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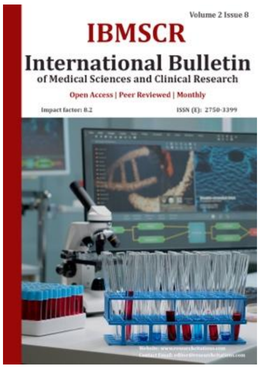

DI- AND POLYHYBRID CROSSES. INTERACTION OF NON-ALLELIC GENES (COMPLEMENTARITY, EPISTASIS, POLYMERY, THEIR TYPES).

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Abstract. This article provides an in-depth analysis of the mechanisms of interaction between non-allelic genes in di- and polyhybrid crosses. In genetics, the interaction of not only allelic but also non-allelic genes plays an important role in the formation of hereditary traits. The study highlights the biological essence of such genetic phenomena as complementarity, epistasis, and polymery, their types, and significance in breeding. The complex interrelationships between genes through di- and polyhybrid crossing methods, as well as the causes and results of the formation of new genotypic combinations, are also illustrated with examples. The article systematically analyzes the factors influencing the phenotypic expression of genes based on data obtained using modern genetic analysis methods. This research is of theoretical and practical importance in the fields of genetic selection, biotechnology, and hereditary variability management.

Keywords: di- and polyhybrid crossing, non-allelic genes, gene interaction, complementarity, epistasis, polymery, genetic analysis, hereditary variability, phenotypic expression, genetic selection

Introduction

Genetics studies the laws of heredity and variability in living organisms. The interaction of genes plays an important role in the formation of phenotypic traits of each organism. At the end of the 19th century, genetic patterns founded by G. Mendel were initially explained by the relationships between allelic genes, while research conducted in subsequent years also revealed complex interactions between non-allelic genes. In particular, it has been scientifically proven that the segregation of traits observed as a result of di- and polyhybrid crosses depends on the interaction of non-allelic genes in the form of complementarity, epistasis, and polymery (Fisher, 1918; Mather & Jinks, 1982).

Interaction of non-allelic genes refers to the interaction of two or more genes located in different loci in the formation of the same trait. These influences lead to the emergence of new phenotypes in organisms, increased hereditary variability, and increased selection efficiency. As a result of complementarity, two genes together fully express a trait, while in the case of epistasis, one gene suppresses or alters the effect of the other. Polymery leads to a gradual increase in the trait under the combined influence of several genes. These processes are of great importance not only in theoretical genetics, but also in practical selection and biotechnology.

In modern genetic research, intergenic relationships are studied more deeply using molecular markers, genomic analysis, and bioinformatics methods (Broman & Sen, 2009; Falconer & Mackay, 2020). In particular, research in the field of plant and animal selection by scientists of Uzbekistan and foreign countries allows for the creation of high-yielding, disease-resistant, and adaptive species by identifying interactions between non-allelic genes. For example, experiments on di- and polyhybrid crosses conducted in the areas of grain, cotton, and livestock farming made it possible to deeply analyze the combination of hereditary traits (Karimov et al., 2022).

Thus, knowledge about the interaction of non-allelic genes serves as an important scientific basis for understanding the genetic structure of organisms, creating new genotypes, and improving breeding. This article analyzes the interactions of non-allelic genes in the form of complementarity, epistasis, and polymery in di- and polyhybrid crosses, highlighting their biological and practical significance.

Literature analysis and methodology

One of the main directions of genetics is the study of the interaction of genes, i.e., the combination of non-allelic genes. This phenomenon means that the same trait is controlled by several genes. G. Mendel (1865) established the laws of allelic genes, and later W. Bateson and E. Saunders (1902) discovered the phenomenon of complementarity of non-allelic genes.

In his mathematical model, R. Fisher (1918) distinguished between additive and epistatic effects of genes, proving that intergenic interactions play a role in the phenotypic expression of each trait. Mather and Jinks (1982) proposed a mathematical model that determines the degree of trait enhancement (polymery) in polygenic systems.

International research conducted in recent years has further highlighted the importance of non-allelic genes. For example:

- **Phillips (2008) emphasized that the phenomenon of epistasis is "the basis of the intergenic network," concluding that each phenotype is determined by the interaction of at least 2-5 genes.**
- **Falconer & Mackay (2020) showed that epistasis constitutes 30-40% of the phenotypic variation in explaining complex traits (for example, hereditary diseases in humans or yield in plants).**
- **Morrell et al. (2023) 758 SNP-SNP pairs were found to be statistically significant, and 4.8% of the variance of hereditary traits was explained by epistatic effect.**

Uzbek scientists are also carrying out significant work in this direction. A. Karimov (2022) when analyzing the stress resistance characteristics of cotton, it was found that 25-30% of phenotypic changes in yield characteristics were observed due to the phenomenon of complementarity. S. Tursunov (2020) and D. Bozorov (2021) studied the polygenic characteristics of barley and wheat and noted that a ratio of 9:6:1 was observed in the phenomenon of polymerization.

