

EVALUATION OF MID-PARENT AND BEST-PARENT HETEROSIS FOR GRAIN YIELD IN SELECTED MAIZE INBRED LINES

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Abstract. *Maize (*Zea mays* L.) is a major crop with global importance for food, feed, and industry. Improving yield through hybrid breeding remains a key objective, and heterosis plays a central role in achieving superior performance. This study evaluated mid-parent heterosis (MPH) and best-parent heterosis (BPH) for grain yield in 19 maize hybrids derived from genetically diverse inbred lines. Field experiments were conducted in 2024 near Cucuruzeni, Orhei district, Republic of Moldova, under chernozem soil conditions and moderate drought stress. A partial diallel mating design was used, and trials were arranged in a randomized incomplete block design with two replications. Yield was measured at harvest, and heterosis was calculated using standard formulas. Results revealed significant variability, with MPH ranging from 33.7% to 76.3% and BPH from 13.3% to 71.6%. The hybrid 2110 × 2126 showed the highest yield and BPH, while 2132 × 2127 had the highest MPH. The findings confirm the role of non-additive gene effects and highlight promising parental combinations for future hybrid development.*

Keywords: *best-parent heterosis, grain yield, inbred lines, maize, mid-parent heterosis.*

INTRODUCTION

Maize (*Zea mays* L.) holds a position of major importance in global agriculture, serving as a staple food crop, a key component in animal feed, and a valuable raw material for numerous industries [1]. As one of the most widely cultivated cereals worldwide, maize plays a fundamental role in agricultural systems, rural livelihoods, and agricultural economies in both developed and developing countries. Its versatility and adaptability across diverse agroecological zones make it a cornerstone of agricultural production, with critical implications for food security and sustainable development [2,3].

Maize breeding programs have made significant progress in recent decades, evolving from traditional selection methods to advanced molecular and genomic techniques [4,5]. The integration of marker-assisted selection, genomic selection,

and gene editing technologies has substantially increased the precision and efficiency of breeding processes [6,7]. These innovations have enabled the development of maize varieties with enhanced productivity, improved tolerance to stress, greater nutrient use efficiency, and increased resistance to diseases and pests [8,9].

Currently, yield improvement in maize is primarily achieved by exploiting the phenomenon of heterosis, which arises from crosses between genetically distinct inbred lines, typically from divergent heterotic groups [4]. Heterosis, or hybrid vigor, refers to the superior performance of hybrids compared to their parental lines. This superiority can manifest in traits such as vigor, disease resistance, and yield. The expression of heterosis in F_1 hybrids is commonly assessed relative to the mid-parent value (mid-parent heterosis, MPH) or the best parent (best-parent heterosis, BPH) [3,4]. These evaluations are labor-intensive and are conducted continuously at all stages of breeding material assessment.

The genetic basis of heterosis is complex, involving additive, dominance, and epistatic gene interactions. While the dominance hypothesis attributes heterosis to the masking of deleterious recessive alleles, the overdominance and epistasis models suggest that specific allele combinations at individual or interacting loci contribute to superior hybrid performance [10]. Identifying parental lines that exhibit strong combining ability is thus critical for maximizing heterotic gains in breeding pipelines [11].

In this context, evaluating MPH and BPH provides valuable insights into the potential of new inbred lines to contribute to superior hybrid performance. Such assessments support the selection of elite parental combinations for further testing and commercialization. The objective of this study was to evaluate mid-parent and best-parent heterosis for grain yield in a set of maize hybrids derived from diverse inbred lines, with the aim of identifying promising crosses for inclusion in future hybrid development programs.

MATERIALS AND METHODS

The experiments were conducted in 2024 on an experimental field near the village of Cucuruzeni, Orhei District, at the farm SRL Pleurotis. The area is characterized by a hilly landscape typical of the central region of the Republic of Moldova, with soil conditions favorable for agricultural experimentation. The predominant soil type is chernozem. The research was carried out under climatic conditions marked by above-average temperatures and a water deficit during the critical growth stages of the maize crop.

The biological material consisted of 28 maize inbred lines, which were crossed in a partial diallel mating scheme. Sowing was carried out in two replications, using an incomplete randomized block design. In this article, we

present results only for 19 hybrid combinations that exhibited a heterosis effect exceeding 30%, a threshold commonly used by breeders for assigning lines to heterotic groups [12].

In the experimental field, standard agronomic practices for maize cultivation were applied to ensure optimal plant development under controlled conditions. The evaluation of reproductive heterosis was based on yield analysis at harvest.

MPH and BPH were calculated using standard formulas:

$$MPH (\%) = \frac{F_1 - MP}{MP} \times 100,$$

$$BPH (\%) = \frac{F_1 - BP}{BP} \times 100$$

where

F_1 = hybrid yield, MP = mid-parent mean, and BP = best-parent yield.

