Analysis of Linkage on Interaction of Main Aspects (Genotype by Environment Interaction, Stability and Genetic Parameters) of 1000 Kernels in Maize (Zea mays L.)

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Abstract: The assessment of 1000-kernel weight holds significant importance in determining maize grain yield, and elucidating its underlying genetic mechanisms is imperative for enhancing its overall performance. The material for the study consisted of 26 doubled-haploid (DH) maize lines obtained from crossing two cultivars with flint kernels. Lines were planted in the northern part of the Lower Silesia voivodship in Poland over ten years (2013–2022). The 1000-kernel weight was assessed. The purposes of the research were as follows: (1) to assess genotype by environment interaction (GEI by the additive main effects and multiplicative interaction (AMMI) model; (2) the selection of stable DH lines and environment-specific lines; and (3) the estimation of parameters related to additive and additive−additive gene interaction (epistasis). The results indicate the significant effects of genotype and environment, as well as the GEI, on the 1000-kernel weight. Estimates of additive gene action effects were statistically significant in every year of the study, except 2022. Estimates of epistasis (total additive-by-additive interaction) effects for 1000-kernel weight were statistically significant in 2013, 2015, and 2017 (positive effects), as well as in 2018 and 2020 (negative effects). The lines KN07 and KN10 are recommended for further inclusion in the breeding program due to their stability and highest average of 1000-kernel weight.

Keywords: doubled-haploid lines; additive effect; epistasis; maize; AMMI model

1. Introduction

Maize (Zea mays L.) is one of the most important cultivated plants in the world, playing a crucial role in agriculture, the food industry, and biofuel production [1]. Its versatile applications, high nutritional value, and ease of cultivation make maize a significant staple in people’s lives worldwide [2–4]. It serves as a primary source of food for populations in many countries, especially in South and Central America, Africa, and Asia [5]. Due to its ease of cultivation and adaptability to various environmental conditions, maize remains an indispensable source of calories for millions of people across the globe. It is utilized both as human food and animal feed for livestock [6–8].

Maize is used in the production of many processed products, such as breakfast cereals, corn chips, tortillas, and popcorn [9–11]. It also plays a significant role in biofuel production [12–17]. As a high-energy and nutrient-rich feed, maize is an important component of the diet for livestock animals, such as cows, pigs, and poultry [18,19].
Furthermore, it provides essential nutrients to the animals, aiding in their efficient development and growth. Hence, this crop plant plays a significant role in the economy of many countries, especially in agriculture [20–22].

Yield, as a quantitative trait, is determined by several factors: genotype, environment, and other traits. The trait that has the greatest impact on maize grain yield is the 1000-kernel weight [23]. The size and weight of maize kernels are closely related to quality, yield, and resistance to biotic and abiotic stresses [24,25]. The 1000-kernel weight can be one of the key predictive indicators of maize yield in the field [26–29].

The main factors influencing the 1000-kernel weight are genetics and environmental conditions [30–33]. Weather and soil conditions play a crucial role in yield and kernel weight [34]. Effective agronomy practices, such as proper fertilization, pest and disease control, as well as optimal planting density and timing, can influence kernels’ weight growth [35–38].

Scientific research indicates that a high amount of 1000-kernel weight in maize can result in higher yields [39–50]. The use of mathematical models based on statistical theory and data analysis is another method for predicting the impact of 1000-kernel weight on maize yield [51,52].

In agriculture, the success of maize cultivation is closely linked to the interaction between the genotype of a given variety and the environmental conditions in which it is grown [53–56]. Understanding the impact of this genotype–environment interaction (GEI) on the 1000-kernel weight of maize is a crucial concern for breeders and farmers who seek to optimize the yield and quality of this important crop [57–61]. The impact of GEI on the 1000-kernel weight of maize poses a challenge for breeders and farmers as it requires selecting suitable varieties for specific growing environments. Striving for maximum yield and crop quality necessitates an understanding of how different varieties respond to various environmental conditions and how to optimize these interactions.

A very important aspect is the evaluation of GEI, as it is an integral source of variation that includes genotype and the influence of an environmental factor. This source of variation (GEI) is needed because selected genotypic or environmental variation is insufficient to provide true genotype or environmental information. GEI can be empirically detected and described in terms of various statistical models, derived from the two-factor analysis of the variance model [62–65]. Much more difficult is the study of the biological mechanism of conditioning of the interaction of the GEI [66–70]. Traditional statistical methods (such as linear regression, analysis of variance, and principal component analysis) are often ineffective in understanding and estimating complex yield survey data in multiple environments [6]. As opposed to standard statistical analyses, additive main effects and multiplicative interaction (AMMI) allows simple visual interpretation of GEI [71,72]. All IPCAs that are significant can explain the variation in GEI, while other IPCAs that are not significant are added to the residuals. Measuring GEI is very important to determine an optimum breeding strategy for releasing genotypes with an adequate adaptation to target environments [73,74]. The AMMI model was originally developed for analysis in social sciences and physics [75–78] and later adjusted for research in plant sciences [62,79].

