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GENETIC AND CYTOLOGICAL EVALUATION OF DIALLEL CROSSES AMONG EIGHT BREAD WHEAT GENOTYPES

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ABSTRACT

The present investigation was carried out to throw some light on the cytological disturbances e. g. frequency of micronuclei and chromosomal aberrations as an indication of the cytological instability and to study the genetic system controlling the inheritance of some agronomic characters using half diallel analysis of eight genetically diverse wheat genotypes. The studied parents exhibited variation frequencies of mitotic activity the highest score was in P_3, P_6 and P_8 and the lowest in P_4, P_5 and P_7. The parental genotypes showed also differences in micronuclei and chromosomal aberration, the highest score was in P_2 and P_7 and the zero score in P_3 and P_8. Most of F_1 hybrids showed less micronuclei and chromosomal aberrations in mitotic division than their parents. However some hybrids had higher percentage of cells containing either micronuclei or chromosomal aberrations than their parents. The additive genetic variance (D) was significant for all studied traits, indicating that additive gene effects played a major role in the inheritance of these traits. Dominance component of variation (H1) was highly significant and greater than (D), for all traits. The component of variation due to the dominance effects associated with gene distribution (H2) was highly significant and greater than D for all traits. Average degree of dominance $(H1/D)^{1/2}$, showed the presence of over dominance for all studied traits, except number of spikes/plant and 1000 kernel weight which exhibited complete dominance. Low heritability estimate in narrow sense was detected for all traits except heading date, number of spikes/plant and 1000 kernel weight which showed high estimate.

Key words: *Wheat, Mitotic activity, Chromosomal aberrations, Micronuclei, Cytology, Dominance, Additive, Heritability, Diallel.*

INTRODUCTION

Wheat is a major crop in the world. It is, therefore, not surprising that since the domestication of wheat, man has been greatly concerned with its improvement through development of varieties which combine high grain yield and desired quality characters. Continuous effects to improve yield and its components have led to extensive use of genetic variations within this species. The breeder needs detailed knowledge about the gene action and genetic system controlling the inheritance of characters. Progress in wheat improvement depends on the amount of genetic variation present in the base population and the type of gene action which controls the

inheritance. Yield of wheat, as in other field crops is a complex character. The most efficient way for improving such character is through studying the behavior of its components (Hassan *et al* 1996).

Chromosomal stability represents one of the major factors maintaining important genes in bread wheat. Therefore, well adapted new varieties with a high rate of cytological stability must be considered in a crossing programmed. Spontaneous abnormalities, either in the form of chromosomal aberrations or micronuclei, represent the major factor responsible for cytological instability. The variable occurrences of these abnormalities have been reported in different bread wheat cultivars (Ducal *et al* 1980, Pukhal *et al* 1980 and Zandorazhanaya *et al* 1997). Such abnormal is also thought to be responsible for wrinkled grains (Suarez and Arteaga 1990). Spontaneous abnormalities are also used as an effective indication for the delirious effect of seed aging in germplasm banks.

The objectives of the present work were to assess the cytological disturbances and genetic system controlling inheritance of different characteristics.

MATERIALS AND METHODS

The fieldwork of this study was carried out at Gemmeiza Agricultural Research Station. Eight wheat genotypes were used to represent a wide range of diversity for several agronomic characters; they were obtained from National Gene Bank, Agricultural Research Center, Egypt. The name and pedigree of these genotypes are presented in Table (1). In 2004/2005 season the eight parents were crossed in all possible combinations excluding reciprocals, to obtain a total of 28 F_1 hybrids. The parental cultivars or lines and their possible twenty eight crosses were sown in 2005/2006 an a field experiment. A randomized complete blocks design (RCBD) with three replicates was used. Each plot comprised two rows, 3 meters long with 30 cm between rows. Plants within rows were 10 cm apart allowing a total number of 60 plants per plot. At maturity, ten plants were randomly selected from each plot for measuring heading date, maturity date, grain filling period, plant height, spike length, number of spikes/plant, number of grains/spike, 1000-grain weight and grain yield/plant.

Cytological studies

Seeds of the parents and their hybrids were germinated on moistened filter paper in Petrie -dishes at room temperature (20-25°C). Root-tips were collected and pretreated with 0.02% colchicine for 2 hours and then fixed in ethanol-glacial acetic acid (3.1). After 24 hours root-tips were transferred to 70% ethyl alcohol and stored. The acteo-carmine staining method was used

Table 1. The names and pedigree of the eight bread wheat cultivars and lines.

No.	Genotypes	Pedigree	Origin
P_1	Sakha 61	Inia /RL4220//7c/Yr's'	Egypt
P_2	Giza 164	KVZ/Buho's'//Kal/Bb=Veery#5CM33027-F-15M-500YOM.	Egypt
P_3	Gemmeiza 7	CMH74A.630/Sx//Seri 82 /Agent CGM4611-2GM-3GM -1GM-OGM.	Egypt
P_4	Sids-7	Maya's'/Mon's'//CMH74A.592/ 3/ Sakha 8^{*2} SD10002 -8SD1SD-1SD -OSD.	Egypt
P_5	line	Gomam/3/Cmt/CDC//PLO ICW 90-0323-5AP-OTS-1AP-OTS-4AP-OL-OAP	ICARDA
P_6	line	LUANCM00587-E-ON-OY-030M-2Y-2Y-OM-24B-O1OU- OB	CIMMYT
P_7	Line	Collection from Qena	Egypt
P_8	Line	Collection from South Sinai	Egypt

to stain the root-tip cells as described by Fayed *et al* (1985) and Sayed-Ahmmed (1985). The fixed root-tips were washed thoroughly with distilled water, macerated by 1N HCl at 60°C for 3 minutes and then washed with distilled water. Subsequently, individual root-tips were warmed gently in a drop of aceto carmine for a short time. The apexes of roots were squashed on a dry clean slide and stained which a small drop of fresh stain. The covers lips were removed by the dry-ice method; the slides were immersed in 96% ethyl alcohol for minutes, then mounted in Canada balsam and dried for each parent and hybrid. Scoring of the cytological criteria was carried out from at least thirteen prepared slides. The prepared slides were used to determine the following cytological phenomena:

