



OPEN Multi-year evaluation of silage yield, quality, and stability of maize (*Zea mays* L.) genotypes in the central Black Sea region of Türkiye

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Maize (*Zea mays* L.) is the dominant silage crop in intensive livestock systems because of its high biomass production and energy-rich, well-fermenting forage. Here, 16 silage maize genotypes were evaluated for four consecutive seasons (2017–2020) under the ecological conditions of Samsun, Türkiye, using a broad set of phenological, morphological, yield, and forage-quality traits (including fiber fractions and energy-based indices such as digestible/gross energy and estimated milk yield). Across years, substantial environmental variation affected several traits, highlighting the importance of multi-year testing for genotype assessment. Among the evaluated materials, TTM 2015–22 showed high fresh biomass productivity (67.1 t ha^{-1}), and one of the highest dry matter yields (22.6 t ha^{-1}), whereas several compositional traits were strongly influenced by seasonal conditions and should be interpreted cautiously. These results emphasize the value of genotype choice to balance yield and forage quality under the conditions tested, although genotype recommendations for quality-related traits require cautious interpretation.

Keywords Silage maize, GEI, Stability analysis, AMMI, GGE biplot, Forage quality

Maize (*Zea mays* L.) is one of the most widely used forage crops for silage production worldwide due to its high biomass yield, nutritional value under optimal growing conditions, and reliable fermentation characteristics¹. Its high energy content, favorable ensiling properties, and strong palatability for ruminants make maize the predominant choice for modern silage systems². Consequently, maize silage constitutes a major component of rations in intensive dairy production systems³.

The contribution of maize genotypes to forage quality varies considerably depending on their genetic background⁴. Silage quality is strongly shaped not only by genotype but also by environmental conditions⁵. Thus, the key determinants of silage yield, chemical composition, and fermentation performance represent a complex interplay between genetic attributes and environmental factors⁶.

An ideal silage maize hybrid is characterized by high biomass and a plant architecture suitable for silage production, which together support high green and dry matter yield and desirable feed value⁷. Optimal silage types generally contain 46–50% grain to meet dietary starch requirements and simultaneously maintain high biomass productivity⁸. A grain proportion of at least 30% is considered desirable even under continental climates⁹. The low correlation between grain and silage yield ($r^2=0.23\text{--}0.25$) further supports the need for separate evaluation trials¹⁰. General combining ability (GCA) has been shown to be more influential than specific combining ability (SCA) for whole-plant biomass production, with moderate heritability estimates^{11–13}. Flint $\times$ Dent combinations typically show greater genetic divergence, whereas Dent endosperm is preferred due to superior starch digestibility^{14–16}.

High biomass accumulation is further influenced by photosynthetic efficiency, cellular architecture, and growth-promoting hormones such as gibberellins and brassinosteroids^{17,18}. Plant architecture is also a major determinant of silage quality, increased leaf number, larger leaf area, narrow leaf angle, and upright orientation enhance photosynthesis and biomass production¹⁹. The preferred leaf–stem ratio ranges from 0.20 to 0.32, and genotypes with higher leaf numbers are generally favored^{20,21}. Leaf area shows positive correlations with dry matter and grain yield²², while photoperiod and temperature play key roles in determining leaf formation^{23–25}.

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The stay-green (SG) trait contributes to delayed senescence, prolonged photosynthetic duration, improved yield, higher sucrose and protein content, and better resistance to lodging and disease^{26–28}. The optimal harvest stage for silage is the half-milkline phase²⁹. Early harvest may result in poor fermentation because of insufficient dry matter, whereas delayed harvest can reduce palatability and digestibility. As maturity progresses, starch content tends to increase and NDF tends to decrease^{30–33}, although excessively delayed harvest may also reduce crude protein and increase lignin and fiber fractions^{34,35}.

Generally, high-quality maize silage is characterized by proper dry matter content, high starch levels, sufficient crude protein, good digestibility, moderate fiber levels, and effective fermentation²⁰. Additionally, silage hybrids should have strong stalks and resistance to lodging. Key developmental traits, such as flowering time, are controlled by genetic factors, such as Vgt1-ZmRap2.7, which are crucial for environmental adaptation^{36,37}. Collectively, high biomass production, an appropriate grain proportion, delayed senescence, robust stalk strength, and high digestibility are the defining features of elite silage maize hybrids²⁰.