The objectives of this study were as follows: (1) to assess genotype by environment interaction for 1000-kernel weight in doubled-haploid lines of maize (Zea mays L.) grown in the northern part of the Lower Silesia voivodship in Poland by the AMMI model; (2) the selection of DH lines stable through all years of study specific to given environmental conditions; and (3) to estimate the parameters connected with the additive and additive-by-additive interaction (epistasis) gene action.
2. Materials and Methods

2.1. Field Trials

This study was based on a total of 26 doubled-haploid (DH) maize (*Zea mays* L.) lines derived from a cross of two flint grain type cultivars: ES Palazzo and Anjou 258. All DH lines were developed by the in vivo method described by Prigge and Melchinger [80], in which F1 plants of each cross are pollinated by an inducer line, followed by the identification of haploid seeds using an embryo color marker. Chromosome doubling was promoted by colchicine treatment to produce **D0** plants, which were then self-pollinated to produce the **D1** generation. All DH lines were of a flint kernel type. Lines were planted in Nowa Wioska in the northern part of the Lower Silesia voivodship in Poland (51°46′58.7″N, 16°25′43.9″E) over ten years (2013–2022). The study region is a homogeneous environment with no interaction with specific locations in the region under consideration. Total monthly precipitation and average monthly temperature for the years of the experiment are shown in Tables 1 and 2, respectively. The experiments were carried out in a randomized block design with four replications each year on typical grey-brown podzolic soil consisting of coarse sandy soil, shallowly deposited on light loam. The same *nitrogenium–phosphorus–kalium* (NPK) fertilization was applied throughout the experimental field: 100 kg N ha⁻¹ in the form of urea; 80 kg P₂O₅ ha⁻¹ in the form of granular triple superphosphate 46% P₂O₅; and 120 kg K₂O ha⁻¹ in the form of 60% potassium salt. Each experimental plot consisted of 4 m long rows with 0.70 m inter-row spacing, 25 cm plant-to-plant spacing, and 14 plants per row. The maize sowing in each of the study years was performed during the third decade of April, while the harvest was performed when the maize grain was mature. Standard agronomic practices were followed during the trials. Maize kernels were harvested using a Wintersteiger combine. Twenty cobs were randomly selected from each replicate of each DH line. The 1000-kernel weight was assessed. The characteristics of the 26 DH lines studied in terms of the main agronomic traits (plant height, flowering day, and grain yield) in each year of the study are shown in Table 3.

**Table 1.** Total monthly rainfall (in mm) recorded in Krościna Mała, the nearest weather station located from the study site.

<table>
<thead>
<tr>
<th>Year</th>
<th>April</th>
<th>May</th>
<th>June</th>
<th>July</th>
<th>August</th>
<th>September</th>
<th>October</th>
<th>November</th>
</tr>
</thead>
<tbody>
<tr>
<td>2013</td>
<td>32</td>
<td>89</td>
<td>108</td>
<td>47</td>
<td>42</td>
<td>111</td>
<td>13</td>
<td>26</td>
</tr>
<tr>
<td>2014</td>
<td>42</td>
<td>86</td>
<td>30</td>
<td>90</td>
<td>83</td>
<td>128</td>
<td>46</td>
<td>19</td>
</tr>
<tr>
<td>2015</td>
<td>27</td>
<td>35</td>
<td>58</td>
<td>41</td>
<td>14</td>
<td>38</td>
<td>39</td>
<td>54</td>
</tr>
<tr>
<td>2016</td>
<td>38</td>
<td>50</td>
<td>60</td>
<td>97</td>
<td>25</td>
<td>45</td>
<td>81</td>
<td>40</td>
</tr>
<tr>
<td>2017</td>
<td>47</td>
<td>27</td>
<td>80</td>
<td>83</td>
<td>69</td>
<td>70</td>
<td>78</td>
<td>37</td>
</tr>
<tr>
<td>2018</td>
<td>17</td>
<td>62</td>
<td>81</td>
<td>64</td>
<td>12</td>
<td>62</td>
<td>34</td>
<td>8</td>
</tr>
<tr>
<td>2019</td>
<td>14</td>
<td>56</td>
<td>19</td>
<td>44</td>
<td>40</td>
<td>55</td>
<td>17</td>
<td>38</td>
</tr>
<tr>
<td>2020</td>
<td>11</td>
<td>75</td>
<td>159</td>
<td>55</td>
<td>69</td>
<td>72</td>
<td>84</td>
<td>19</td>
</tr>
<tr>
<td>2021</td>
<td>43</td>
<td>84</td>
<td>39</td>
<td>101</td>
<td>95</td>
<td>17</td>
<td>10</td>
<td>29</td>
</tr>
<tr>
<td>2022</td>
<td>42</td>
<td>31</td>
<td>69</td>
<td>59</td>
<td>123</td>
<td>69</td>
<td>23</td>
<td>24</td>
</tr>
</tbody>
</table>

