_G estimates, the breeding strategy should focus on selection for wide environment. But for those traits where high CV_P estimates were observed specific environment should be considered.

To conclude, since the investigation of phenotypic stability and adaptability of durum wheat genotypes in this study has clearly showed that the evaluated genotypes were sensitive to the diverse growing conditions of the Eastern Shoa region of Ethiopia, where the main variety testing sites for the program are situated, thus future recommendations for variety release should take into account these findings. The AMMI biplot classified Debre Zeit as a high yielding environment, Akaki and Chefe Donsa as medium and Alem Tena and Selale as low yielding environments for most of the traits except Alem Tena which was categorized as best location for evaluating genotypes for high protein content.

Stability analysis of yield, yield components, phenological and morphological traits and protein content across the test environments appears to be of value for recommending varieties for general or specific adaptation in environments.

According to linear regression and AMMI stability models, genotypes CD97383, CIGM91-349 and DZ3117 were classified as best genotypes. The better performance of genotype CD97383 may be due to its high yield with stable performance, higher

number of effective tillers per plant and thousand-kernel weight; that of genotype CIGM91-349 may be due to short plant height, higher biological yield and higher number of kernels per spike. The better performance of genotype DZ3117 may be related to the phenological traits since it exhibited earlier heading, medium maturity and longer grain filling period in addition, it was best genotypes in terms of grain protein content. Therefore, the future breeding strategies should consider not only yield but also yield components, morphological and phenological traits to release varieties with high yield and stable performance. Further studies on more locations and years for spatial and temporal stability analysis should be conducted for conclusive results.

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DECLARATION

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

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