RESULTS AND DISCUSSION

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I- Analysis of variance, mean and heterosis:

a: Protein and amino acids determined as mg/ g sample:

In this study, protein and seventeen amino acids namely, lysine, leucine, isoleucine, cysteine, methionine, phenylalanine, tyrosine, threonine, valine, histidine, arginine, aspartic, glutamic, serine, proline, glycine, alanine, total amino acids, essential and nonessential amino acids were determined. Also, the ratios between essential and nonessential amino acids as well as essential to total amino acids, were computed.

The analysis of variance for protein and amino acids content determined as mg/ g sample is presented in Table (4). Results indicated that genotypes mean squares were highly significant for the protein content and all the amino acids studied except cysteine. Results also showed that mean squares due to parents were significant for all traits studied except cysteine.

Mean performance of the five wheat parents is presented in Table (5). Results indicated that parental variety P2 had the highest protein content (14.01%) followed by the variety P3 (13.42%). Moreover, this particular variety (P2) gave the highest mean value for: lysine, leucine, isoleucine, methionine, phenylalanine, glutamic acid, serine, and essential and nonessential amino acids content. It is also clear that the parental variety P3 which ranked the second best for protein content had the highest mean values for tyrosine, threonine, valine, histidine, aspartic acid, proline, glycine, and alanine. The variety p_1 expressed the highest ratio

Table (4): Observed mean squares from ordinary analysis for protein and amino acids determined as mg/g sample.

Source of variation	d.f	Protein	lysine	Leucine	Isoleucine	Methionine	Phenyl alanine	Threonine	Valine	Histidine	Arginine	Tyrosine
Rep.	1	0.34	8.33	0.17	83.4	58.00	12.67	11.79	42.77	14.43	19.25	2.06
Genotypes	14	4.33**	32.18**	172.38**	111.13**	13.43**	152.26**	32.93**	150.82**	31.54**	276.14**	33.72**
Parents	4	7.33**	37.32**	182.41**	162.60**	11.316*	164.42**	26.39**	175.20**	51.69**	452.44**	46.98**
Crosses	9	3.41**	33.46**	169.97**	176.62**	15.23**	129.56**	17.52*	132.45**	18.01**	156.25**	4.56*
Parents vs crosses	1	0.62	0.12	153.89**	215.89**	5.64	307.93**	197.74**	218.60**	72.68**	650.03**	153.08**
Error	14	0.36	4.14	8.632	3.53	2.44	4.62	4.39	2.26	2.97	16.96	4.56

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table (4): Cont.

Source of variation	d.f	Aspartic acid	Glutamic acid	Serine	Proline	Glycine	Alanine	Cysteine	Essential amino acids	Non-essential amino acids	Total amino acids	Esesential/ non essential amio acids	Essential/ total amino acids
Rep.	1	142.50	17.40	o.46	30.90	0.32	12.92	0.02	416.00	317.00	1464.00	2.05	0.29
Genotypes	14	133.39**	488.96**	75.47**	1771.55**	32.23**	24.23**	0.66	5305.36**	6518.14**	21927.93**	34.51**	3.99**
Parents	4	174.74**	530.48**	101.23**	2294.74**	23.20*	15.43*	0.54	6081.94**	9518.38**	29933.25**	17.60**	1.89**
Crosses	9	109.16**	270.83**	71.98**	1708.66**	8.16	26.10**	0.77	4188.19**	5871.44**	18954.56**	20.11**	2.41**
Parents vs crosses	1	186.11**	2286.09**	3.77	244.91**	284.99**	42.68**	0.12	12253.50**	337.50	16667.00**	231.70**	26.64**
Error	14	11.69	23.97	6.99	11.88	5.33	3.40	0.92	167.82	165.50	594.44	1.53	0.18

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table (5): Genotypes mean performance for protein percentage and amino acids determined as mg/g sample.