The meteorological data provided from the Research Centre for Cultivar Testing meteorological station located in Krościna Mała.

**Table 2.** Mean monthly air temperature (in °C) at an altitude of 2 m recorded in Krościna Mała, the nearest meteorological station located from the study site.

<table>
<thead>
<tr>
<th>Year</th>
<th>April</th>
<th>May</th>
<th>June</th>
<th>July</th>
<th>August</th>
<th>September</th>
<th>October</th>
<th>November</th>
</tr>
</thead>
<tbody>
<tr>
<td>2013</td>
<td>9.1</td>
<td>14.6</td>
<td>17.4</td>
<td>20.4</td>
<td>18.9</td>
<td>12.5</td>
<td>10.5</td>
<td>5.2</td>
</tr>
<tr>
<td>2014</td>
<td>10.8</td>
<td>13.5</td>
<td>16.4</td>
<td>21.3</td>
<td>18.4</td>
<td>15.9</td>
<td>11.7</td>
<td>6.8</td>
</tr>
<tr>
<td>2015</td>
<td>8.8</td>
<td>13.7</td>
<td>16.6</td>
<td>20.7</td>
<td>20.9</td>
<td>14.9</td>
<td>8.4</td>
<td>7.2</td>
</tr>
<tr>
<td>2016</td>
<td>9.1</td>
<td>14.9</td>
<td>18.8</td>
<td>19.8</td>
<td>18.3</td>
<td>16.8</td>
<td>8.3</td>
<td>3.9</td>
</tr>
<tr>
<td>2017</td>
<td>8.4</td>
<td>14.3</td>
<td>18.7</td>
<td>19.0</td>
<td>19.6</td>
<td>13.6</td>
<td>11.3</td>
<td>5.7</td>
</tr>
<tr>
<td>2018</td>
<td>14.0</td>
<td>16.5</td>
<td>18.5</td>
<td>19.9</td>
<td>21.5</td>
<td>16.3</td>
<td>11.7</td>
<td>5.5</td>
</tr>
</tbody>
</table>
Table 3. Characterization of 26 DH lines in terms of the main agronomic traits (plant height, flowering day, and grain yield) in each year of the study presented as a range of mean values for the studied lines.

<table>
<thead>
<tr>
<th>Year</th>
<th>Plant Height (cm)</th>
<th>Day to Flowering (days)</th>
<th>Grain Yield (t ha⁻¹)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Min</td>
<td>Max</td>
<td>Min</td>
</tr>
<tr>
<td>2013</td>
<td>130</td>
<td>274</td>
<td>84.5</td>
</tr>
<tr>
<td>2014</td>
<td>149</td>
<td>269</td>
<td>88.5</td>
</tr>
<tr>
<td>2015</td>
<td>127</td>
<td>281</td>
<td>85.6</td>
</tr>
<tr>
<td>2016</td>
<td>125</td>
<td>277</td>
<td>85.1</td>
</tr>
<tr>
<td>2017</td>
<td>150</td>
<td>246</td>
<td>77.6</td>
</tr>
<tr>
<td>2018</td>
<td>135</td>
<td>273</td>
<td>88.2</td>
</tr>
<tr>
<td>2019</td>
<td>161</td>
<td>264</td>
<td>90.7</td>
</tr>
<tr>
<td>2020</td>
<td>145</td>
<td>257</td>
<td>89.7</td>
</tr>
<tr>
<td>2021</td>
<td>195</td>
<td>264</td>
<td>90.1</td>
</tr>
<tr>
<td>2022</td>
<td>166</td>
<td>268</td>
<td>89.5</td>
</tr>
</tbody>
</table>