A- Mitotic index (MI) and frequencies of the mitotic phases

The mitotic index represented the percentage of divided cells to the total cells examined. The percentage of each mitotic phase was calculated by dividing the number of cells in this phase on the total number of dividing cells per each parent or hybrid.

B- Micronuclei

The number of micronuclei was determined in interphase cells as well as in dividing cells. The estimation included the two different distinguishable types of micronuclei, i.e. compact and non-compact as reported by Hesemann and Fayed (1982) and Fayed (1990).

C- Chromosomal aberrations

The total number of chromosomal aberrations was estimated in dividing cells. The abnormalities included cells with fragments, laggards, stickiness and bi-nucleate cells.

Statistical and genetic analysis

The statistical analysis of data collected from RCBD was done according to Jinks 1954, singh and chanudhary 1985. Analysis of Hayman (1954 a and b) was carried out to estimated genetic components. The differences in mitotic activity as well as mitotic abnormalities between the two parents involved in each hybrid and between the parents and the F_1's were statistically tested using chi^2-test by means of a 2 x 2 contingency table.

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance for heading and maturity dates, grain filling period, plant height, number of spikes/plant, spike length, number of kernels/spike, 1000-kernels weight, mitotic index and grain yield/plant is presented in Table (2). Test of significance indicated that the mean squares due to genotypes were highly significant for all studied traits. The significance of mean squares indicated the presence of true differences among these genotypes. Mean squares due to parents and crosses were highly significant for all traits. These findings indicate that parental varieties and/or lines and their F_1 differed in their mean performance in all traits. Similar results were previously reported by Afiah *et al* (2000).

Parents vs crosses mean squares (Table 2) as an indication to average heterosis overall crosses were found to be highly significant for all studied traits.

Table 2. Analysis of variance for morphological and yield component characters.

Source of variation	d. f	Mean squares				
		Heading date	Maturity date	Grain filling period	Plant height	Spike length
Replications	2	1.042	0.632	1.347	5.495	0.514
Genotypes	35	236.821**	214.211**	142.016**	174.972**	3.411**
Parents (P)	7	208.453**	205.644**	116.675**	183.588**	3.27.**
Crosses	27	196.866**	155.788**	153.218**	27.368**	3.561**
P vs crosses	1	1514.201**	1851.586**	16.952**	2776.99**	0.346**
Error	70	0.684	0.729	1.275	1.462	0.371

Table 2. Continued

Source of variation	d. f	Mean squares			
		Spikes/ plant	Kernels/ spike	1000. kernel weight	Grain yield /plant
Replications	2	0.840	8.333	4.666	0.724
Genotypes	35	27.090 **	124.570 **	103.860 **	201.314 **
Parents (P)	7	47.16**	258.151*	146.250**	152.221**
Crosses	27	22.796**	65.801**	96.179**	207.736**
P vs crosses	1	2.509**	776.293**	14.523**	371.557**
Error	70	0.660	8.502	3.016	1.901

* and ** significant at 5% and 1% level of probability.

Mean performance

The mean performance of the eight parental genotypes of wheat is presented in Table (3).The parental cultivar (P_1) ranked the third for spike length and the second for number of kernels /spike. Also, it showed a moderate value for mitotic index. The parental cultivar (P_2) ranked the first for grain filling period and the third for number of kernels /spikes while it had a moderate value for mitotic index. The parental cultivar (P_3) ranked the first for spike length and number of spikes/plant and the second for maturity date and the third for heading date; grain filling period, plant height and mitotic index .The parental cultivar (P_4) ranked the first for plant height and the third for number of spikes/plant and had moderate value for most of studied traits while it was the last for mitotic index. The parental line (P_5) ranked the first for heading date and number of kernels /spike and the second for 1000 kernel weight and the third for maturity date. Also, it was the least in grain yield. The parental line (P_6) ranked the first for maturity date, 1000 kernel weight and mitotic index and the second for heading date and grain yield/plant. The parental line (P_7) ranked the second for number of spikes/plant. Also, it was moderate for mitotic index. The parental line (P_8) ranked the first for grain yield /plant and the second for spike length and mitotic index.

The mean performances of the tested twenty eight crosses are presented in Table (3). Early heading was found in the cross P_4xP_6 followed by P_5xP_6 and then by P_3xP_5, while the cross P_1xP_7 and P_7xP_8 had the latest heading date. For maturity date, the crosses P_4xP_5, P_5xP_6, P_3xP_7 and P_3xP_5 were the earliest. However, the two crosses P_1 xP_8 and P_2xP_8 were latest in maturity date. Earliness in wheat is favorable for escaping from yellow rust and other diseases as well as from high temperature at maturity and other stress conditions. For grain filling period, it was found that cross P_1xP_3

Table 3. Mean performance for studied traits of eight wheat genotypes and their F_1 crosses.