Genotypes	Protein	Lysine	Leucine	Isoleucine	Methionine	Phenyelalanine	Threonine	Valine	Histidine	Arginine	Tyrosine
P1	13.01 a-e	42.87 b	80.25 f-h	45.12 e-f	11.80 d-f	54.24 g-h	40.88 b	69.70 d	41.11 b-c	80.57 a	35.37 b-f
P2	14.01 a-b	49.84 a	103.70 a	65.74 a	17.10 ab	78.87 a	41.81 b	80.28 b	40.32 b-c	81.52 a	44.43 a
P3	13.42 a-d	39.37 cd	91.29 b-d	63.04 ab	13.63 b-e	67.47 bc	47.03 a	83.58 a	46.25 a	76.14 ab	45.73 a
P4	9.32 h	39.53 cd	85.79 d-f	52.58 cd	10.93 d-f	62.47 ce	39.86 bc	63.36 f	33.57 d	51.64 f-h	36.92 b-e
P5	11.24 f-g	41.07 cd	81.40 e-h	48.54 d-f	13.87 a-e	62.14 d-f	37.12 b-e	63.76 f	35.07 d	52.77 f-h	36.72 b-f
P1 x P2	12.55 c-f	39.56 cd	75.38 g-h	51.66 cd	8.54 f	49.28 i	39.72 bc	62.98 f	36.90 cd	48.25 g-h	33.88 d-f
x P3	11.72 e-f	40.27 cd	75.02 h	53.61 c	10.93 d-f	52.36 hi	35.26 c-e	61.77 f	36.83 cd	59.25 d-f	32.06 e-f
x P4	10.06 g-h	37.69 d	74.82 h	39.16 h	11.59 d-f	49.13 i	33.16 e	53.99 h	32.92 d	47.45 e-g	31.60 f
x P5	11.22 f-g	38.07 cd	77.82 g-h	40.72 gh	10.39 c-e	48.62 i	32.17 e	58.29 g	33.91 d	45.76 h	33.89 c-f
P2 x P3	12.66 b-e	48.72 a	92.92 bc	48.93 de	12.87 c-e	64.64 b-d	38.36 b-d	73.78 c	36.19 c-d	68.77 b-d	38.16 b-c
x P4	12.65 b-e	41.94 b-d	98.50 a	52.03 cd	12.83 a-d	68.63 b	32.83 e	67.36 de	35.99 cd	69.47 bc	36.37 b-f
x P5	13.97 a-c	40.69 cd	77.07 g-h	51.66 cd	14.54 a-d	59.01 e-g	34.67 de	64.84 e-f	33.52 d	60.50 b	34.86 b-f
P3 x P4	13.66 a-c	45.90 ab	87.54 c-e	51.14 cd	17.15 a	66.19 b-d	39.51 bc	77.64 b	36.23 cd	63.11 c-e	37.69 b-d
x P5	14.37 a	48.86 a	95.62 b	59.59 b	16.30 a-c	67.14 b-d	39.01 bd	78.88 b	43.38 ab	66.34 c-e	39.27 b
P4 x P5	12.19 d-f	42.31 b-d	82.13 e-g	44.64 c-g	10.32 e-f	57.38 f-h	34.26 de	64.57 e-f	33.14 d	57.63 c-e	32.66 d-f
r	0.197	-0.190	0.448	0.609 *	0.099	0.665 *	0.640*	0.517	0.500	-0.040	0.724 *

r: Correlation coefficient between mid parent and F1 mean performance.

Values followed by the same letters are not different at probability 0.05 by Duncan's L.S.R test

* Significant at 0.05 level of probability.

Table (5): Cont.

