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SUMMARY

One of the most important choices breeders make is the selection of parental materials. The probability of developing new high-yielding lines with other desirable characters is enhanced by crossing elite high-yielding parents. The major goals of this study are; (i) evaluation of parental genotypes for their yielding ability and leaf rust reaction under Nubaria conditions. (ii) Studying the heterosis, general and specific combining ability, heritability and correlation for yield and yield components. (iii) Detection of genetic polymorphism among parental genotypes. (vi) Assessment the usefulness of microsatellite markers as predictors of the amount of specific combining ability and heterosis. (v) Tagging and mapping of the important leaf rust resistance gene (*Lr26*) with SSR markers using F_2 population.

Ten bread wheat genotypes (Gemmiza 7, Sakha 61, Sakha 69, Sakha 93, Sakha 8, Sids 6, Line 1, Line 2, Line 6 and Line 8) representing a wide local and exotic germplasm were evaluated under recommended conditions at Nubaria in 1999/2000 and 2000/2001. Grain yield and its components; number of spikes per m^2, number of kernels per spike and 1000- kernel weight were recorded during the genotypes evaluation and study the possibility to use these parameters as indices in selection breeding programs. The analysis of variance indicated highly significant variation and the genotypes taken in consideration revealed differences for all characters studied in this experiment. The genotypes Sakha 93 and Gemmiza 7 were the most productive, while Line 8 resulted in poor yielding and for

number of spikes per m^2. Gemmiza 7 and Line 6 showed highest and lowest values for number of kernels per spike and 1000-kernel weight. The other genotypes showed different behavior and revealed variability between them under recommended conditions. For leaf rust reaction, the monogenic lines (Line 1 and Line 2) showed a resistant type of reaction to leaf rust, while other genotypes revealed a susceptible type of reaction to leaf rust except Line 6 and Line 8 showed moderate resistance and Sakha 61 showed a moderate susceptibility. Highly significant positive correlation was noticed between grain yield and number of spikes per m^2, number of kernels per spike and 1000-kernel weight. The results indicated that the most important sources of variation in grain yield are the direct effect of number of kernels per spike followed by number of spikes per m^2 and 1000-kernel weight. Indirect effects of yield components in grain yield revealed that the interaction between number of kernels per spike and number of spikes per m^2 was the first indirect effect followed by interaction between number of kernels per spike and 1000-kernel weight.

A diallel cross set involving six wheat genotypes (Gemmiza 7, Sakha 69, Sakha 93, Sakha 8, Line 1 and Line 2) was conducted in order to estimate the expression of heterosis and combining ability. The study was undertaken to investigate the variability among F_1 hybrids and mode of gene action, The six parental genotypes and their 15 F_1 hybrids were evaluated for grain yield and its components in 2002/2003. The results showed that the parents and their F_1 hybrids differed significantly for all the quantitative characters. The

best heterotic hybrids were (Gemmiza 7 x Sakha 93 and Line 1 x Line 2) which exhibited significant positive heterosis over both mid and better parent for grain yield.

Combining ability analysis by Griffing's method II indicated significance of both GCA and SCA genetic effects, but the former was more than important the latter. The diallel analysis indicated that Gemmiza 7 and Sakha 93 were the best general combiner parents for grain yield and some yield components. The hybrids, Gemmiza 7 x Sakha 93, Sakah 93 x Sakha 8 and Gemmiza 7 x Line 6 showed the best specific combining ability (SCA) for grain yield.

For segregating populations in F_2 generation, the analysis of variance indicated highly significant variation and the genotypes taken in consideration revealed differences for all characters studied in this experiment. The results showed that the genotypes (Gemmiza 7 x Sakha 93, Gemmiza 7 x Sakha 8, Sakha 93 x Sakha 69 and Sakha 93 x Sakha 8) were the most productive, while genotypes (Sakha 69 x Line 1 and Sakha 69 x Line 2) resulted in poor yielding. The other genotypes showed different behavior and revealed variability between them under recommended conditions. The study of heritability in broad sense in F_2 generation indicated that the heritability values were high to moderate for grain yield and its components. Heritability estimates for grain yield 84% and 73% for number of spikes per m^2, respectively, while these values were similar for number of kernels per spike and 1000-kernel weight (82% and 81%, respectively).

The phenotypic correlation was highly significant positive between

grain yield and number of spikes per plant, while it was significant positive for number of kernels per spike and 1000-kernel weight. The results indicated that the most important sources of variation in grain yield are the direct effect of number of spikes per plant followed by 1000-kernel weight and number of kernels per spike. Indirect effects of yield components in grain yield revealed that the interaction between number of kernels per spike and number of spikes per plant was the first indirect effect followed by interaction between number of spikes per plant and 1000-kernel weight.