Genotypes	Plant Height (Cm)	Spike Length (Cm)	Heading date (days)	Maturity date (days)	Grain filling period (days)	Spikes / plant	Kernels / spike	1000-kernel weight (g)	Grain yield/ plant (g)
P_1	100.66	15.40	95.56	141.96	46.40	19.60	86.33	45.63	45.54
P_2	104.13	14.40	99.36	137.13	37.76	17.40	86.30	36.66	36.33
P_3	112.33	16.36	88.06	129.56	41.50	20.36	67.96	41.90	36.23
P_4	115.63	14.80	91.13	140.46	49.33	19.73	68.56	46.73	42.80
P_5	101.43	13.16	76.56	133.86	57.30	9.46	93.00	55.43	26.30
P_6	100.50	15.43	81.86	128.46	4.64	13.53	74.43	57.97	46.66
P_7	114.40	15.13	99.23	152.20	52.96	19.93	86.20	43.46	43.78
P_8	120.06	16.33	96.23	147.06	50.83	14.30	77.06	48.60	46.70
P_1x P_2	91.40	14.80	86.80	134.30	47.50	18.20	72.00	35.86	36.40
P_1x P_3	94.80	15.23	92.43	122.96	30.53	21.00	70.03	49.36	46.73
P_1x P_4	97.66	13.63	95.00	132.90	37.90	20.03	72.80	49.96	34.83
P_1x P_5	94.23	15.46	81.20	134.46	53.26	13.76	79.43	49.63	38.40
P_1x P_6	86.96	15.13	85.16	134.50	49.33	14.33	79.03	50.76	34.00
P_1xP_7	87.76	15.76	95.10	134.80	39.70	16.83	75.73	48.23	36.00
P_1x P_8	97.70	15.56	95.23	141.86	46.63	19.03	73.03	42.10	34.40
P_2x P_3	92.80	15.80	80.70	125.70	45.00	17.96	71.76	36.93	26.04
P_2x P_4	100.83	13.56	82.23	137.23	55.00	13.16	74.40	39.50	21.53
P_2x P_5	91.63	15.46	85.90	128.53	42.63	13.76	79.03	42.93	36.36
P_2x P_6	89.76	15.26	72.26	124.80	52.53	14.00	66.46	48.76	33.93
P_2xP_7	97.06	15.20	87.30	136.50	49.20	16.53	67.26	47.16	46.63
P_2x P_8	99.10	14.46	84.53	137.96	53.43	18.63	70.13	44.80	48.43
P_3x P_4	105.13	16.83	88.13	132.26	44.13	20.46	64.80	39.93	35.43
P_3x P_5	93.66	17.26	72.10	120.60	48.50	14.03	79.76	43.00	24.50
P_3x P_6	94.00	14.86	75.43	121.73	46.30	13.76	72.50	49.03	25.76
P_3xP_7	96.83	14.46	88.53	120.26	31.73	15.13	74.93	50.56	33.46
P_3x P_8	105.90	13.36	76.43	123.60	47.16	17.70	64.86	48.63	45.46
P_4x P_5	96.20	14.66	74.63	109.50	34.86	12.30	78.56	52.80	27.56
P_4x P_6	97.30	15.23	69.40	124.56	55.16	19.16	76.83	56.23	48.70
P_4xP_7	99.76	14.36	77.06	127.00	49.93	18.70	67.76	51.73	37.10
P_4x P_8	96.43	14.66	82.50	128.96	46.46	20.10	78.93	51.80	48.56
P_5x P_6	91.20	16.10	69.43	118.50	49.06	13.33	79.40	57.56	35.23
P_5xP_7	94.86	17.36	77.43	134.16	56.73	13.06	79.10	50.23	34.06
P_5x$P8$	98.76	15.26	78.66	133.06	54.40	12.26	71.20	47.86	25.00
P_6xP_7	99.63	15.06	75.36	126.03	50.66	16.60	70.70	50.63	42.83
P_6x P_8	102.30	15.13	72.53	128.03	55.50	18.20	73.86	58.70	47.93
P_7x P_8	106.83	15.40	94.40	133.86	39.46	17.80	74.60	47.36	25.00
L.S.D $_{0.05}$	1.95	0.98	1.33	1.38	1.82	1.313	4.71	2.80	2.22

followed by P_3xP_7 and then cross P_4 xP_5 had the shortest while the cross P_5xP_7 and P_6xP_8 had the longest grain filling period. For plant height, the shortest three crosses where P_1xP_6, P_1xP_7 and P_2xP_6. The three crosses P_7xP_8, P_3xP_8 and P_3xP_4 were the tallest in the same order. The three crosses P_5 x P_6, P_5x P_7 and P_3xP_5 possessed the longest spikes and two crosses P_3xP_8 and P_2xP_4 had the shortest ones. For number of spikes/plant the four crosses P_1xP_3, P_3xP_4, P_4xP_8 and P_1xP_4 had the highest number. However the two crosses P_4xP_5 and P_5xP_8 gave the lowest number of spikes. The four crosses P_3xP_5, P_1xP_5, P_5xP_6 and P_5xP_7 possessed the highest number of grains/spikes but the two crosses P_3xP_4 and P_3xP_8 had the lowest number. The three crosses P_6xP_8, P_5xP_6 and P_4xP_6 possessed the highest 1000-grain weight while the three crosses P_1xP_2, P_2xP_3 and P_2xP_4 showed the lowest weight. The four crosses P_4xP_6, P_4xP_8, P_2xP_8 and P_6xP_8 possessed the highest grain yield while the two crosses P_2xP_4 and P_3xP_5 gave the lowest mean grain yield/plant.