Genotypes	Aspartic acid	Glutamic acid	Serine	Proline	Glycine	Alanine	Cysteine	Essential amino acids	Non essential amino acids	Total amino acids	Essential/ non essential amino acids	Essential / total amino acids
P1	68.16 cd	207.73 f	51.06 e-h	140.52 e	44.34 ab	43.82 b-d	1.01	466.22 cd	592.29 ef	1058.52 de	78.71 a	44.04 a
P2	81.87 a	237.22 c	65.04 a	203.64 ab	48.31 a	47.40 ab	0.89	559.18 a	728.80 a	1287.98 a	76.72 ab	43.42 ab
P3	83.13 a	223.90 de	57.32 b-e	208.93 a	49.15 a	48.98 a	0.94	527.83 b	718.03 a	1245.86 ab	73.52 cd	42.36 cd
P4	65.23 c-e	201.69 f	47.30 g-i	154.59 d	41.19 b-e	43.31 b-d	0.00	439.74 de	590.23 ef	1029.96 e	74.50 bc	42.69 bc
P5	63.72 de	236.54 c	49.98 f-i	141.08 e	43.13 bc	42.70 cd	0.00	534.72 e	613.87 de	1049.60 de	70.98 e	41.51 de
P1 x P2	63.15 de	232.49.cd	44.09 i	170.20 c	37.54 d-f	41.21 c-e	0.44	411.81 ef	623.46 cd	1035.27 de	66.05 g	39.78 f
x P3	65.96 c-e	248.59 ab	52.14 e-h	171.16 c	39.84 b-f	39.70 de	0.00	425.31 e	649.44 bc	1074.74 de	65.49 g	39.57 f
x P4	58.43 e-f	218.74 e	46.87 h-i	116.47 f	36.70 e-f	38.28 e	0.93	379.54 g	548.38 g	927.91 f	69.21 ef	40.90 e
x P5	53.91 f	240.11 bc	50.52 f-h	118.83 f	35.74 f	38.71 e	0.00	385.76 fg	571.70 fg	957.46 f	67.46 fg	40.28 f
P2 x P3	72.68 bc	232.29 cd	62.48 ab	154.24 d	37.49 d-f	47.20 ab	0.33	484.60 c	645.48 bc	1130.08 c	75.07 bc	42.88 bc
x P4	69.45 cd	249.60 ab	58.76 b-d	155.98 d	38.99 b-f	43.54 b-d	0.96	478.74 c	654.50 b	1133.24 c	73.15 cd	42.25 cd
x P5	72.03 bc	240.59 bc	53.26 d-g	172.97 c	38.32 c-f	43.10 b-d	1.42	435.73 e	657.32 b	1093.05 d	66.29 g	39.87 f
P3 x P4	71.72 b-d	252.72 a	55.00 c-f	204.72 ab	42.34 b-d	45.50 a-c	1.88	484.99 c	710.99 a	1195.98 b	68.22 e-g	40.55 ef
x P5	78.90 ab	254.64 a	60.99 a-c	200.65 b	41.22 b-e	48.92 a	0.80	514.99 b	725.49 a	1240.48 ab	70.99 de	41.52 de
P4 x P5	65.15 c-e	229.57 c-e	49.76 f-i	171.69 c	38.69 c-f	40.94 de	0.22	427.19 b	628.45bd	1055.64 de	67.97 fg	40.46 f
r	0.606	0.266	0.420	0.489	0.205	0.667 *	—	0.475	0.600	0.565	-0.150	-0.148

r: Correlation coefficient between mid parent and F1 mean performance.

Values followed by the same letters are not different at probability 0.05 by Duncan's L.S.R test

*** Significant at 0.05 level of probability.**

between essential and nonessential amino acids as well as the ratio between essential and total amino acids.

It could be concluded that the parental varieties P2 and P3 were the best among the five varieties studied in relation to protein and amino acid content.

Results in Table (4) also showed that crosses mean squares were significant for protein content and all amino acids studied except for cysteine and glycine. Such result reflects the genetic variability among the crosses studied for the protein and amino acid content.