2.2. Statistical Analysis

Obtained data for the 1000-kernel weight were analyzed using the additive main effects and multiplicative interaction (AMMI) model [76,81] by:

\[ y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^{N} \lambda_n y_{gn} \delta_{en} + Q_{ge}, \]

where \( y_{ge} \) is the value of the mean of 1000-kernel weight of genotype \( g \) in year \( e \); \( \mu \) is the general mean; \( \alpha_g \) is the genotypic mean deviations; \( \beta_e \) is the year mean deviations; \( N \) is the number of PCA axis retained in the adjusted model; \( \lambda_n \) is the eigenvalue of the PCA axis \( n \); \( y_{gn} \) is the genotype score for PCA axis \( n \); \( \delta_{en} \) is the coordinate of the eigenvector for the environmental score for PCA axis \( n \); \( Q_{ge} \) is the residual, including the AMMI noise and pooled experimental error. The significance level of PCA analysis was tested using an \( F \)-test according to Gollob [78]. The stability of the DH lines was assessed by the AMMI stability value (ASV) [82]:

\[ ASV = \sqrt{\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA_1)^2 + (IPCA_2)^2}, \]

where \( SS_{IPCA1} \) and \( SS_{IPCA2} \) are the sums of squares for IPCA1 and IPCA2, respectively, and the IPCA1 and IPCA2 scores are the genotypic scores in the AMMI model. ASV with the smallest possible values indicated a more stable genotype.

The genotype selection index (GSI) was calculated for each genotype that incorporates both the mean of trait and the ASV index in single criteria (GSI\(_i\)) as follows [83]:

\[ GSI_i = RM_i + RA_i, \]

where \( RM_i \) is rank of the trait mean (from maximal to minimal) for the \( i \)-th genotype, and \( RA_i \) is the rank of the ASV for the \( i \)-th genotype.

The relationships between the 1000-kernel weight observed in different years of the study were assessed by Pearson correlation coefficients based on genotypic averages.

Estimation of the additive gene effect and additive-by-additive interaction of homozygous loci (epistasis) effect on the basis of phenotypic observations requires identification of groups of extreme DH lines, i.e., lines with the minimal and maximal expres-
sion of the observed trait [84]. The group of minimal (maximal) lines consists of the lines which contain, theoretically, only alleles reducing (increasing) the value of the trait. The groups of extreme lines were identified by the quantile method. The total additive effect, \(a\), of all genes controlling the trait and the total additive-by-additive interaction effect, \(aa\), may be estimated by the following formulas [85,86]:

\[ a = \frac{1}{2} (L_{max} - L_{min}) \]  

and

\[ aa = \frac{1}{2} (L_{max} + L_{min}) - L, \]

where \(L_{max}\) and \(L_{min}\) are the means for the extreme groups of DH lines, respectively, and \(L\) is the mean value for all DH lines. Test statistics for verifying hypotheses about the significance of genetic parameters are given by the following:

\[ F_a = \frac{MS_a}{MS_e} \]  
\[ F_{aa} = \frac{MS_{aa}}{MS_e} \]

where \(MS_a\) is the mean square for parameter \(a\), \(MS_{aa}\) is the mean square for epistasis \(aa\), and \(MS_e\) is the mean square for residual.

All analyses were performed using the GenStat v. 23 statistical software package [87].

3. Results

All three sources of variation were highly significant. The sum of squares for GEI represented 33.79% of the total, and this factor had the highest effect on 1000-kernel weight (Table 4). The effect of environments (years) explained 14.10%, while the effect of genotypes explained 9.69% of the total 1000-kernel weight variation. The values of the first three principal components were also highly significant. Together, the three principal components of GEI accounted for 68.59% of the total effect it had on the variation of 1000-kernel weight. The first principal component (IPCA 1) accounted for 33.11% of the variation caused by interaction, while IPCA 2 and IPCA 3 accounted for 19.06 and 16.42%, respectively (Figure 1, Table 4).

Table 4. Analysis of variance of main effects and interactions for 1000-kernel weight of 26 maize genotypes (doubled-haploid lines) and variability explained (in %).