Mitotic activity

The data of mitotic activity, expressed by the mitotic index (MI), in the parents and their hybrids are given in (Table 4). Results showed that the variation in MI between different parents is observable. The mitotic index ranged from the highest score in P_3 and P_6 (15.70 and 15.15, respectively) to its lowest estimate in the P_7, P_4 10.61 and $P_5$10.94. The line P_8 was close to the highest score found in P_3 and P_6. The high MI in the P_3, P_6 and P_8 probably, indicates that, these lines are more adapted to the Egyptian conditions than the P_4, P_5 and P_7 where MI was sharply reduced. The decrease in MI could be attributed to the increase in the length of interphase period Dulaut and Olivero 1984. The frequencies of interphase observed in the lines which showed low MI in the present study were obviously higher than that of high MI, indicating the role of prolonged interphase as suggested by the later investigators. El-Bayoumi *et al* 1979 suggested that, the increase in MI could mostly be due to the appearance of high frequency of prophase. The data of the present study could be used to confirm such suggestion, since the frequencies of prophase in the lines showing MI were mostly higher than these of the low MI (Table 4). The hybrids exhibited a varied behavior for MI according to their parents. Based on the single estimate of MI, the hybrids could be classified into three groups ,the first group includes the hybrids that possess a lower MI than either of parents (P_1x P_2 , P_1 x P_6 , P_1x P_8 , P_2 x P_4 , P_3 x P_6 , P_4 x P_8 , P_5 x P_8 , P_6 x P_7 and P_6x P_8) ; the second group includes the hybrids that possess a higher MI than the higher parents (P1x P4, P_1x P_5 , P_1x P_7 , P_2 x P_5 , P_2 x P_8 , P_3 x P_8 , P_4 x P_5 , P_4 x P_7, P_5x P_6, P_5 x P_7 and P_7 x P_8) and the third group includes the hybrids that are characterized by an intermediate MI between the parents (P_1x P_3 , P_2 x P_3, P_2 x P_6 , P_2 x P_7, P_3 x P_4, P_3 x P_5 , P_3 x P_7 and P_4 x P_6).

Table 4. Mitotic index (MI) and frequency of mitotic phases in the wheat parents and their hybrids.

Parents and hybrids	Total studied cells	Total divided cells	MI %	Frequency of mitotic phases %		
				prophase	metaphase	Ana-telophase
P_1	3442	384	11.16	8.89	1.05	1.22
P_2	3325	372	11.19	8.60	1.23	1.35
P_3	3980	625	15.70	12.74	1.43	1.53
P_4	3757	411	10.94	8.60	1.01	1.33
P_5	3721	407	10.94	8.36	1.16	1.42
P_6	4054	614	15.15	12.43	0.79	1.92
P_7	3855	409	10.61	8.38	0.88	1.35
P_8	3884	529	13.62	10.38	1.57	1.67
P_1x P_2	32256	286	8.78	6.60	0.86	1.32
P_1x P_3	3554	464	13.06	9.79	1.55	1.72
P_1x P_4	3699	454	12.27	9.27	1.35	1.65
P_1x P_5	3480	612	17.59	13.42	1.78	2.39
P_1x P_6	3274	304	9.28	7.06	0.95	1.28
P_1x P_7	3516	498	14.16	10.98	1.45	1.73
P_1x P_8	3379	365	10.80	7.75	1.18	1.86
P_2x P_3	3420	405	11.84	8.98	1.02	1.84
P_2x P_4	3531	379	10.73	8.07	1.08	1.59
P_2x P_5	3502	495	14.13	10.51	1.37	2.26
P_2x P_6	3615	421	11.65	9.38	0.94	1.33
P_2x P_7	3602	396	10.99	8.38	1.17	1.44
P_2x P_8	3790	550	14.51	11.19	1.66	1.66
P_3x P_4	3550	516	14.54	11.18	1.44	1.92
P_3x P_5	3552	541	15.23	11.97	1.41	1.86
P_3x P_6	3430	499	14.55	11.02	1.90	1.63
P_3x P_7	3703	546	14.74	11.10	1.35	2.30
P_3x P_8	3355	540	16.10	12.28	1.79	2.03
P_4x P_5	3710	579	15.61	11.73	1.73	2.13
P_4x P_6	3410	382	11.20	8.50	1.29	1.41
P_4x P_7	3626	510	14.07	10.70	1.41	1.96
P_4x P_8	3383	359	10.61	7.89	1.21	1.51
P_5x P_6	3603	575	15.96	12.18	2.25	1.53
P_5x P_7	3448	468	13.57	10.12	1.54	1.91
P_5x P_8	3394	282	8.31	6.36	0.80	1.15
P_6x P_7	3191	327	10.25	7.87	1.00	1.38
P_6x P_8	3052	366	11.99	8.85	1.34	1.80
P_7x P_8	3072	477	15.53	11.91	2.05	1.56

Results regarding the differences in mitotic index between the two parents involved in each hybrid on the basis of X^2 test are given in Table (5). The data of this table showed that, there were significant differences in mitotic index between the parental pairs as well as between their F_1 hybrids in many cases.

Table 5. Significant X^2 estimates for the MI resulting from the comparison of wheat parents and their F_1 hybrids at the mitotic division.