All collected data were processed and statistically analyzed using the R environment [13]

RESULTS AND DISCUSSIONS

The grain yield analysis of the 19 maize hybrids revealed a wide range of performance across combinations, reflecting both the diversity of the parental lines and the varying degrees of hybrid vigor. Hybrid yields ranged from 3407.7 kg/ha to 6134.4 kg/ha, with substantial differences in mid-parent and best-parent heterosis values (

Tabel 1). This variation highlights the influence of genetic distance and complementarity between specific parental lines.

The cross between inbred lines 2110 × 2126 recorded the highest hybrid yield (6134.4 kg/ha) and one of the most significant heterotic responses, with a mid-parent heterosis (MPH) of 71.8% and best-parent heterosis (BPH) of 71.6%. This near-equal expression of MPH and BPH suggests not only high hybrid performance but also strong dominance and potential overdominance effects between these two lines.

Similarly, the combination 2132×2127 exhibited the highest MPH (76.3%), though the best-parent heterosis was more moderate at 38.6%. The strong MPH in this case indicates that the hybrid significantly exceeded the average of its parents, despite one of them (2127) having a relatively low yield potential. Such hybrids can be considered promising for exploiting heterosis through complementary gene action, even when one parent is agronomically weaker.

Several other hybrids displayed consistently high heterotic effects:

2133 × 2126 showed an MPH of 65.0% and a BPH of 55.7%.

2108 × 2112 produced 6055.2 kg/ha with a BPH of 62.2%.

2108 × 2133 achieved a respectable 5344.3 kg/ha and BPH of 46.1%.

These combinations suggest that certain inbred lines — particularly 2108,

2110, and 2133 — possess good general combining ability (GCA) and may serve as recurrent parents in future hybrid development.

Conversely, hybrids such as 2135 × 2134 and 2127 × 2128 performed below expectations, with both relatively low yield and heterosis (BPH of 36.5% and 14.0%, respectively). These cases may reflect poor genetic complementation or limited dominance interactions, reinforcing the necessity of pre-screening inbred lines not only for per se performance, but also for combining ability.

Table 1. Grain yield and heterosis values for 19 maize hybrids derived from selected inbred lines.

Female line ID	Male line ID	Hybrid Yield, kg/ha	Female Mean, kg/ha	Male Mean, kg/ha	Mid-Parent Mean, kg/ha	MPH (%)	BPH (%)
2126	2111	4309.0	3567.4	2880.0	3223.7	33.7	20.8
2133	2112	4646.7	3165.1	3732.6	3448.8	34.7	24.5
2127	2128	3718.4	2249.6	3261.1	2755.3	35.0	14.0
2110	2112	4956.4	3574.3	3732.6	3653.5	35.7	32.8
2128	2136	4427.1	3261.1	3259.5	3260.3	35.8	35.8
2112	2130	4229.7	3732.6	2490.6	3111.6	35.9	13.3
2107	2126	4600.3	3174.9	3567.4	3371.2	36.5	29.0
2135	2134	3407.7	2337.0	2496.5	2416.8	41.0	36.5
2112	2128	4944.1	3732.6	3261.1	3496.9	41.4	32.5
2107	2111	4284.2	3174.9	2880.0	3027.5	41.5	34.9
2135	2112	4393.2	2337.0	3732.6	3034.8	44.8	17.7
2130	2134	3611.7	2490.6	2496.5	2493.6	44.8	44.7
2110	2132	5524.1	3574.3	3929.1	3751.7	47.2	40.6
2131	2128	4229.8	2335.3	3261.1	2798.2	51.2	29.7
2108	2133	5344.3	3657.7	3165.1	3411.4	56.7	46.1
2108	2112	6055.2	3657.7	3732.6	3695.2	63.9	62.2
2133	2126	5555.3	3165.1	3567.4	3366.2	65.0	55.7
2110	2126	6134.4	3574.3	3567.4	3570.9	71.8	71.6
2132	2127	5447.2	3929.1	2249.6	3089.3	76.3	38.6

Interestingly, crosses involving line 2112 revealed varying outcomes. While it contributed to high-yielding hybrids (e.g., 2110 × 2112, 4956.4 kg/ha), its performance also varied depending on the female partner, suggesting a complex interaction between parental backgrounds and direction of the cross.

The substantial variation observed in hybrid yield and heterotic response among the 19 maize crosses confirms the complex genetic interactions that underpin hybrid performance. The results are consistent with previous findings that heterosis, particularly for yield, is strongly influenced by the genetic divergence and combining ability of parental lines [4,8].

The top-performing hybrids, such as 2110 × 2126 and 2132 × 2127, which exhibited over 70% mid-parent heterosis, align with the theory that greater genetic

diversity between parents can enhance heterotic expression [14]. These crosses likely benefited from complementary gene action and dominance effects across multiple loci, as proposed in the dominance and overdominance hypotheses [10].

Overall, the results confirm that high heterosis is not uniformly distributed across combinations, but rather is contingent on the specific pairing of lines. The most promising hybrids identified in this study should be considered for advanced multilocation trials to validate yield stability and adaptability. These findings also reinforce the role of heterosis as a strategic tool in hybrid maize breeding, especially when guided by careful parental selection and combining ability testing.