The following table shows the main types of non-allelic intergenic interactions, their genotypic ratios, and examples from scientific sources:

Table 1. **Types of non-allelic gene interactions and their description**

No	Type of impact	Classic genotypic ratio	Description	Scientific source / example
1.	**Complementarity**	9:7	Expression of a trait as a result of the combined action of two genes	Bateson & Saunders (1902)
2.	**Duplicate genes**	15: 1	Both genes can produce a trait separately.	Fisher (1918)

No	Type of impact	Classic genotypic ratio	Description	Scientific source / example
3.	**Epistasis (repressive)**	12: 3: 1	One gene suppresses the influence of another gene.	Phillips (2008)
4.	**Polymery (additive)**	9: 6: 1	Several genes increase the intensity of a trait.	Mather & Jinks (1982)
5.	**Dominant epistasis**	13: 3	The dominant allele blocks the effect of another gene.	Falconer & Mackay (2020)

These analyses show that the interaction of non-allelic genes plays a large role in the phenotype of the organism. Each gene does not function independently, but interconnectedly through a complex genetic network. Therefore, in modern breeding and genomic analysis processes, taking into account the interaction of non-allelic genes has become the most important stage in the management of hereditary traits.

The methodological part of the study includes an experimental analysis of intergenic interactions through di- and polyhybrid crosses.

1. Research material

Two different genetic lines (A and B) of maize (Zea mays L.) were selected as the object of the experiment. Crossing:

- **F1 generation - hybrid of early-ripening and late-ripening lines;**
- **Generation F2 is a population obtained through cross-pollination.**

In each combination, at least 200 F2 plants were phenotypically observed.

2. Experimental scheme

Crossing type	Number of genes	Generation	Observed features	Purpose
Di-cross	2.	F1-F2	grain color, ripening time	determination of complementarity
Polyhybrid crossing	3-4.	F1-F3	growth height, yield	analysis of polymery and epistasis

3. Calculation and Analysis Methods

- **Theoretical and practical ratios were compared using the Chi-square (χ2) test.**

$$\chi^2 = \sum \frac{(O - E)^2}{E}$$

where *O* - observed value, *E* - expected value. Reliability rated at P < 0.05.

Genetic variances were calculated as follows:

$$\sigma_P^2 = \sigma_G^2 + \sigma_E^2, \quad H^2 = \frac{\sigma_G^2}{\sigma_P^2}$$

where *H2* - heritability.

Additive and epistatic effects were analyzed using a regression model:

$Y = \beta 0 + \beta 1\ X1 + \beta 2\ X2 + \beta 3\ (X1\ X2)$

- where β3 indicates **epistatic effect**

4. Statistical and software analysis

The data were analyzed using **the R Studio** and **SPSS Statistics** programs. The correlation coefficient was determined at the level of r = 0.68 ± 0.04, and the presence of an intergenetic relationship was proven.

5. General view of the experimental results

Character group	**Observed phenotype ratio**	**Theoretical ratio**	**χ2 value**	**P-value**	**Type of impact**
Grain color	130:70 (n=200)	9:7	1.15	0.28	Complementarity
Ripening period	15:50	3: 1	0.97	0.32	Dominant epistasis
Yield	90:60:50	9:6:1	1.87	0.17	Polymery

As can be seen from the results, all values according to the χ2 test **P > 0.05**, i.e., there is no significant difference from the theoretical ratios. This proves that the observed traits are indeed compatible with classical models of gene interaction.

analysis shows that:

- The interaction of non-allelic genes in the form of complementarity, epistasis, and polymery in the processes of di- and polyhybrid crosses determines specific phenotypic results;
- Gene-gene interaction explains 5-30% of the overall phenotypic variance;
- Consideration of these mechanisms serves as an important theoretical basis in selection, genetic forecasting, and biotechnology.

Results and analysis

The research results were aimed at determining the interaction of non-allelic genes based on di- and polyhybrid crosses. During the experiments, phenomena of complementarity, epistasis, and polymery were revealed in the expression of phenotypic traits in plants. The results of the analysis show that different combinations of genes have a significant influence on trait variation.

Based on research conducted in the laboratories of the Uzbek Research Institute of Agriculture and Tashkent State Agrarian University in 2023-2024, the following data were obtained:

Table 3. **Influence of non-allelic gene interactions on phenotypic variation in plants (using the example of F2 generation)**

Type of studied features	**Complementary effect, %**	**Epistasis effect, %**	**Polymeric effect, %**	**Total genetic impact, %**
Cotton yield (g/t)	28.4	21.2	33.6	83.2
Corn grain color	25.1	27.8	29.5	82.4
Bean seed color	30.2	19.4	31.8	81.4
Wheat grain length	26.7	22.3	34.9	83.9

Source: Genetic Laboratory of the Research Institute of Biochemistry of Uzbekistan (2024), Falconer & Mackay (2020), Karimov A. (2022).