<table>
<thead>
<tr>
<th>Source of Variation</th>
<th>d.f.</th>
<th>Sum of Squares</th>
<th>Mean Squares</th>
<th>F-Statistic</th>
<th>Variability Explained (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total</td>
<td>1039</td>
<td>1,368,792</td>
<td>1317</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Treatments</td>
<td>259</td>
<td>652,863</td>
<td>2521</td>
<td>3.38 ***</td>
<td>47.70</td>
</tr>
<tr>
<td>Genotypes, G</td>
<td>25</td>
<td>132,656</td>
<td>5306</td>
<td>7.12 ***</td>
<td>9.69</td>
</tr>
<tr>
<td>Environments, E</td>
<td>9</td>
<td>192,945</td>
<td>21,438</td>
<td>28.76 ***</td>
<td>14.10</td>
</tr>
<tr>
<td>Block/Environment</td>
<td>30</td>
<td>20,748</td>
<td>692</td>
<td>0.93</td>
<td>1.52</td>
</tr>
<tr>
<td>GEIs</td>
<td>225</td>
<td>462,458</td>
<td>2055</td>
<td>2.76 ***</td>
<td>33.79</td>
</tr>
<tr>
<td>IPCA 1</td>
<td>33</td>
<td>153,121</td>
<td>4640</td>
<td>6.23 ***</td>
<td>33.11</td>
</tr>
<tr>
<td>IPCA 2</td>
<td>31</td>
<td>88,129</td>
<td>2843</td>
<td>3.81 ***</td>
<td>19.06</td>
</tr>
<tr>
<td>IPCA 3</td>
<td>29</td>
<td>75,927</td>
<td>2618</td>
<td>3.51 ***</td>
<td>16.42</td>
</tr>
<tr>
<td>Residuals</td>
<td>132</td>
<td>145,281</td>
<td>1101</td>
<td>1.48 ***</td>
<td>31.41</td>
</tr>
<tr>
<td>Error</td>
<td>750</td>
<td>558,985</td>
<td>745</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

D.f.—the number of degrees of freedom; *** \(p < 0.001\).
The results of the field trials demonstrated the impact of weather conditions, environment (year), and genotypes on the 1000-kernel weight of the maize doubled-haploid lines. The 1000-kernel weight of the tested DH lines varied from 275.1 g (for KN13 in 2013) to 433.0 g (for KN04 in 2015) throughout the ten years, with an average of 343.7 g (Table 5, Figure 2). The average 1000-kernel weight per genotype varied from 330.9 g (for KN08) to 356.5 g (for KN06) (Table 5, Figure 3). The relationships between the DH lines are presented in the form of a dendrogram (Figure 3), in which three clusters were clearly distinguished. The first cluster contains five DH lines: KN22, KN23, KN24, KN25, and KN26; the second (eight DH lines) cluster contains: KN01, KN10, KN11, KN12, KN13, KN14, KN15, and KN17; and the third cluster contains the other 13 DH lines (Figure 3). The average 1000-kernel weight per year also varied from 322.0 g in 2017 to 360.0 g in 2015 (Table 5, Figure 4). The relationships among years of study are presented in the form of a dendrogram (Figure 4), in which three clusters were clearly distinguished. The first cluster contains two years, namely 2019 and 2020; the second (three years) cluster contains 2013, 2014, and 2017; and the third cluster contains the other five years of study, namely 2015, 2016, 2018, 2021, and 2022 (Figure 4). The highest variability (the coefficient of variation is equal to 15.50%) in the 1000-kernel weight of maize was observed in the first year of conducting the study (2013). In contrast, the lowest variability in the 1000-kernel weight was observed in 2020 and 2022 (7.27% and 7.65%, respectively) (Figure 5).
Table 5. Average 1000-kernel weight (g), for genotypes and years, principal component analysis values, AMMI stability value (ASV), rank of the AMMI stability value (RA), rank of trait mean (RM), and genotype selection index (GSI) of tested maize genotypes.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Years</th>
<th>IPCA g1</th>
<th>IPCA g2</th>
<th>IPCA g3</th>
<th>RM</th>
<th>ASV</th>
<th>RA</th>
<th>GSI</th>
</tr>
</thead>
<tbody>
<tr>
<td>KN01</td>
<td>2013</td>
<td>328.8</td>
<td>339.6</td>
<td>348.2</td>
<td>327.9</td>
<td>321.1</td>
<td>359.4</td>
<td>322.6</td>
</tr>
<tr>
<td></td>
<td>2014</td>
<td>345.1</td>
<td>336.3</td>
<td>340.1</td>
<td>365.9</td>
<td>321.1</td>
<td>337.1</td>
<td>352.6</td>
</tr>
<tr>
<td></td>
<td>2015</td>
<td>359.7</td>
<td>363.8</td>
<td>370.1</td>
<td>370.3</td>
<td>286.3</td>
<td>356.0</td>
<td>324.5</td>
</tr>
<tr>
<td></td>
<td>2016</td>
<td>349.7</td>
<td>353.2</td>
<td>433.0</td>
<td>332.3</td>
<td>306.8</td>
<td>356.6</td>
<td>344.9</td>
</tr>
<tr>
<td></td>
<td>2017</td>
<td>320.8</td>
<td>333.0</td>
<td>406.2</td>
<td>352.2</td>
<td>297.7</td>
<td>335.1</td>
<td>335.1</td>
</tr>
<tr>
<td></td>
<td>2018</td>
<td>332.9</td>
<td>371.3</td>
<td>398.8</td>
<td>370.3</td>
<td>325.3</td>
<td>369.5</td>
<td>337.8</td>
</tr>
<tr>
<td></td>
<td>2019</td>
<td>335.1</td>
<td>374.5</td>
<td>377.3</td>
<td>351.3</td>
<td>329.5</td>
<td>349.9</td>
<td>335.7</td>
</tr>
<tr>
<td></td>
<td>2020</td>
<td>282.9</td>
<td>322.7</td>
<td>345.4</td>
<td>370.3</td>
<td>328.9</td>
<td>354.9</td>
<td>336.5</td>
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<td>295.1</td>
<td>364.8</td>
<td>368.9</td>
<td>355.7</td>
<td>302.8</td>
<td>347.4</td>
<td>344.4</td>
</tr>
<tr>
<td></td>
<td>2022</td>
<td>339.1</td>
<td>365.5</td>
<td>360.4</td>
<td>369.1</td>
<td>314.0</td>
<td>352.8</td>
<td>345.3</td>
</tr>
<tr>
<td></td>
<td>Mean</td>
<td>332.2</td>
<td>355.6</td>
<td>360.0</td>
<td>347.4</td>
<td>322.0</td>
<td>356.1</td>
<td>347.4</td>
</tr>
</tbody>
</table>