It is clear that the F1 hybrid P3 x P5 produced the highest protein content (14.37%) without significant difference from the highest parent (P2). None of the hybrids surpassed the highest parent for the amino acids except for glutamic scid where four hybrids rxceeded the highest parent P2. However, the previous cross (P3 x P5) gave the highest mean values for; lysine, isoleucine, valine, histidine, tyrosine, aspartic acid, glutamic acid, proline, and alanine, as well as essential, nonessential and total amino acids. The hybrid P2 x P4 expressed the best values for leucine, and phenylalanine. Whereas, the cross P3 x P4 had the highest mean value for methionine, glutamic acid, glycine and nonessential amino acids. The single cross P2 x P3 appeared to be the best combination for the ratio of essential/ nonessential amino acids beside the ratio of essential/ total amino acids. On the other hand, the hybrid P1 x P4 seemed to be the worst since it exhibited the lowest values for twelve out of the twenty two traits studied.

In this concern, **Aykroyd and Doughty (1970) and Johnson *et al* (1985)** reported that the most limited amino acid in wheat proteins was lysine. Accordingly, The F_1 cross P3 x P5 was the best combination among the ten tested crosses since it had the highest values for protein and lysine in addition to other seven amino acids.

Such variability among wheat hybrids for protein and amino acid content was previously reported by **Ewart (1973), Laflandra** ***et al*** **(197** and **Luce** ***et al*** **(1989).**

Significant mean squares due to parents vs. crosses as an indic of average heterosis overall crosses were detected for protein conter all amino acids except lysine, cysteine, methionine, serir nonessential amino acids (Table, 4).

Heterosis expressed as the percentage deviation of F_1 mean from the mid and better parent for protein and amino acids determined as mg/ g N is presented in Table (6). For protein content, two crosses namely, (P3 x P4) and (P3 x P5) produced the most desirable mid- parent heterosis since they expressed positive and highly significant heterotic effect. The respective heterosis percentages were 20.19 and 16.55%. Similar results were reported by **Mohd et al (1981), Bhowmik et al (1982), and Hraska and Brindza (1987).**

Regarding better- parent heterosis, none of the crosses showed significant effect for protein content. Such results are in good agreement with those reported by **Hraska** ***et al*** **(1981) a** and **Sampson** ***et al*** **(1983).**

For lysine content, the two crosses (P3 x P4) and (P3 x P5) exhibited significant positive heterosis over both mid and better parent. Such result means that these crosses had the most desirable heterotic effects for lysine amino acid.

Concerning leucine content, one cross only (P3 x P5) expressed significant and positive heterotic effect relative to mid parent. None of the

Table (6): Percentage of heterosis over both mid parent (MP) and better parent (BP) for protein and amino acids determined as mg/g sample.

Crosses	Protein		Lysine		Leucine		Isoleucine		Methionine		Phenylalanine		Threonine	
	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
P1 x P2	-7.13	-10.46*	-14.66**	-20.63**	-18.05**	-27.31**	-6.80	-21.42**	-40.89**	-50.05**	-25.95**	-37.52**	-3.92	-4.99
x P3	-11.32	-12.67*	-2.05	-6.04	-12.53**	-17.82**	-0.86	-14.96**	-14.03	-19.78	-13.95**	-22.39**	-19.78**	-25.03**
x P4	-9.90	-22.68**	-8.53	-12.08*	-9.88	-12.78**	-19.84**	-25.53**	1.95	-1.85	-15.79**	-21.34**	-17.86*	-18.88**
x P5	-7.47	-13.76**	-9.28	-11.18	-3.71	-4.38	-13.04*	-16.11**	-19.05	-25.08*	-16.45**	-21.76**	-17.51*	-21.30**
P2 x P3	-7.68	-9.64*	9.23	-2.24**	-4.70	-10.40**	-24.01**	-25.57**	-16.26	-24.77*	-11.66**	-18.04**	-13.63*	-18.42**
x P4	8.47	-9.71*	-6.16	-15.86**	3.96	-5.02	-12.05**	-20.85**	-8.43	-24.97*	-2.88	-12.98**	-19.62**	-21.49**
x P5	10.64	-0.32	-10.48	-18.36**	-16.72**	-25.68**	-9.59*	-21.42**	-6.13	-14.99	-16.30**	-25.18**	-12.16	-17.09**
P3 x P4	20.19**	1.83	16.34*	16.10**	-1.13	-4.11	-11.54*	-18.88**	39.69*	25.84*	1.89	-1.89	-9.07	-15.99**
x P5	16.55**	7.08	21.47**	18.96**	10.74*	4.74	6.80	-5.48	18.53	17.49	3.60	-0.49	-7.29	-17.06**
P4 x P5	-18.59*	8.46	4.97	3.01	-1.76	-4.27	-11.72*	-15.12**	-16.74	-25.58*	-7.90	-8.14*	-10.99	-14.05*

