NUMBER OF GENES INTERACTIVE MODELS IN PLANTS GROWN UNDER STRESS VARIABLES

M. M. Elsahookie
Professor / Plant Breeding
elsahookieemeritus@yahoo.com
Dept. of Field Crops – Coll. of Agric. – Univ. of Baghdad

ABSTRACT
To acquire more information on genotype x environment interactions in plants grown under abiotic and/or biotic stresses, and to understand a new approach on the complex mechanism of tolerance, a formula was set-up to estimate the number of genes interactive models (NGIM) acting in plants under stress. Some of previous results and ideas on this topic were taken into consideration, including morpho-physiological traits and molecular approaches. The formula was: NGIM = n^2 - x, when n = number of stress variables and x = n-1. Genes of stress variables were sketched as circles, and the sectors of each group of genes and their interactions were identified. Sketches explained that in two stress variables, these sectors will appear, as two of genes groups acting alone, and one sector represents the interaction. If three variables taken, there will be seven sectors, three of them of genes groups acting alone, three sectors of two groups interactions, and one sector of three groups interaction. In case of four variables, four sectors will be of genes groups acting alone, four sectors of two groups interactions, four sectors of three groups interactions, and one sector of the four groups interaction (total 13). In case of five variables taken, the sectors will be 21, in case of six variables taken, the sectors will be 31, and for seven variables the sectors will be 43. Sectors of eight variables will be 57, namely, 8 sectors of genes groups acting alone, 8 sectors of two groups interactions, 8 sectors of three groups interactions, 8 sectors of four groups interactions, 8 sectors of five groups interactions, 8 sectors of six groups interactions, 8 sectors of seven groups interactions, and one sector for the eight groups interaction. However, using this formula for any number of stress variables will give similar trend of interactions. The results of applying this formula showed the complexity of multi-gene actions and interactions in plants grown under stress variables. This implies the need of a larger area of plots to grow thousands of genotypes individuals repeated under several levels of that stress, several traits taken under study, and genetically wide genotypes, planted in a honeycomb design to enable the breeder identifying tolerant individuals and/or genotypes under those environments.

Key words: epigenetics, helitrons, peroxisomes, SSR, DNA-methylation.

M. M. Elsahookie
University of Baghdad
Dept. of Field Crops
 elsahookieemeritus@yahoo.com

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97
Introduction
Many researchers around the world searched into the area of plant adaptation and distribution, i.e., genotype x environment interaction. Wilsie (27) summarized several ideas of those researchers, such as Shelford, Good, Cain, and others. Their ideas were focused on what so called: Tolerance Theory. They explained that environmental variables have an influence on plant growth and distribution. Thus, adaptation has a genetic basis. One the best explanations of those researchers that came from Billings (5). He explained the relationship of 15 environmental variables and plant growth in a schematic diagram called holocoenotic environment. That scheme explained that every variable has an influence on another, and that the plant growth and distribution will be the result of those interactions. On the other side, plant adaptation in a specific environment or environmental variables of stress has been replaced by the term genotype x environment interaction (G x E). Chapman et al. (6) explained that plants grown under stressed environment are a result of G x E interactions. Thousands of genes could be involved in tolerance of plants grown under stressed environment. There are two groups of environmental stresses; abiotic and biotic. The problem of salinity and water stress deficit have the most dramatic negative influence of abiotic stress in today's agriculture. These two problems are being more important to study on plants genotypes grown under these stresses, especially with the increasing effect of global warming and scarcity of good quality irrigation water in the world.

Several researchers suggested using some statistical parameters to determine stability of performance of genotypes grown across environments. Some of these models became more common in use, such as Wricke (29), Finlay and Wilkinson (15), Eberhart and Russell (8), Shukla (25) and others (9, 11, 12, 16, 20). However, G x E interactions have been studied on two levels; morpho-physiological traits (1, 2, 17, 18, 14, 22) and molecular level (4, 7, 13, 14, 21, 23, 28). The morpho-physiological traits included plant characteristics, such as plant height, leaf area, flowering mechanism, yield components, plant growth rate, root traits, leaf cuticle, and other traits. The molecular approach focused on DNA-methylation, epigenetics, and many compounds of protein origin decrease or increase under stress. This article was written and discussed to explain some thoughts on genes interactions in plants under stress to expand the area of understanding the mechanism of genotype tolerance to abiotic and/or biotic stress. This will be through determining the number of genes interactive models (NGIM) acting in plants under stress. NGIM = \( n^2 - x \), when \( n \) is the number of groups of genes of tolerance to any biotic or abiotic stress (salinity, drought, low fertility, toxicity, population density, etc.) and \( x = n - 1 \). The sketches obtained by applying this formula will shed new light on some dimensions of this phenomenon.