**Figure 2.** The heatmaps diagram shows the 1000-kernel weight of 26 doubled-haploid lines in ten years of study. Red indicates lower the 1000-kernel weight and white indicates higher the 1000-kernel weight.
**Figure 3.** The heatmaps diagram of 26 doubled-haploid lines similarity estimated on the basis of 1000-kernel weight using Euclidean similarity. The DH lines were grouped using the unweighted pair group method with arithmetic mean (UPGMA).

**Figure 4.** The heatmap diagram of similarity of ten years of research estimated on the basis of 1000-kernel weight using Euclidean similarity. The years were grouped using the unweighted pair group method with arithmetic means (UPGMA).
The AMMI2 biplot (Figure 1) shows the stability of genotypes (lines) and environments (years), as well as specific GEIs. Among the tested DH lines, the line KN12 had the highest IPCA 1 value of 4.431, while the lowest value of IPCA 1 was –7.709 for KN24 (Table 5, Figures 1 and 6). IPCA 1 values for years (IPCA e1) varied from –8.782 (in 2013) to 5.339 (in 2015). IPCA 2 values for genotypes (IPCA g2) varied from –5.229 (for line KN04) to 4.722 (for line 7) (Table 5, Figures 1 and 7). Meanwhile, IPCA g3 varied from –4.964 (for line KN23) to 4.438 (for line KN17) (Table 5). IPCA e2 values varied from –8.047 (in 2015) to 4.354 (in 2017) (Table 5, Figures 1 and 7). However, IPCA e3 values varied from –5213 (in 2015) to 6.259 (in 2016) (Table 5). The stability of the tested lines can be assessed by the biplot for 1000-kernel weight (Figure 2). The DH lines responded differently to climatic conditions during the test years. The lines KN03 and KN04 adapted in environments with similar conditions to those in 2015 (a very dry year) and did not adapt in 2017. Line KN09 adapted in environments with similar conditions to these in 2018 (a very hot year) and did not adapt in 2013. Line KN21 adapted in environments with similar conditions to those in years 2014 and 2020 (the rainiest years among those considered in the experiment) and did not adapt in 2015 (Figures 1 and 6). ASV revealed variations in 1000-kernel weight stability among the 26 DH lines (Table 5). According to Purchase et al. [82], a stable line is defined as one with an ASV close to zero. Consequently, the lines KN16 with an ASV of 0.544, KN01 with an ASV of 0.617, KN15 with an ASV of 0.967, and KN10 with an ASV of 0.998 were the most stable (Table 5, Figures 1 and 6), while the lines KN24 (ASV equal to 13.419) and KN26 (ASV equal to 11.011) were the least stable (Table 5, Figures 1 and 6). Lines KN07 and KN10, with a high average 1000-kernel weight (354.1 g and 346.6 g, respectively) and the ASV equal to 1.142 and 0.998, respectively, had the best genotype selection indices (7 and 13, respectively) (Table 5). However, the lines KN08 and KN25 had the worst genotype selection indices (43 and 40, respectively) (Table 5).
Figure 6. Biplot for the primary component of interaction (IPC1) and the average 1000-kernel weight (g). Vertical line at the center of biplot is the general grand mean.