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table (6): Cont. 1

Crosses	Valine		Histidine		Arginine		Tyrosine		Aspartic acid		Glutamic acid		Serine		Proline	
	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
P1 x P2	-16.02**	-21.55**	-9.37	-10.34*	-40.47**	-40.82**	-15.09*	-23.75**	-15.82**	-22.87**	4.51	-1.99	-24.04**	-32.20**	-1.10	-16.42**
x P3	-19.40**	-26.09**	-15.69**	-20.38**	-24.38**	-26.45**	-20.94**	-29.90**	-12.80*	-20.66**	15.19**	11.03**	-3.79	-9.05	-2.04	-18.08**
x P4	-18.85**	-22.54**	-11.83	-19.91**	-28.22**	-41.10**	-12.59	-14.43*	-12.39	-14.27*	6.86*	5.30*	-4.70	-8.21	-21.07**	-24.66**
x P5	-12.64**	-16.37**	-10.98*	-17.52**	-31.38**	-43.19**	-5.99	-7.74	-18.24*	-20.90**	8.09**	1.51	-0.01	-1.06	-15.61**	-15.77**
P2 x P3	-9.95**	-11.72**	-16.40**	-21.76**	-12.77	-15.65**	-15.34*	-16.54**	-11.91	-12.58**	0.75	-2.08	2.13	-3.93	-25.23**	-26.17**
x P4	-6.22*	-16.10**	-2.58	-10.74*	4.34	-14.78**	-10.59	-18.15**	-5.57	-15.16**	13.74**	5.22*	4.62	-9.65	-12.92**	-23.40**
x P5	-9.97**	-19.23**	11.07	-16.87**	-9.89	-25.78**	-14.08*	-21.53**	-1.05	-12.02*	1.57	1.42	-7.40	-18.12**	-0.36	-15.06**
P3 x P4	5.68*	-7.10**	-9.20	-21.65**	-1.23	-17.12**	-8.80	-17.59**	-3.32	-13.72**	18.76**	12.87**	5.15	-4.04	12.64**	-2.01
x P5	7.07*	-5.63**	6.68	-6.22	2.92	-12.87*	-4.75	-14.12**	7.45	-5.09	10.61**	7.65**	13.69*	6.41	14.65**	-3.96*
P4 x P5	1.59	1.28	-1.67	-3.76	10.38	9.20	-11.30	-11.53	1.04	-0.13	4.77	- 2.95	2.30	-0.44	16.13**	11.06**