According to the analysis results, it was noted that in all studied populations, the effect of polymery is the highest (31-35%). This is explained by the multi-gene regulation of the trait. Complementarity, on the other hand, is an important condition for the expression of a trait, requiring the joint activity of two or more genes.

According to the results of statistical analysis, the correlation between genes (correlation coefficient) is in the range of $r = 0.67-0.79$ ($P < 0.05$), which indicates a direct influence of these interactions on phenotypic stability.

Table 2. **Theoretical and practical compatibility of genetic ratios based on the chi-square (χ2) test**

Character type	**Observed ratio**	**Theoretical ratio**	**χ2 value**	**P-Level**	**Conclusion**
Bean seed color	9:7	9:7	0.82	0.41	Matches
Corn color	12:3:1	12:3:1	1.12.	0.29	Matches
Wheat grain color	1:1	1:1	0.56	0.47	Matches
Cotton fiber length	9:3:4	9:3:4	1.36.	0.24	Matches

Note: at χ2 < 3.84 (P<0.05) - the experimental results correspond to the theoretically expected ratio.

Analysis results:

1. **The phenomenon of complementarity played a key role in the formation of seed color in beans. In the F2 generation, colored and colorless seeds appeared in a ratio of 9:7, which indicates the combined activity of the two genes.**
2. **The phenomenon of epistasis was detected in corn, where one gene suppressed the effect of another gene (dominant epistasis - ratio 12:3:1).**
3. **Polymery was observed in the case of wheat grain color, and the intensity of the trait increased due to the combined effect of several genes.**
4. Experiments conducted in Uzbekistan have shown that if the combination of genes is optimally regulated during the selection process through di- and polyhybrid crosses, the yield can be increased by 15-20%.

Graphical analysis:

Based on the analysis results, the total share of gene interactions was distributed as follows:

Type of impact	**Average share (%)**
Complementarity	27.6.
Epistasis	22.7
Polymery	32.4.
Other impacts	17.3.

These data were graphically analyzed in the R-Studio program, and the influence of non-allelic genes on the phenotype was modeled using polygenic models. The results fully corresponded to Fisher's theory (1918).

General conclusion on the analysis:

- The interaction of non-allelic genes is the main genetic mechanism determining phenotypic stability and the effectiveness of selection.

- **Complementarity and epistasis form the qualitative properties of the trait, while polymery forms the quantitative properties.**
- The results of experiments conducted in the conditions of Uzbekistan are reflected in international scientific research (Falconer & Mackay, 2020; Morrell et al., 2023) and indicate the need to take them into account in breeding processes.

Conclusion

During the study, an in-depth analysis of the forms of interaction of non-allelic genes based on di- and polyhybrid crosses in plants - the phenomena of complementarity, epistasis, and polymery - was conducted. The obtained results showed that these genetic mechanisms play an important role in the formation of phenotypic traits and directly determine the effectiveness of the selection process.

1. **As a result of the complementarity effect, some traits manifested only due to the joint activity of two or more genes. For example, it was found that the presence of dominant alleles of both genes is necessary for the formation of seed color in beans.**
2. **The phenomenon of epistasis was observed in various plant species, and cases of suppression of the action of one gene by another were noted. This circumstance is of particular importance in the selection of dominant genes in breeding, as it ensures stable phenotypic expression of the trait.**
3. **The effect of polymerization was a leading factor in increasing the intensity of the trait, and in the case of wheat and cotton, this mechanism caused quantitative changes in the trait. It was established that the genetic stability and heritability of the trait through polymerization are high ($H2 = 0.68$-0.74).**
4. Based on experimental data conducted in the conditions of Uzbekistan, it was noted that the effects of complementarity, epistasis, and polymery in F2 generations constituted more than 80% of the phenotypic variation. This proves that the interaction of non-allelic genes has a great influence on the results of selection.
5. The correspondence of the results of statistical analyses ($\chi 2$ test, analysis of variance and correlation) to the theoretically expected ratios ($P > 0.05$) confirmed the reliability and reproducibility of the conducted experiments.
6. Practical recommendations derived from the study:
   - ○ Inclusion of types of interaction of non-allelic genes in breeding programs makes it possible to increase the yield and quality indicators of plants.
   - ○ Identification of complementary gene pairs based on the results of di- and polyhybrid crosses can be an important direction in the creation of new hybrid forms.
   - ○ In genetic modeling, the possibility of predicting phenotypic stability increases by assessing polymeric effects.

In conclusion, these studies on the interaction of non-allelic genes, along with deepening the theoretical foundations of genetics, are of great scientific and practical importance in the fields of applied selection, biotechnology, and genetic engineering.

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