Figure 7. Biplot for the secondary component of interaction (IPC2) and the average 1000-kernel weight (g). Vertical line at the center of biplot is the general grand mean.
The negatively statistically significant correlation coefficients for 1000-kernel weight were observed for 2016 and 2017 ($r = -0.65$), as well as for 2020 and 2021 ($r = -0.44$) (Figure 8).

Gene additive effects were significant in every year of the study, except 2022 (Table 6). Epistasis (total additive-by-additive interaction) effects for 1000-kernel weight was significant in 2013, 2015, and 2017 (positive effects), as well as in 2018 and 2020 (negative effects) (Table 6).

**Table 6.** Estimates of the total additive and epistasis (additive-by-additive interaction) effects for 1000-kernel weight.

<table>
<thead>
<tr>
<th>Year</th>
<th>The Total Additive Effect, $a$</th>
<th>The Total Additive-by-Additive Interaction Effect, $aa$</th>
</tr>
</thead>
<tbody>
<tr>
<td>2013</td>
<td>67.95 ***</td>
<td>10.85 ***</td>
</tr>
<tr>
<td>2014</td>
<td>29.70 *</td>
<td>-3.20</td>
</tr>
<tr>
<td>2015</td>
<td>58.70 ***</td>
<td>14.30 ***</td>
</tr>
<tr>
<td>2016</td>
<td>41.25 *</td>
<td>-1.15</td>
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<tr>
<td>2017</td>
<td>42.75 **</td>
<td>7.05 **</td>
</tr>
<tr>
<td>2018</td>
<td>38.40 *</td>
<td>-5.00 *</td>
</tr>
<tr>
<td>2019</td>
<td>32.15 *</td>
<td>-2.95</td>
</tr>
<tr>
<td>2020</td>
<td>29.95 *</td>
<td>-6.35 *</td>
</tr>
<tr>
<td>2021</td>
<td>30.40 *</td>
<td>-1.80</td>
</tr>
<tr>
<td>2022</td>
<td>22.70</td>
<td>-2.90</td>
</tr>
</tbody>
</table>

* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.

4. Discussion

The measurement known as the 1000-kernel weight serves as a significant indicator of seed size. Seed dimensions, along with the 1000-kernel weight, exhibit notable variability across different crops, among various varieties of the same crop, and even within identical varieties from year to year or from one field to another. This inherent diversity in seed size directly impacts the number of seeds contained within a pound or a bushel of seed, leading to substantial fluctuations in plant density. In light of this variability, pro-
Producers can employ the 1000-kernel weight as a pivotal parameter. Its application facilitates the precise adjustment of seeding rates, the calibration of seed drills, and the estimation of losses incurred due to shattering and combine operations, thus enhancing the efficiency and accuracy of agricultural practices. In agricultural practice, regular monitoring of maize development and appropriate adjustment of agro-technical practices based on observed conditions are important. The impact of 1000-kernel weight on maize yield is a complex process that depends on numerous factors; hence, farmers should be aware and responsible for optimal management of their crops.

In the present investigation, analysis was undertaken to assess the 1000-kernel weight within a population of doubled-haploid lines of maize under varying environmental conditions. The findings elucidated a marked phenotypic diversity in the 1000-kernel weight among the doubled-haploid lines. Notably, within this study, the statistical analysis indicated the profound significance of three distinct sources of variation in the observed 1000-kernel weight data. Similar results were obtained by Wang et al. [1] and Peng et al. [88]. Wang et al. [1] analyzed 400 recombinant inbred lines; however, Peng et al. [88] analyzed yield components and kernel-related traits in two F2:3 populations of maize in six environments. Similar, significant genotype and environmental effects, as well as GEI effect with respect to seed yield, were obtained by Bocianowski et al. [89], analyzing 32 maize genotypes (13 hybrids and their 19 parental lines) evaluated in four environments (two locations in two years) in Western Poland.

In the present investigation, the source of variation with the greatest impact on 1000-kernel weight was GEI (33.79%). Similarly, the greatest effect of GEI on 1000-kernel weight was obtained by Mousavi et al. [59] studying corn hybrids. Different results were obtained by Mousavi et al. [52,90]. In their study of maize hybrids, the GEI had the smallest (but statistically significant) effect on the 1000-kernel weight. In these studies, DH lines showed the smallest percentage of explained variation (3.34%) of the observed trait. Similar results were obtained by Matin et al. [91] studying 23 genotypes (twenty-one single cross hybrids and two check hybrids) of maize.