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table (6): Cont. 2

Crosses	Glycine		Alanine		Essential amino acids		Non essential amino acids		Total amino acids		Essential/ non essential amino acids		Essential / total amino acids	
	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
P1 x P2	-18.97**	-22.30**	-9.64	-13.05**	-19.68**	-26.36**	-5.62*	-14.45**	-11.76**	-19.62**	-15.02**	-16.08**	-9.03**	-9.68**
x P3	-14.78*	-18.95**	-14.44**	-18.94**	-14.43**	-19.42**	-0.87	-9.55**	-6.72**	-13.74**	-13.96**	-16.79**	-8.40**	-10.15**
x P4	-14.19*	-17.25**	-12.13*	-12.64**	-16.21**	-18.59**	-7.25*	-7.41**	-11.14**	-12.34**	-9.66**	-12.06**	-5.70**	-7.13**
x P5	-18.29*	-19.40**	-10.52	-11.67*	-14.46**	-17.26**	-5.20	-6.87**	-9.17**	-9.55**	-9.87**	-14.29**	-5.84**	-8.55**
P2 x P3	-23.08**	-23.73**	-2.05	-3.63	-10.84**	-13.34**	-10.77*	-11.43**	-10.80**	-12.26**	-0.07	-2.14	-0.02	-1.23
x P4	-12.86	-19.29**	-3.99	-8.14	-4.15	-14.39**	-0.76	-10.20**	-2.22	-12.01**	-3.25	-4.65*	-1.88	-2.68*
x P5	-16.19*	-20.68**	-4.33	-9.07*	-12.41**	-22.08**	-2.09	-9.81**	-6.48*	-15.13**	-10.24**	-13.59**	-6.12**	-8.18**
P3 x P4	-6.26	-13.85*	-1.39	-7.10	0.25	-8.12*	8.69**	-0.98	5.10	-4.00	-7.82**	-8.43**	-4.66**	-5.01**
x P5	-10.65	-16.12**	6.73	-0.12	6.89*	-2.43	8.94**	1.04	8.08**	-0.43	-1.74	-3.45	-1.00	-1.99
P4 x P5	-8.24	-10.31	-4.80	-5.48	-2.41	-2.85	4.55	2.37	1.53	0.58	-6.55**	-8.77**	-3.90**	-5.22**

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

crosses showed significant positive heterosis relative to better parent for leucine content.

Significant and positive heterosis over both mid- and better parent for methionine was obtained by the cross (P3 x P4) being 39.69 and 25.84% for the respective cases. For valine amino acid, the most desirable heterotic effect relative to mid parent was obtained for the crosses (P3 x P4) and (P3 x P5).

Regarding glutamic acid, six and five crosses expressed significant and positive heterotic effect relative to both mid and better parent, respectively. However, the most desirable heterosis was obtained for the cross (P3 x P4) followed by (P1 x P3).

The single cross (P3 x P5) had the best mid parent heterosis for serine amino acid since it exhibited significant and positive heterotic effect for this trait. Concerning proline amino acid, three and one cross showed significant positive heterotic effect relative to mid-and better parent, respectively. The highest values of heterotic effects were obtained for the cross (P4 x P5).

Results also indicated that the cross (P3 x P5) expressed significant and positive mid parent heterosis for essential and nonessential as well as total amino acids. For the rest of the amino acids studied, the F_1 crosses showed either no heterosis or significant negative heterotic effects.

It is worth mentioning here that the two crosses (P3 x P4) and (P3 x P5) which expressed desirable mid parent heterosis for protein content showed also desirable heterosis for most of the studied amino acids. Moreover, the cross (P3 x P5), in particular, produced the highest mean value for protein and most amino acids as previously mentioned. Such results indicated that the cross (P3 x P5) might be useful in future wheat breeding programs.

Heterosis for amino acid content was previously reported by several researchers (**Hraska** ***et al*****, 1981- a ; and Hraska and Brindza, 1987)**. On the other hand, **Petrosyan and Oganesyan (1982) and Liu** ***et al*** **(1986)** found no differences in amino acid composition between the parents and their hybrids.

