

Breeding studies on common wheat

Nadya Adly Riad Abd El-nour

The main objective of the present study was to determine the genetic variance components for some quality traits in wheat. Five wheat varieties and/or lines were chosen on the basis of their variabilities in the studied traits. A half diallel set of crosses involving the five parents was evaluated for, protein, amino acids, gluten, hydration coefficient, moisture, ash, fiber and extracted flour, shorts, fine bran and bran (AACC, 1983). Seventeen amino acids were determined as mg/g sample. Analysis of variance was performed for each quality trait. Heterosis was computed as the percentage deviation of F1 mean performance from mid-parent and better-parent. Data were genetically analyzed according to Griffing (1956), method 2, model I, Hayman (1954 a and b) and Jinks (1954). Heritability was estimated as Mather and Jinks (1971). The obtained results can be summarized as follows:

1- Analysis of variance, mean and heterosis:

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

- 1- Significant mean squares due to genotypes along with parents and crosses were detected for protein and most amino acids (mg/g sample).
- 2- The parental variety P2 gave the highest mean value for protein and seven amino acids. The F1 cross (p3 x PS) was the best combination for protein and nine amino acids since it gave the highest mean values.
- 3- The two crosses (p3 x P4) and (p3 x PS) expressed the best heterosis for protein and most of the studied amino acids.

b: Other quality traits:

- 1- Mean squares due to genotypes along with parents and crosses were significant for gluten, ash, fiber, as well as extracted flour and fine bran.
- 2- The parent P2 expressed the best mean performance for gluten and extracted flour, while parent P1 had the highest value for ash and fiber. The best F1 mean values for gluten, ash, and fiber were obtained for the crosses (p2 x P5), (p2 x P3) and (P1 x P4), respectively.
- 3- Significant and positive heterotic effects were obtained for gluten in the crosses P3 x P4, P3 x P5 and P4 x P5 and for extracted flour in both P1 x P3 and P3 x P5.

1.1- Combining ability analysis:

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

- 1- Significant mean squares due to both general and specific combining ability were detected for protein and all amino acids studied. High GCNSCA ratios which largely exceeded the unity were obtained for most traits, indicating that the largest part of the total genetic variability associated with these traits was a result of additive and additive x additive types of gene action.
- 2- The parents P2 and P3 seemed to be the best general combiners for protein and all amino acids.
- 3- The most desirable SeA effects for protein and most amino acids were detected in the cross (p3 x P5), followed by the cross (p3 x P4).

b: Other quality traits:

- 1- General and specific combining ability variances were significant for gluten, ash, fiber and extracted flour. The GCNSCA ratio revealed that additive and additive x additive gene effects were more important than non additive ones for such traits.
- 2- Parent P2 appeared to be the best general combiner for gluten, fiber and extracted flour.
- 3- The best SCA effects were obtained in the crosses (p3 x P4), and (P3 x P5) for gluten, and extracted flour, respectively. Four crosses expressed desirable SCA effects for fine bran.

1.1.1- Genetic components analysis:

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

- 1- The additive component D was appreciable for all traits except alanine amino acid, while the two dominant components H1 and H2 were significant for all traits except serine amino acid.
- 2- Dominance of heterozygous loci (h2) was unidirectional in 17 out of the studied 22 traits with increasing alleles being dominant over decreasing ones. Overdominance was detected for all traits under study.
- 3- The alleles of positive and negative effects were not equally distributed among the parental populations for protein and most amino acids.
- 4- High heritability values in broad sense were detected for all traits. However, narrow sense heritability values ranged from high to low for the traits under study.

b:

Other quality traits: 1- Appreciable values for both additive and dominance components were detected for the traits; gluten, ash, fiber, and extracted flour and fine bran. 2- Increasing alleles of dominance seemed to be dominant over the decreasing ones at heterozygous loci and for fiber and fine bran overdominance was indicated for all traits. 3- Negative and positive alleles are equally distributed among the parents for fiber and flour traits. 4- High heritability values in broad sense accompanied by low to moderate values in narrow sense were obtained for the traits under study.

IV- Graphical analysis: 1- The intersection of regression line below the origin point for most studied traits, revealed overdominance for such traits. 2- The distribution of parental varieties along the regression line showed that varieties P2, P3, and P5 possess an excess of genes behaved as dominant, while the variety P4 possess an excess of genes behaved as recessive ones for most of the traits studied. 3- Significant and positive correlation values between Y_r and $W_r + V_r$ were detected for fiber and leucine, phenylalanine, tyrosine, threonine, and total amino acids (mg/g sample). This indicated that decreasing genes were dominant over increasing ones for these traits. Appreciable negative correlation values were obtained for protein, gluten; as well as glutamic acid and proline (mg/g sample), revealing that increasing genes were dominant over decreasing ones.