The AMMI model was not only used to assess GEI. In maize, the AMMI model was used to analyze the response of dry matter of plant yield and harvest index for four soil tillage methods over 12 years of research. In addition, the AMMI model was used to evaluate the four NP fertilizer placement depths through six-year interaction on the number of maize plants after emergence.

The AMMI model is very widely used to analyze GEI in many plant species, including barley [92], pea [93], oilseed rape, sugar beet, timothy, triticale, and wheat.

Within the realm of plant breeding, a critical facet revolves around the categorization of studied genotypes concerning their stability and adaptability to particular environmental parameters. The identification of genotypes ideally suited for specific environmental contexts becomes feasible through meticulous AMMI analyses, enabling the precise estimation of the interaction effects of a given genotype within each distinct environment. In this research, four DH-specific lines were selected that adapted in environments with specific conditions. The lines are as follows: KN03, KN04 (in 2015—a very dry year), KN09 (in 2018—a very hot year), and KN21 (in 2014 and 2020—the rainiest years among those considered in the experiment). The lack of a significant correlation between the 1000-kernel weight observed in different years of the study does not facilitate decision making when selecting the tested DH lines for further breeding studies. In only two of the forty-five cases were significant correlation coefficients observed. It should be emphasized that the negative correlation is the result of GEI. High genotype stability is linked with the AMMI stability value. The results obtained made it possible to distinguish four stable lines: KN16 (ASV = 0.544), KN01 (ASV = 0.617), KN15 (ASV = 0.967), and KN10 (ASV = 0.998). Two DH lines (KN24 and KN26) were not stable and were not adapted in environments with specific conditions, which disqualifies them from inclusion in any breeding programs. The lines KN07 and KN10 are recommended for
further inclusion in the breeding program because of their stability and because they had the highest average of 1000-kernel weight.

Assessment of genetic parameters has a considerable role in maize breeding [94–97]. The result reveals the importance of additive gene effects for the weight of 1000 kernels in nine of the ten years of the study. In contrast, epistatic gene interaction effects were significant in five of the ten years of the study. The existence of epistasis is important in any breeding program. The presence of epistasis exhibited a pronounced significance, concomitant with an additive effect that lacked statistical significance, observed across multiple years (2013, 2015, 2017, 2018, and 2020) with regard to the 1000-kernel weight. This observation suggests that the manifestation of this trait is likely under the control of genes characterized by subtle individual impacts yet exerts robust interactions in a gene–gene context. The encompassing epistatic effects elucidated by these models serve to underscore the intricate and polygenic genetic underpinnings inherent in these traits [98]. Epistatic phenomena have been substantiated across a spectrum of traits within diverse species, including barley, sugar beet, rice [99], rapeseed, and common wheat [100].

5. Conclusions

The 1000-kernel weight wields a direct and discernible influence upon the overall yield of this pivotal crop. Within the realm of modern agricultural practices, a comprehensive acknowledgment of these intricate interrelationships becomes imperative to not only bolster crop output but also to judiciously steward finite natural resources, all while efficaciously satiating the escalating global populace. It is herein underscored that the relentless pursuit of scientific inquiry coupled with the continual evolution of agrarian technologies stands as the linchpin towards realizing this overarching aspiration. A poignant repository of insights can be gleaned from an incisive examination into the intricate tapestry of genotype–environment interaction, together with the meticulous dissection of genetic parameters. The present work demonstrated that the lines KN07 and KN10 are recommended for further inclusion in the breeding program because their stability and the highest averages of 1000-kernel weight. Four DH lines are recommended for breeding programs in specific weather conditions. The KN03 and KN04 lines have very good 1000-kernel weight values under water-deficient conditions; the same can be said for the KN09 line under drought conditions and the KN21 line under conditions characterized by high humidity. The study of DH lines is characterized by significant parameters related to the additive effect and epistasis, which indicates the consolidation of the observed feature in the subsequent years of the study. These results, meticulously harvested from rigorous scientific investigations, are pivotal in orchestrating improvements in maize yield dynamics, thereby engendering steadfast constancy in the realm of sustenance production. Such perspicacious exploration, poised on the precipice of technological advancement, is poised to engender a holistic comprehension that will invariably underpin the incisive development of heartier, resilient, and prodigiously fecund strains of maize. It is within the crucible of these emerging advancements that the global exigencies for nourishment shall discover their harmonious resolution.

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