Evaluation of Genetic Diversity in Some Inbred Maize Lines

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Abstract. The genetic value of maize inbred lines is determined by the source of germplasm that they are extracted from, the selection methods used during the successive inbreeding generations, as well as by the combination capacity expressed in the obtained heterosis. In the field of applied genetics, quantifying genetic distance can be considered a tool for predicting heterosis, which serves to the prognostication of hybridization formulas with the best possible performance. The priority objectives that need to be studied in the assessment of genetic diversity are numerous and need to be discussed systematically. Considering the importance and timeliness of research knowledge on phenotypic diversity and genetic inbred lines, our analysis methods pursued the following objectives: evaluating genetic diversity; controlling, conservation, utilizing and maintaining the existing germplasm on a rigorous scientific basis. The biological material used in the conducted research was represented by: 5 inbred lines, considered to be indicators of the heterotic groups, and 12 lines, new creations of the maize breeding team at ARDS Turda. Analysis of additive effects corresponding to quantitative characters is one of the most effective ways to determine the amelioration value of donor sources of favourable genetic material for complementarily perfecting the initial material during recurring selection works. The calculation of additive and non-additive genic effects, allowed the prediction of genetic performance in simple and trilinear hybrids, with maximum chances of confirmation by the competition experiments, for homologation.

Keywords: genetic diversity, inbred lines, maize

Introduction. Phenotypic diversity and genetic diversity in particular of the parental forms is one of the most important causes of heterosis expression. Since the beginning of modern maize improvement it has been observed that heterosis is obtained especially when extreme phenotypes are cross-bred, mainly convarieties like dentiformis and indurata, and that this kind of cross gave a more pronounced heterosis than when botanical origins of the same convarietv were bred (Richey, 1922). Remarkable success was achieved in maize improvement by using heterosis and nucleocytoplasmic phenomena, which made it possible to obtain hybrids with high genetic potential, which yield a harvest of over 150-200 q/ha (Palli, 2008). Obtaining corn genotypes that are superior to the existent ones involves the development of new gene combinations and the number and value of these combinations depend largely on the diversity and the value of the collection that the breeder has available (Săulescu et. al. 2010). The genetic value of maize inbred lines is determined by the source of germplasm that they are extracted from, the selection methods used during the successive inbreeding generations, as well as by the combination capacity expressed in the obtained heterosis. In the field of applied genetics, quantifying genetic distance can be considered a tool for predicting heterosis, which serves to the prognostication of hybridization formulas with the best possible performance.

Aims and objectives. The priority objectives that need to be studied in the assessment of genetic diversity are numerous and need to be discussed systematically. Considering the importance and timeliness of research knowledge on phenotypic diversity and genetic inbred lines, our analysis methods pursued the following objectives:
- evaluating genetic diversity;
- controlling, conservation, utilizing and maintaining the existing germplasm on a rigorous scientific basis;

**Materials and methods.** The biological material used in the conducted research was represented by: 5 inbred lines, considered to be indicators of the heterotic groups, and 12 lines, new creations of the maize breeding team at ARDS Turda. Estimating the diversity has been achieved by calculating the genetic diversity:

- at the level of the homozygous loci for the additive genetic effects ($\hat{g}$)
- for the factorial system

$$\hat{g}_m \text{ or } \hat{g}_n = X_{m..} \cdot X_{..} \quad (Căbulea, 1975)$$


$$X_{m..} = \text{sum of the values in which the paternal parent participates constantly}$$

$$X_{..} = \text{sum of the values in the factorial system}$$

- at the inter and intra-allelic interactions, for the non-additive genetic effects ($\hat{s}_{mn}$)
- for the factorial system

$$\hat{s}_{mn} = X_{mn} - X_{..} - (\hat{g}_m + \hat{g}_n)$$

- for the diallel system

$$\hat{s}_{mn} = \frac{2}{2} \left( \frac{X_{m+n} - X_{m} - X_{n} + X_{mn} + X_{m} + X_{n} + 2X_{m+n} + X_{m+n}}{p-1}(p-2) \right)$$

$\hat{s}_{mn}$ = genetic effect of the interactions of the genes of the two parents ($X_m$ and $X_n$)

$X_{mn}$ or $X_{nm}$ = phenotypic values of the hybrids

The characterization of a genotypic structure as part of a population was performed by bio-metricization and summing quantitative and/or qualitatively multivariable data.

**Results and Discussion.** Data analysis for the three years of experimentation showed that the following lines expressed genes favourable for production: TC344, TC243, TC365; for resistance to breaking and falling: TC314, TC344, TC365, other lines can be used as sources of favorable genes for improvement of other quantitative characters.

Analysis of non-additive genic effects, reflecting the specific gene interactions at intra and interallelic level, revealed a favourable interaction for production of crosses such as TC335x A 635 (9,93); TC335xA 619 (8,87); TC331xF 564 (13,41); TC 331xA 619 (12,25) TC 314xA 619 (11,57).

**Conclusion.** Analysis of additive effects corresponding to quantitative characters is one of the most effective ways to determine the amelioration value of donor sources of favourable genetic material for complementarily perfecting the initial material during recurring selection works.

The calculation of additive and non-additive genic effects, allowed the prediction of genetic performance in simple and trilinear hybrids, with maximum chances of confirmation by the competition experiments, for homologation.

**REFERENCES**