Hybrid	Interrelation between the hybrid and		The parents involved the hybrids
	P_1	P_2	
P_1x P_2	8.51**	8.67**	-
P_1x P_3	4.75*	7.98**	24.85**
P_1x P_4	-	-	-
P_1x P_5	43.73**	48.96**	-
P_1x P_6	5.11*	45.05**	19.67**
P_1x P_7	11.06**	16.66**	-
P_1x P_8	-	10.24**	7.92**
P_2x P_3	-	17.19**	22.51**
P_2x P_4	-	-	-
P_2x P_5	10.32**	13.00**	-
P_2x P_6	-	15.32**	18.77**
P_2x P_7	-	-	-
P_2x P_8	13.36**	-	8.09**
P_3x P_4	-	16.65**	28.78**
P_3x P_5	-	22.69**	27.59**
P_3x P_6	-	-	-
P_3x P_7	-	22.45**	33.95**
P_3x P_8	-	6.40**	5.09*
P_4x P_5	27.12**	26.90**	-
P_4x P_6	-	19.12**	23.27**
P_4x P_7	12.94**	16.17**	-
P_4x P_8	-	11.96**	9.90**
P_5x P_6	31.02**	-	23.38**
P_5x P_7	9.06**	11.80**	-
P_5x P_8	11.52**	41.35**	9.94**
P_6x P_7	29.40**	-	27.96**
P_6x P_8	11.16**	-	-
P_7x P_8	28.54**	3.86*	12.67**

*=P < 0.05 **=P < 0.01 - = non values significant

The data presented in Table (6) showed that, the percentage of cells containing either micronuclei or chromosomal aberrations in mitotic divisions depended on the parental genotypes examined. These differences ranged from the highest score of micronuclei and chromosomal aberrations in the P_2 and P_7 to the zero estimates in the P_3 and P_8. However, P_5 and P_6 exhibited higher frequencies of micronuclei than P_1 and P_4. Data also showed that, P_4 exhibited higher frequencies of chromosomal aberrations than P_1. Most of F_1 hybrids showed less micronuclei and chromosomal aberrations in mitotic than their parents. However some hybrids have higher percentage of cells containing either micronuclei or chromosomal aberrations than their parents. The increase of abnormalities in such hybrids could be explained on the basis of cytological differences between different genetic back grounds. Such variation included chromosomal length (Fan 1985), nuclear DNA content (Lee *et al* 1997) and heterochromatin (Friebe and Gill 1994 and Vahidy *et al* 1994). The combination of different parental genotypes might, therefore, be responsible for chromosomal instability in the hybrids and subsequently introduce more chromosomal aberrations, which in turn, could be eliminated and subsequently form more micronuclei. In other words, the increased abnormalities in the hybrids may be due to genetic and structural heterozygosity. In this respect, Palitti (1998) hypothesized that chromosomal aberration could be attributed to the following 1-heterogeneity regarding the induction of initial DNA lesions and their repair among chromosomes or regions of the same chromosome, 2-The ratio between symmetrical and asymmetrical exchange, 3-Influence of DNA repeats, chromatin condensation and cell cycle checkpoints on the formation of chromosome aberrations.

The types of micronuclei, compact and non-compact, previously described by Hesseman and Fayed (1982) in *Vicia faba* were also detected in the present study in mitosis of the parents and their hybrids (Figure 1a and b). The frequency of compact micronuclei was, in general, more than that of non-compact type in the parents and their hybrids. The various types of chromosomal aberrations were presented in Table (6). The types observed in mitosis were fragments, laggards, stickiness and binucleate cells (Figures 1c to 1f). Fragments and stickiness represented the most frequent types of chromosomal aberrations in mitosis of studied materials. The other kinds of aberrations were found in low frequencies.

Table 6. Number and percentage of micronuclei and chromosomal aberrations in at the mitotic division of studied wheat parents and their F_{1s}.