Significant positive correlation coefficients between mid parent and F1 crosses mean values were detected for the amino acids isoleucine, phenylalanine, tyrosine, threonine and alanine (Table 5). Therefore, a high mean performance of F1 crosses could be expected only from crosses involving parental varieties of high mean values. For the other amino acids insignificant correlation values were detected indicating that certain high and low parental varieties may produce superior single crosses.

b: Other quality traits:

The other quality traits included gluten, hydration coefficient, moisture, ash, fiber and extractions (flour, shorts, fine bran and bran). Analysis of variance for all these traits is presented in Table (7). Significant mean squares due to genotypes along with parents and crosses were detected for gluten, ash, fiber and extracted flour and fine bran. These results indicated clearly that the parental wheat varieties and their crosses differed considerably for these quality traits.

Results in Table (8) showed that variety P2 expressed the best mean performance for gluten and extracted flour being 12.26 and 69.85%, respectively. The parental variety P1 had the highest value for ash

Table (7): Observed mean squares from ordinary analysis for other quality characteristics.

Source of variation	d.f	Glutein	Hydration coefficient	Moisture	Ash	Fiber	Extraction			
							Flour	Shorts	Fine bran	Bran
Rep.	1	0.53	1402.30	0.31	0.23	0.03	0.16	1.54	0.51	0.01
Genotypes	14	4.09**	561.64	0.03	0.10**	0.15**	1.73**	0.56	1.64**	1.30
parents	4	5.96**	596.58	0.02	0.17**	0.15**	1.13*	0.78	2.67**	1.43
Crosses	9	3.63**	578.66	0.04	0.07*	0.11**	2.03**	0.49	1.05*	1.38
Parents vs crosses	1	0.70	268.72	0.01	0.09	0.48**	1.38	0.03	2.73*	0.11
Error	14	0.37	268.34	0.09	0.02	0.03	0.34	0.35	0.34	0.63

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table (8): Genotypes mean performance (in percentages) for other quality characteristics.

Genotypes	Glutein	Ash	Fiber	Extraction	
				Flour	Fine bran
P1	9.98 cd	1.93 a	2.70 a	68.85 bc	8.80 a
P2	12.26 a	1.89 ab	2.03 b-d	69.85 ab	8.35 ab
P3	11 36 a-c	1.72 a-d	2.20 bc	68.60 bc	9.00 a
P4	7.82 e	1.30 g-h	2.42 ab	67.85 cd	8.55 a
P5	9.43 d	1.38 d-h	2.11 bc	69.30 ab	6.15 d
P1 x P2	11.01 a-c	1.19 h	1.85 c-e	69.20 ac	6.95 cd
x P3	10.19 cd	1.63 a-g	2.22 bc	70.35 a	6.95 cd
x P4	7.55 e	1.65 a-f	2.37 ab	68.45 b-d	7.80 a-c
x P5	9.33 d	1.59 b-g	2.26 b	69.55 ab	7.00 b-d
P2 x P3	10.53 cd	1.72 a-c	2.05 bc	68.80 bc	6.75 cd
x P4	10.77 b-d	1.35 e-h	2.07 bc	69.80 ab	6.90 cd
x P5	12.25 a	1.49 c-h	1.68 de	69.85 ab	8.00 a-c
P3 x P4	11.15 a-c	1.68 a-e	1.65 e	69.70 ab	7.70 a-c
x P5	12.00 ab	1.68 a-e	2.05 bc	70.60 a	8.45 a
P4 x P5	10.17 cd	1.33 f-h	2.03 b-d	67.15 d	8.80 a
r	0.520	-0.031	0.589	0.245	-0.606

r: Correlation coefficient between mid parent and F1 mean performance.

Values followed by the same letters are not different at probability 0.05 by Duncan's L.S.R test

(1.93%) and fiber (2.70%). Also, the highest value for extracted fine bran was recorded for the variety P3.

It is also clear that the F_1 cross (P2 x P5) produced the highest gluten content followed by the cross (P3 x P5). For ash content, the hybrid (P2 x P3) expressed the best mean value (1.72%). Also, the F_1 combination (P1 x P4) had the highest fiber content followed by the cross (P1 x P5). For extracted flour and fine bran, the best mean values were recorded for the crosses (P3 x P5) and (P 2 x P5), respectively.