The aim of this study was to evaluate the silage performance of diverse maize (*Zea mays* L.) genotypes in terms of yield, biomass components, chemical composition, and digestibility, and to elucidate the combined influence of environmental conditions and genetic structure on forage quality. Within this framework, genotypes were compared based on key silage quality criteria—including biomass productivity, grain proportion, stay-green expression, stalk strength, and dry matter accumulation—to identify the most suitable materials for silage production.

Materials and methods

Plant material

A total of 1100 initial materials obtained from diverse domestic and international sources—including populations, F1 hybrids, local landraces, and segregating materials—were evaluated based on morphological characteristics such as tassel structure, ear architecture, plant appearance, and leaf morphology. Negative selection was applied annually during inbred line development (2008–2014) using predefined, quantitative agronomic and health criteria. Lodging and foliar disease severities were assessed in the field, with lodging and leaf blight scored on a 1–9 scale; lines showing scores outside the acceptable range were discarded, and lines with visible rust were excluded. Trait components related to plant/ear quality and uniformity were evaluated using 1–5 scoring scales, and only lines meeting the predefined acceptance thresholds were advanced. In addition, lines outside the target flowering window (65–80 days) and those that failed to produce sufficient seed for advancement were eliminated. Using these criteria, 154 inbred lines were advanced to the S6 generation.

After generating 56 hybrid combinations in 2016 (Supplementary Table 1), the hybrids were screened prior to entry into the multi-year trials to ensure suitability for replicated testing. Hybrids were excluded if they produced insufficient seed for multi-environment experiments (≤ 500 g), showed poor within-hybrid uniformity (uniformity scored on a 1–5 scale; only hybrids scoring ≤ 2 were retained), had undesirable ear or whole-plant appearance (1–5 scales; only ≤ 2 were retained), or exhibited inadequate germination/emergence capacity ($< 90\%$). In addition, hybrids that performed below the trial mean in preliminary observations and those exhibiting non-uniform flowering/pollen synchrony, which could compromise reliable evaluation, were removed from further testing (Fig. 1). A total of 16 maize genotypes were evaluated across 2017–2020, comprising 12 experimental hybrids and 4 commercial check hybrids (controls) (AGA, BURAK, Kilowatt, and SAMADA-07) (Supplementary Table 1).

Experiment site

The experiment was conducted in Çarşamba, Samsun, within the Black Sea region of Türkiye, across successive growing seasons from 2017 to 2020. The experimental site is situated inland from the Turkish Black Sea coast. According to the Köppen-Geiger climate classification, the region has a Cfa climate, characterized by mild winters, hot summers, and year-round rainfall (Beck et al., 2018⁷¹). Mean annual precipitation for the growing seasons was 191.42 mm, 183.27 mm, 230.02 mm, and 183.20 mm from 2017 to 2020.

According to the International classification system, the field trial soil has a clay loam (CL) texture, with 45.3% loam, 29.2% clay, and 25.5% sand. It has a slightly alkaline reaction and a medium calcareous structure. Available phosphorus is insufficient, and the organic matter content is low (IUSS 2015).

Regional environmental data indicated marked interannual variability in temperature and precipitation across the 2017–2020 growing seasons. Mean temperatures increased from approximately 12–15 °C in April to peak values of 25–30 °C during July–August, and then declined again in September. Precipitation patterns also differed among years: 2019 was the wettest season, 2018 and 2020 were comparatively drier, and 2017 was intermediate in rainfall. These climatic differences were the primary environmental drivers shaping maize growth dynamics and the observed yield–quality variation among genotypes (Fig. 2).