Parents and hybrids	Total studied cells	Total divided cells	Number and percentage of		Percentage of types of micronuclei		Percentage of types of Chromosomal aberrations			
			Micronuclei	Chromosomal aberration	Compact	Non. compact	Fragment	Laggards	Stickiness	Binucleate cells
P_1	3442	384	5 (0.14)	1(0.26)	(0.14)	-	(0.26)	-	-	-
P_2	3325	372	8(0.24)	6(1.61)	(0.18)	(0.06)	(1.07)	-	(0.54)	-
P_3	3980	401	-	-	-	-	-	-	-	-
P_4	3757	418	8(0.21)	5(1.19)	(0.16)	(0.5)	(0.24)	(0.24)	(0.71)	-
P_5	3721	397	11(0.30)	-	(0.16)	(0.14)	-	-	-	-
P_6	4054	614	12(0.30)	-	(0.23)	(0.07)	-	-	-	-
P_7	3855	409	9(0.23)	12(2.93)	(0.13)	(0.10)	(1.22)	(0.73)	(0.73)	(0.25)
P_8	3884	529	-	-	-	-	-	-	-	-
P_1x P_2	3256	286	15(0.46)	-	(0.25)	(0.21)	-	-	-	-
P_1x P_3	3554	464	10(0.28)	5(1.09)	(0.14)	(0.14)	(0.65)	(0.22)	(0.22)	-
P_1x P_4	3699	454	11(0.29)	1(0.22)	(0.16)	(0.13)	(0.22)	-	-	-
P_1x P_5	3480	621	-	-	-	-	-	-	-	-
P_1x P_6	3274	304	-	-	-	-	-	-	-	
P_1x P_7	3516	498	-	-	-	-	-	-	-	-
P_1x P_8	3379	365	10(0.30)	14(3.84)	(0.18)	(0.12)	(1.10)	(0.55)	(1.37)	(0.82)
P_2x P_3	3420	405	9(0.26)	-	(0.23)	(0.03)	-	-	-	-
P_2x P_4	3531	379	13(0.37)	-	(0.26)	(0.17)	-	-	-	-
P_2x P_5	3502	495	-	-	-	-	-	-	-	-
P_2x P_6	3615	4217	(0.19)	-	(0.19)	-	-	-	-	-
P_2x P_7	3602	396	-	8(2.02)	-	-	(2.02)	-	-	-
P_2x P_8	3790	550	9(0.24)	-	(0.24)	-	-	-	-	-
P_3x P_4	3550	516	-	-	-	-	-	-	-	-
P_3x P_5	3552	541	15(0.24)	-	(0.25)	(0.17)	-	-	-	-
P_3x P_6	3430	499	-	-	-	-	-	-		-
P_3x P_7	3703	546	12(0.32)	-	(0.18)	(0.14)	-	-		-
P_3x P_8	3355	525	-	-	-	-	-	-		-
P_4x P_5	3710	579	-	-	-	-	-	-		-
P_4x P_6	3410	382	-	10(2.61)	-	-	(0.78)	-	(1.83)	-
P_4x P_7	3626	510	-	-	-	-	-	-	-	-
P_4x P_8	3383	359	-	-		-	-	-	-	-
P_5x P_6	3603	575	-	-	-	-	-	-	-	-
P_5x P_7	3448	468	10(0.29)	-	(0.17)	(0.12)	-	-	-	-
P_5x P_8	3394	282	-	-	-	-	-	-	-	-
P_6x P_7	3191	327	6(0.19)	8(2.45)	0.13	0.06	0.61	-	-	-
P_6x P_8	3052	366	13(0.42)	10(3.01)	0.26	0.16	0.82	0.31	1.53	-
P_7x P_8	3072	477	-	-	-	-	-	0.55	1.37	-

( ) percentage

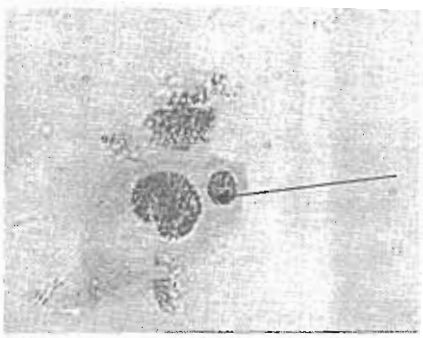

Fig a. Compact micronuclei

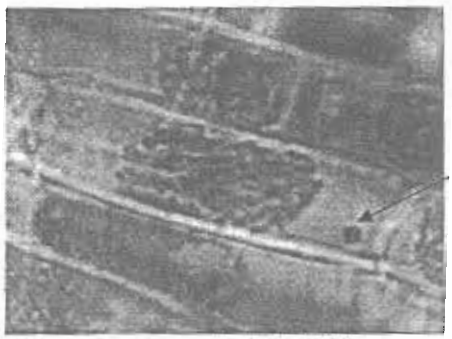

Fig b. Non-compact micronuclei

Fig. 1 a and b. Types of micronuclei compact and non-compact

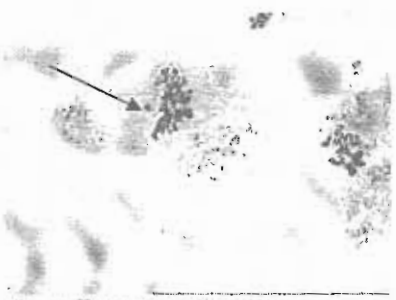

Fig. c. Fragment chromosome

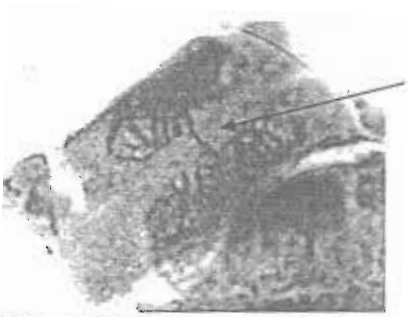

Fig. d. Laggard chromosome

Fig. e. Stickiness in chromosomes

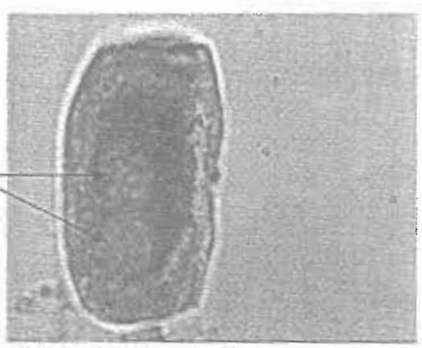

Fig. f. Binucleate cells

Fig. 1c to 1f. Types of chromosome aberration in mitotic cell division

From Tables (7 and 8) it could be seen that there were significant differences in number of cells containing either micronuclei or chromosomal aberration between the parental pairs and their corresponding F_1hybrids, in many cases. These results reflect some sort of genotypic variation in spontaneously occurring abnormalities among these parents, which might be due to their divergent origin and eventually their genetic back grounds. These results are in well agreement with those of Ducal *et al* (1980) and Pukhal *et al* (1980), who found differences in meiotic abnormalities within different varieties of bread wheat. But, Gvaladze *et al* (1990) found a high percentage of abnormalities including micronuclei in the meiosis of intra specific wheat hybrids.