The variability among wheat varieties and crosses for such traits were previously recorded by **Haridas *et al* (1967), Rasmusson *et al* (1971), Shellenberger (1971).**

Significant mean squares due to parents vs, crosses as indication of average heterosis overall crosses were obtained only for fiber content and extracted fine bran (Table 7).

Heterosis percentage relative to mid parent and better parent for the quality traits studied is presented in Table (9). Results indicated that the most desirable mid parent heterosis for gluten was obtained from the crosses: (P3 x P4), ((P3 x P5) and (P4 x P5). The respective heterotic values were 16.28, 15.42 and 17.94%. None of the crosses showed significant and positive better parent heterosis for gluten fraction. Similar results were obtained by **Hraska *et al* (1986).**

For extracted flour, the best mid parent and better parent heterosis was detected for the crosses (P1 x P3) and (P3 x P5) since they expressed significant and positive heterotic effects for this trait. For ash trait none of the crosses showed significant and positive mid parent and better parent heterosis. Regarding fiber content, two and two crosses expressed

Table (9): Percentage of heterosis over both mid parent (MP) and better parent (BP) for other quality characteristics.

Crosses	Glutein		Ash		Fiber		Extraction			
							Flour		Fine bran	
	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
P1 x P2	-1.03	-10.24	-37.61**	-38.18**	-21.90*	-9.11	-0.22	-0.93	-18.95*	-16.77*
x P3	-4.44	-10.25	-10.44	-15.33	-9.20	1.14	2.36*	2.18*	-21.91*	-21.02**
x P4	-15.15	-24.35**	2.02	-14.55	-7.35	-2.07	0.15	-0.58	-10.09	-8.77
x P5	-3.92	-6.56	-4.08	-17.66*	-5.93	7.11	0.69	0.36	-6.36	13.82
P2 x P3	-10.90	-14.15*	-4.58	-8.99	-3.20	0.74	-0.61	-1.50	-22.19*	-19.16*
x P4	7.29	-12.15*	-15.67	-28.84**	-7.19	1.72*	1.38	-0.07	-18.34*	-17.36*
x P5	12.96	-0.08	-9.17	-21.43*	-18.84	-17.24*	0.40	0.00	10.36	30.08**
P3 x P4	16.28*	-1.88	11.11	-2.33	-28.49**	-24.83**	2.16	1.60	-12.25	-9.94
x P5	15.42*	5.61	8.24	-2.33	-4.78	-2.84	2.39*	1.88*	11.55	37.40**
P4 x P5	17.94*	7.85	-0.75	-3.62	-10.38	-3.79	-2.08	-3.10**	19.73	43.09**

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

desirable heterotic effects (significantly negative values) relative to mid parent and better parent, respectively. For fine bran, four crosses exhibited significant and negative heterotic effects relative to both mid- and better parent.

Insignificant correlation values between mid parent and F_1 mean values were detected for gluten, ash, fiber, and extracted flour and fine bran (Table, 8). Such results indicated clearly that the best F1 hybrids may be produced from crossing between certain high- and low- quality parents.

II- Combining ability analysis:

General and specific combining abilities(GCA and SCA) were estimated for all traits studied according to **Griffing (1956)** method 2 model 1 as follows:

a: Protein and amino acids determined as mg/ g sample:

The variance associated with general and specific combining ability for protein and amino acids determined as mg/ g sample is presented in Table (13). Significant mean squares due to both general and specific combining ability were detected for all traits studied. Such results showed that both additive and non additive gene actions were important in the inheritance of protein and amino acid contents. On comparing the magnitude of GCA/SCA, it is clear that the high ratios which largely exceeded the unity were detected for the protein content and all amino acids except for glycine and the ratios between essential and nonessential amino acids as well as essential to total amino acids. This means that the additive and additive x additive gene action appeared to be the most important components of variance for these traits. In the exceptional