Molecular markers display an important role and are considered as a complementary tool with conventional breeding for wheat improvement. The first step to design breeding program for useful trait is choosing parental genotypes based on its genetic dissimilarity. Detection of polymorphism among ten wheat genotypes under study, Euclidean distance and Nei's genetic distance were used in this investigation

Morphological markers analysis indicated that the range of Euclidean distance among all genotypes (1.04-9.97) is relatively wide. Also, the average of Euclidean distances (5.50) among all genotypes was high. This indicates that the amount of phenotypic variation among the genotypes is relatively high. Therefore, the dendogram illustrated that the most unique genotypes appear to be Gemmiza 7, Line 1, Sakha 93, Sakha 8 and Line 8. All genotypes formed three different groups and the studied morphological traits contributed significantly in differentiating the three groups from each other.

Genetic relationship using simple sequence repeat (Microsatellites or (SSRs) experiment was conducted using fifty SSR's developed and provided by Dr. P. Cregan, USDA-ARS, Maryland, USA, These were used to detect the genetic relationships between genotypes and to develop the molecular marker data. The results showed that the similarity matrix of genetic distance ranged from 0.10 between Gemmiza 7 and Line 8 to 0.875 between Sakha 69 and Sakha 61. The average of similarity among varieties was 0.49.

Among the fifty SSR loci, ten microsatellite markers (20%) generated polymorphism between parents with a total of 92 fragments. From the total scorable SSR bands, 27 alleles were detected for polymorphism. This represented an average of 2.7 alleles per locus with a range of two to five alleles detected by a single SSR locus. Nei's genetic distance (GD) was measured using the 27 polymorphic SSR alleles and showed that the genetic distance for each genotype combination ranged from 0.27 to 0.72 and the studied varieties formed two main clusters. The first main cluster separated two sub-clusters, the first sub-cluster included Gemmiza 7 and Sids 6 at a genetic similarity about 0.66 and the second sub-cluster included Line 1 and Line 6 at a genetic similarity about 0.49. In relation to second main cluster, this cluster formed two sub-clusters at a genetic similarity about 0.55, the first sub-cluster included Sakha 69 and Sakha 61 at a genetic similarity about 0.68 and Sakha 8 which represented an individual variety at a genetic similarity about 0.58. For the second sub-cluster, the results indicated that it included two varieties, Line 2 and Line 8, separated at genetic

similarity about 0.72.

Predicting F_1 common wheat hybrid performance using DNA markers is one of the important applications of DNA markers and evaluation of hybrids for heterosis or combining ability in the field is expensive and time-consuming. Therefore, an amplification products which were detected by the ten microsatellite markers were used to study the relationship of genetic diversity measurments using SSR markers with the amount of specific combining ability and heterosis in wheat genotypes under study. The results indicated that the amount of heterosis and specific combining ability for grain yield per plant were highly significantly correlated with Nei's genetic distance (GD) (0.60 and 0.49, respectively). The results showed that heterosis only was significantly correlated with Nei's GD for number of spikes per plant (0.31), while SCA was significantly correlated with Nei's GD for 1000-kernel weight (0.40). On the other hand, all other traits revealed weak correlation between Nei's GD, heterosis and SCA. With regard to correlation of heterosis with SCA, heterosis was also significantly or highly significantly correlated with SCA for all traits under study.

Identifying molecular markers linked to different leaf rust resistance genes is an important step in long-term strategy for rust disease resistance. Identfying microsatellite markers linked to *Lr26* resistance gene was an objective of this investigation. A cross between the resistant *Lr26* donor line (monogenic Line 1) and Gemmiza 7 as a susceptible variety, The F_2 segregating population

was used to identify the SSR markers linked to leaf rust resistance genes. Bulked DNA from each of resistant plants and susceptible plants were tested by using fifty primer pairs of SSR loci on the 21 wheat chromosomes. Among these primers, *Xbarc80* and *Xbarc81*, showed polymorphism between susceptible and resistant bulked DNA. Both primers could be analyzed as codominant markers and the results showed that the segregation ratio for the previous F_2 population was 1:2:1 (Chi-square=0.59, $p< 0.05$).

A regression analysis was performed to test the significance of the linkage between *Lr26* and the polymorphic markers. The results showed that the regression analysis for the markers *Xbarc80* and *Xbarc81* were significant. In relation to infection type, the calculated r^2 for *Xbarc80* and *Xbarc81* were 0.28 and 0.55, respectively. On the other hand, the calculated r^2 for *Xbarc80* and *Xbarc81* were 0.33 and 0.50 for disease severity, respectively.

The two closest microsatellite loci and the resistance gene *Lr26* were assigned to chromosome 1B. A standard maximium-likelihood technique was used to analyze the linkage between the two microsatellite loci and resistance gene *Lr26*. The map distance between *Lr26* and *Xbarc80* was 8.1 cM, while the distance between this resistance gene *Lr26* and *Xbarc81* was 18.5 cM, respectively. *Lr26* was flanked on either side by *Xbarc80* and *Xbarc81*, with a total map length of 26.6 cM, with LOD scores ranging from 10 to 18.6, respectively.