Table 7. Significant X^2 estimates for the total number of micronuclei calculated from the comparison of wheat parents and their F_1 hybrids at the mitotic division.

Hybrid	Interrelation between the hybrid and		The parents involved the hybrids
	P_1	P_2	
P_1x P_2	5.63*	-	-
P_1x P_3	-	11.27**	5.87*
P_1x P_4	-	-	-
P_1x P_5	5.00*	10.22**	-
P_1x P_6	4.62*	9.82**	-
P_1x P_7	5.00*	8.20**	-
P_1x P_8	-	11.27**	5.42*
P_2x P_3	-	10.28**	9.77**
P_2x P_4	-	-	-
P_2x P_5	8.41**	10.22**	-
P_2x P_6	-	-	-
P_2x P_7	8.84**	6.57*	-
P_2x P_8	-	8.71**	9.29**
P_3x P_4	-	7.61**	8.41**
P_3x P_5	16.69**	-	10.86**
P_3x P_6	-	10.15**	11.61**
P_3x P_7	12.83**	-	9.41**
P_3x P_8	-	-	-
P_4x P_5	8.00**	11.00**	-
P_4x P_6	7.24**	10.12**	-
P_4x P_7	7.61**	8.56**	-
P_4x P_8	7.22**	-	8.41**
P_5x P_6	10.61**	10.53**	-
P_5x P_7	-	-	-
P_5x P_8	-	9.89**	11.40**
P_6x P_7	-	-	-
P_6x P_8	-	16.52**	11.57**
P_7x P_8	7.18**	-	9.01**

*=P < 0.05 **=P < 0.01 - = non values significant

Table 8. Significant X^2 estimates for the total number of chromosomal aberrations calculated from the comparison of wheat parents and their F_1 hybrids at the mitotic division.

Hybrid	Interrelation between the hybrid and		The parents involved the hybrids
	P_1	P_2	
$P_1 x P_2$	-	4.61*	-
$P_1 x P_3$	-	428*	-
$P_1 x P_4$	-	-	-
$P_1 x P_5$	-	-	-
$P_1 x P_6$	-	-	-
$P_1 x P_7$	-	14.28**	8.48*
$P_1 x P_8$	13.06**	19.84**	-
$P_2 x P_3$	6.48 *	-	6.40*
$P_2 x P_4$	6.06 *	4.54*	-
$P_2 x P_5$	7.89 **	-	6.34*
$P_2 x P_6$	6.69*	-	9.66**
$P_2 x P_7$	-	-	-
$P_2 x P_8$	8.95**	-	8.40**
$P_3 x P_4$	-	6.10*	4.74*
$P_3 x P_5$	-	-	-
$P_3 x P_6$	-	-	-
$P_3 x P_7$	-	15.56**	11.42**
$P_3 x P_8$	-	-	-
$P_4 x P_5$	6.84*	-	4.67*
$P_4 x P_6$	-	15.65**	6.25*
$P_4 x P_7$	6.03*	14.54**	-
$P_4 x P_8$	4.24*	-	6.26*
$P_5 x P_6$	-	-	-
$P_5 x P_7$	-	13.34**	11.31**
$P_5 x P_8$	-	-	-
$P_6 x P_7$	14.67**	-	17.50**
$P_6 x P_8$	16.34**	14.00**	-
$P_7 x P_8$	-	13.58**	15.08**

*=P < 0.05 **=P < 0.01 - = non values significant

Genetic components and heritability

Data presented in Table (9) revealed that the additive variance (D) was significant for all studied traits. These results indicated that the additive gene effects played a major role in the inheritance of all studied traits in F_1's. The dominance component of variation (H_1) was highly significant and greater than D, for all traits. The second component of dominance which was associated with gene distribution (H_2) was highly significant. All H_2 estimates were smaller than H_1 estimates for all studied traits, indicating

Table 9. Additive (D), dominance (H) and environmental (E) variance together with the derived genetics parameters for studied characters in 8 X 8 diallel cross of wheat in F_1.

Parameter	Plant height	Spike length	Grain filling period	Days to maturity	Heading date
D	60.67 ± 5.77**	0.96±0.59	38.46±15.01*	68.30±19.75**	69.25±11.23**
H_1	112.36±13.28**	5.64±1.37**	189.95±34.50**	173.18±45.40**	149.73±25.81**
H_2	110.29±11.55**	3.73±1.19**	144.65±30.02**	149.83±39.50**	121.40±22.46**
F	16.96±13.65	2.33±1.41	48.17±35.46	24.79±46.367	5.63±26.53
h^2	455.37±7.75**	0.002±0.80	2.59±20.13	303.66±26.49**	248.32±15.06**
E	0.52±1.92	0.12±0.19	0.42±5.00	0.24±6.58	0.23±3.74
$(H_1/D)^{1/2}$	1.36	2.41	2.22	1.59	1.47
$H_2/4\ H_1$	0.24	0.16	0.19	0.21	0.20
KD/KR	1.22	3.00	1.78	1.25	0.94
h^2/H_2	4.12	0.0005	0.017	2.02	2.04
Heritability(N.S)	0.44	0.20	0.32	0.46	0.62