Materials and Methods
Going back to some basics of genetics and the hypothesis of Tatum (26) (one gene - one enzyme) that every gene controls the production, functions, and specificity of a particular enzyme, and the hypothesis of Elsahookie (10); one enzyme – one gene, implies that if we get the specific enzyme (s) of a specific gene (s), we will be able to prescribe a good therapy for any dysfunction in a living organism, including human cancer. That will be through the application of that specific enzyme (s) on that organism living under that specific stress. This short introduction was necessary to keep in mind the schematic diagram of genes of plants under stress how to interact. Seki et al. (24) showed two schemes of three groups of genes each, how they interact and produce seven genes groups acting (as sectors) under stress. When studying those two diagrams, a question was raised: how many groups of genes we will have if we draw four, five, six…etc circles?. The number of those groups of genes (sectors in the scheme) acting in plants under stress variables will follow the formula: \( \text{NGIM} = n^2 - x \), when NGIM is the expected number of genes of that interactive models, \( n \) = number of groups of genes of that stress variable, and \( x = n - 1 \). The forthcoming diagrams will be shown and discussed.
Results and Discussion

When two circles (two groups of genes) interact, there will be three NGIM acting in plants for stress tolerance (Fig. 1). However, the area of the intersect will differ as the number of genes control the traits differ. This difference will be true for abiotic or biotic stress tolerance.

Fig. 1. Two groups of genes are interacting. Three NGIM are shown. The area of intersect is different between the interacted circles.

The same trend of interactions will hold true when three groups of genes are taken into consideration (Fig. 2). Seven sectors appear in the diagram. The sectors 1, 2, and 3 represent the action of genes groups of an environmental variable alone, 4, 5, and 6 represent interactions of two groups of genes, and one sector (no. 7) represents the interaction of the three groups of genes.

Fig. 2. Three groups of genes are interacting. Seven NGIM appears in the diagram.

The formula \( \text{NGIM} = n^2 - x \) will also hold true when four groups of genes are taken. Fig. 3 shows that there are 1, 2, 3, and 4 sectors represent the action of genes of the four variables acting alone, 5, 6, 7, and 8 represent interactions of two groups of genes, 9, 10, 11, and 12 represent interactions of three groups of genes, while only one sector (no. 13) represents the interaction of all of the four groups of genes. If we take 5 or 7 groups of genes, NGIM will be 21, and 43 sectors, respectively.

Fig. 3. Four groups of genes are interacting. Number of intersect is 13.

However, Fig. 4 shows that there are 31 sectors in that scheme. The numbers; 1, 2, 3, 4, 5, and 6, represent the action of the six groups of genes acting alone, 7, 8, 9, 10, 11, and 12 represent the interactions of two groups of genes, 13, 14, 15, 16, 17, and 18 represent the interactions of three groups of genes, 19, 20, 21, 22, 23, and 24 represent the interactions of the four groups of genes, 25, 26, 27, 28, 29, and 30, represent the interactions of the five groups of genes, while only one intersect (no. 31) represents all of the six groups of genes interacting with each other.

Fig. 4. Six groups of genes are interacting and showing that NGIM is 31 sectors.

The schematic diagram (Fig. 5) shows that there are 57 sectors for eight groups of genes interacting. Only one sector (no. 57) represents
all of the eight groups of genes interacting together. Eight sectors will be for each of the eight groups of genes acting alone, two groups, three groups, four groups, five groups, six groups, and seven groups.

Fig. 5. Eight groups of genes are interacting and showing that NGIM is 57 sectors.

In the foregoing illustrations and discussion, it showed clearly the complexity of gene action nature in multi-genes traits of a genotype living under stress variables. This implies that it will not be easy to identify a single gene or even a single QTL totally responsible of the tolerance of a genotype to any abiotic or biotic stress variable. Allard and Bradshaw (3) reported a formula estimated numbers of interactions (phenotypes) of a 10 genotypes grown in a 10 environments to be $10^{145}$. This number is robust, but they did not explain how. On the other hand, Liu et al. (21) estimated the number of alleles in a QTL in some maize (Zea mays L.) inbreds equal to 21.7 alleles each. Keeping this in mind and taking several environmental variables in the study, such as salinity, drought, low fertility, elemental toxicity, low radiation, …etc, and proposing 200-300 genes acting for each variable, the number of plants having different ranks of tolerance will be very high. If we take the number of combinations of a padlock of 3 sets of Arabic integers from 0-9, the number will one thousand. While if we take it of 6 sets, the number of combinations will be one million. This explains the huge numbers of varied plants of a genotype grown under stress variables. Seki et al. (24) showed a schematic diagram of three groups of genes governing salinity, drought, and ABA. The number of genes given for those three variables were 213, 299, and 245, respectively. Some researchers count on morpho-physiological traits to test salinity of genotypes living under stress variables as we have mentioned before. Genetic distance among genotypes differs as the traits differ. Yadav and Singh (30) found that genetic distance was between 1.6 to 10.8 among maize inbreds when morphological traits were taken into consideration. However, genetic distance for same inbreds became only 0.35 to 1.92 when physiological traits were taken into consideration. Meanwhile, RAPD analysis of same inbreds revealed that genetic distance became very low (0.42 to 0.65). Dashti et al. (7) identified 6 QTL related to wheat kernel weight, one QTL for grain yield, 3 QTL for spike length, and 5 QTL for number of kernels in a spike. However, epigenetics, DNA-methylation, SSR, helitrons, RNAi, and peroxisomes could play important roles under stress. These findings imply that to study G x E interactions of plant genotypes, a large area of many widely diversified genotypes, thousands of plants for each genotype should be grown in a honeycomb design, and many morpho-physiological traits should be taken to identify some tolerant plants or genotypes under that abiotic and/or biotic stress variables.

References