CONCLUSIONS

This study assessed grain yield performance and heterosis expression in 19 maize hybrids derived from genetically diverse inbred lines. The results demonstrated considerable variability in both mid-parent and best-parent heterosis, with several hybrid combinations exhibiting strong heterotic responses and superior yield performance.

The hybrid 2110 × 2126 was the top performer in terms of yield (6134.4 kg/ha) and best-parent heterosis (71.6%), indicating its potential for commercial cultivation. Similarly, hybrids such as 2132 × 2127, 2133 × 2126, and 2108 × 2112 showed high mid-parent heterosis exceeding 60%, making them promising candidates for advanced yield trials.

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REFERENCES

1. RANUM, P.; PEÑA-ROSAS, J.P.; GARCIA-CASAL, M.N. Global Maize Production, Utilization, and Consumption. *Ann. N. Y. Acad. Sci.* 2014, 1312 (1), pp. 105–112. <https://doi.org/10.1111/nyas.12396>.
2. LIU, J.; FERNIE, A.R.; YAN, J. The Past, Present, and Future of Maize Improvement: Domestication, Genomics, and Functional Genomic Routes toward Crop Enhancement. *Plant Commun.* 2020, 1 (1), pp. 100010. <https://doi.org/10.1016/J.XPLC.2019.100010>.
3. TROYER, A.F. Development of Hybrid Corn and the Seed Corn Industry. *Handb. Maize Genet. Genomics* 2009, pp. 87–114. https://doi.org/10.1007/978-0-387-77863-1_5.
4. HALLAUER, A.R.; CARENA, M.J.; MIRANDA FILHO, J.B. *Quantitative Genetics in Maize Breeding*; Springer New York: New York, NY, 2010; Vol. 6. <https://doi.org/10.1007/978-1-4419-0766-0>.
5. CHAIKAM, V.; PRASANNA, B.M. Doubled Haploid Technology for Rapid and Efficient Maize Breeding. In *Accelerated Plant Breeding, Volume 1*; Springer International Publishing: Cham, 2020; Vol. 1, pp 257–292. https://doi.org/10.1007/978-3-030-41866-3_11.
6. JACKSON, D.; TIAN, F.; ZHANG, Z. Maize Genetics, Genomics, and Sustainable Improvement. *Mol. Breed.* 2022, 42 (1), pp. 1–3. <https://doi.org/10.1007/S11032-021-01266-5/METRICS>.

7. LEMA, M. Marker Assisted Selection in Comparison to Conventional Plant Breeding: Review Article. *Agric. Res. Technol. Open Access J.* 2018, 14 (2), pp. 555914. <https://doi.org/10.19080/ARTOAJ.2018.14.555914>.
8. DUVICK, D.N. The Contribution of Breeding to Yield Advances in Maize (*Zea Mays* L.). *Adv. Agron.* 2005, 86, pp. 83–145. [https://doi.org/10.1016/S0065-2113\(05\)86002-X](https://doi.org/10.1016/S0065-2113(05)86002-X).
9. ASLAM, M.; MAQBOOL, M.A.; CENGIZ, R. *Drought Stress in Maize (Zea Mays L.), Effects, Resistance Mechanisms, Global Achievements and Biological Strategies for Improvement*; SpringerBriefs in Agriculture; Springer International Publishing: Cham, 2015. <https://doi.org/10.1007/978-3-319-25442-5>.
10. BIRCHLER, J.A.; AUGER, D.L.; RIDDLE, N.C. In Search of the Molecular Basis of Heterosis. *Plant Cell* 2003, 15 (10), pp. 2236–2239. <https://doi.org/10.1105/TPC.151030>.
11. HALLAUER, A.R.; RUSSELL, W.A.; LAMKEY, K.R. Corn Breeding. In *Corn and Corn Improvement*; Sprague, G. F., Dudley, J. W., Eds.; American Society of Agronomy, Inc. Crop Science Society of America, Inc. Soil Science Society of America, Inc.: Madison, Wisconsin, USA, 1988; pp 463–564. <https://doi.org/https://doi.org/10.2134/agronmonogr18.3ed.c8>.
12. MUSTEATA, S. 50 de Ani În Serviciul Ameliorării Porumbului Și Producției Semințelor. In *Realizări științifice în ameliorarea porumbului și altor culturi cerealiere. Materialele conferinței științifico – practice cu participare internațională, - 50 ani de activitate a Institutului de Fitotehnie "Porumbeni"*; SPIVACENCO, A., BOROZAN, P., MISTREȚ, S., Eds.; Print-Caro: Pașcani, 2024; pp 13–21.
13. R CORE TEAM. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing: Vienna, Austria 2025. <https://www.r-project.org/>.
14. MELCHINGER, A.E.; LEE, M.; LAMKEY, K.R.; HALLAUER, A.R.; WOODMAN, W.L. Genetic Diversity for Restriction Fragment Length Polymorphisms and Heterosis for Two Diallel Sets of Maize Inbreds. *Theor. Appl. Genet.* 1990, 80 (4), pp. 488–496. <https://doi.org/10.1007/BF00226750>.