Table 9. Continued

Parameter	Spikes/ plant	Kernels/ spike	1000- kernel weight	Grain yield
D	15.49±1.51**	83.21 ±7.86**	47.72±4.11**	50.11 ±15.41**
H_1	16.27±3.48**	115.11±18.07**	50.15±9.45**	232.08±35.46**
H_2	12.61±3.03**	83.70±15.72**	42.90±8.22**	229.23±30.85**
F	7.12±3.58*	85.80±18.58**	3.500±9.72	17.15±36.45
h^2	0.31±2.03	126.12±10.54**	1.93±5.51	60.68 ±20.69**
E	0.22±0.50	2.83±2.62	1.02±1.37	0.62±5.14
$(H_1/D)^{1/2}$	1.00	1.17	1.00	2.15
$H_2/4\ H_1$	0.19	0.18	0.21	0.24
KD/KR	1.57	2.56	1.07	1.17
h^2/H_2	0.024	1.50	0.045	0.26
Heritability (N.S)	0.64	0.37	0.68	0.23

*=P<0.05 **=P<0.01 N.S.= narrow sense

unequal allele frequency. The overall dominance effect of heterozygous loci (h^2) were significant for all traits, except for grain filling period, spike length, number of spikes/plant and 1000 kernel weight in the F_1 generation. These results are in agreement with those reported by Hamada (1993) and Abdel-Sabour *et al* (1993).

The covariance of additive and dominance (F) was not significant for all studded traits, except spikes/plant and kernels/spike, indicating an equality of the relative frequencies of dominant and recessive alleles in the parents for studied traits. These findings were in line with those reached by Ashoush (1996).

The relative size of (D) and (H_1) estimated as $(H_1/D)^{½}$ used as a weight measure of the average degree of dominance at each locus, showed the presence of over dominance for all studied traits except spikes/plant and 1000-kernel weight, which showed complete dominance. Similar results were obtained by Hamada (1993). The mean value of UV over all loci ($H_2/4H_1$) were slightly below the maximum value of 0.25, indicating that the positive and negative alleles were not equally distributed among the parents for all studied traits. The ratio KD/KR was more than unity for almost all traits, confirming presence of excess of dominant genes which govern these traits. The h^2/H_2 estimates for all studied traits suggest that there were one or more pairs of genes or genes groups affecting the inheritance of these traits. These results are in agreement with those reported by Hamada (2003).

Heritability estimates in narrow sense are given in Table (9). Low heritability values in narrow sense were detected for all studied traits except days to heading, number of spikes/plant and 1000-kernel weight which should high heritability, indicating that most of the genetic variance was due to non-additive genetic effects. This finding supported the previous results regarding the genetic components where the H_1 estimates played a greater role than D (Table 9). Therefore, the bulk method of selection might be quite promising most traits. Similar conclusion was reported by Hamada (2003).

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التقييم الوراثي والسيتولوجي للهجن التبادلية لثمانية اباء من قمح الخبز

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أجريت الدراسة الحالية في محاولة لإلقاء الضوء على قيم الإضطراب السيتولوجي (أي التكرار النووى الصغير والتغيرات الكروموسومية) في الإنقسام الميتوزي كدليل على عدم الثبات السيتولوجي وأيضاً دراسة النظام الوراثي المتحكم في بعض الصفات المحصولية مستخدماً الهجن التبادلية بين ٨ تراكيب وراثية مختلفة من قمح الخبز وهي (الصنف سخا ٦١ الأب رقم ١) ، (الصنف جيزة ١٦٤ الأب رقم ٢) ، (الصنف جميزة ٧ الأب رقم ٣) ، (الصنف سدس ٧ الأب رقم ٤) ، (السلالة المستوردة من الإيكاردا الأب رقم ٥) ، (السلالة المستوردة من

السمت الأب رقم 6)، (سلالة مجمعة من محافظة قنا الأب رقم 7)، (سلالة مجمعه من محافظة شمال سيناء الأب رقم8) أظهرت الدراسة أن النشاط الميتوزي كان مختلفا بين الأباء حيث تبين أن الآباء رقم8,6,3 ذات نشاط ميتوزي عالي والأباء رقم7,5,4 ذات نشاط ميتوزي منخفض. أظهرت الآباء إختلافات في التكرار النووي الصغير والتغيرات الكروموسومية حيث أظهرت الآباء رقم 7, 2 محتوى عالي منها في حين لم يظهر اي نوع من التغيرات الكروموسومية والنووية الصغيرة في الآباء رقم 8 ,3 ولذلك يوصي بإدخال هذه التراكيب الوراثية في برامج التربية لأنها ذات ثبات سيتولوجي عالي وايضا ذات صفات محصولية متميزة. كما أظهرت الهجن إختلافاً واضحاً في النشاط الميتوزي مقارنةً بالآباء الداخلة في التهجين فقد أظهرت أيضاً بعض الهجن في محتوى اعلى من التغيرات الكروموسومية والنووية الصغيرة مقارنةً بالآباء الداخلة في التهجين.

كان تباين الفعل الجيني المضيف (D) معنوى في كل الصفات المدروسة وهذه النتيجة توضح معنوية التباين الوراثي من النوع المضيف في توريث هذه الصفات. كانت مكونات التباين السيادي (H_2, H_1) معنويةً وعالية مقارنةً بالتباين المضيف (D). كان متوسط درجة السيادة $(H_1 / D)^{1/2}$ أعلى من الوحدة في كل الصفات موضحاً تأثير السيادة الفا ئقة ما عدا صفة عدد سنابل / النبات ووزن الآلف حبة التي كانت السيادة الكاملة تلعب دوراً في تأثيرها على هذه الصفات. كانت كفاءة التوريث بالمعنى الضيق منخفضة ما عدا صفة عدد سنابل/ النبات ووزن الألف حبة حيث كانت أعلى من 50 % .