Experimental design and field management

The field trial followed the principles of a Randomized Complete Block Design (RCBD) with three replications. Each plot consisted of two rows with 0.70 m row spacing and 6 m row length for a total of approximately 9 m². Before sowing, 15:15:15 compound fertilizer was applied at 666.7 kg ha⁻¹, corresponding to 100 kg ha⁻¹ each of N, P₂O₅, and K₂O. At the V6 stage, urea (46% N) was applied at 150 kg ha⁻¹ (equivalent to 69 kg N ha⁻¹) as a side-dress between rows, followed immediately by irrigation. Field preparation involved autumn plowing followed by spring harrowing with a disc harrow. Sowing took place by hand on May 5–6 from 2017 to 2020. Drip irrigation was applied at approximately 5-day intervals to maintain non-limiting soil moisture. Each irrigation event was continued until the soil in the effective root zone approached field capacity as assessed by feel method, and irrigation was terminated at the dough stage.

Maize Breeding Progress

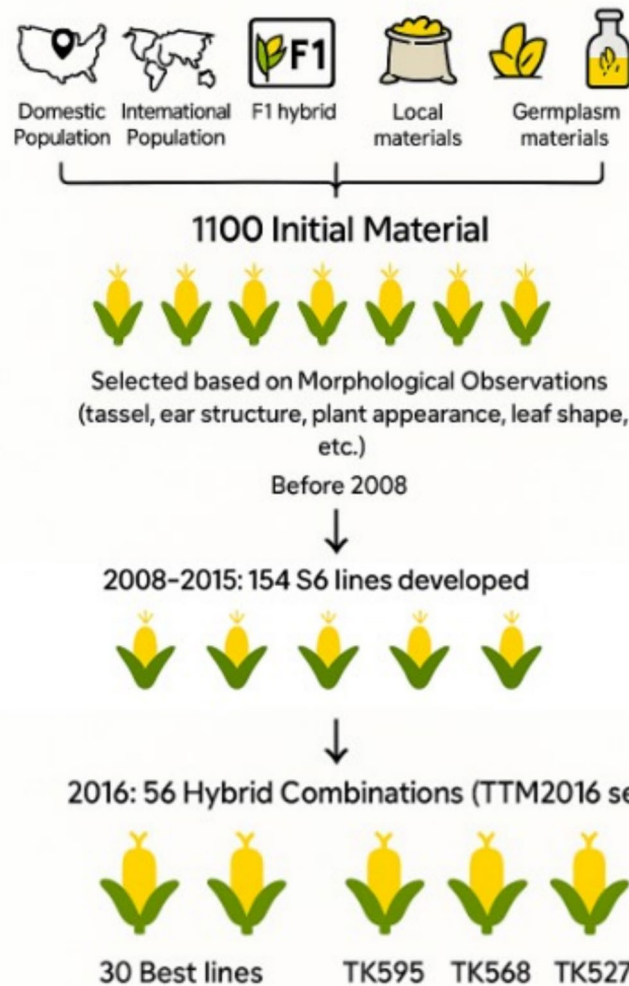


Fig. 1. Breeding and selection workflow for the silage maize panel evaluated in this study: 1100 source materials were screened, and negative selection during 2008–2014 advanced 154 inbred lines to the S6 generation. In 2014, 125 inbreds were testcrossed with three testers (270 hybrids) and evaluated at two locations in 2015; 30 lines were retained based on combining ability/heterotic grouping, generating 56 hybrids in 2016. Hybrids were then pre-screened before multi-year testing (seed > 500 g, germination $\geq 90\%$, and field uniformity plus plant/ear appearance scores ≤ 2 on 1–5 scales; below-mean performers discarded), resulting in 16 genotypes (including commercial checks) tested across 2017–2020 under Samsun (Çarşamba), Türkiye.

Weed management was initiated through manual methods. Due to substantial weed pressure, hand weeding continued until maize plants reached the 3- to 5- leaf stage, at which point hoeing was implemented. Plots were manually harvested at the dough stage from the 1st to 6th of September across the 2017–2020 growing seasons, depending on the maize genotype. For compositional analyses, three representative plants per plot were randomly sampled from the two central rows. The harvested material was pooled to form a composite sample per plot, and two subsamples were analyzed using near-infrared spectroscopy³⁸.

Data collection of the genotypes' yield and nutrient composition

Field-based phenotypic characterization was performed in accordance with the standard operating procedures issued by Türkiye's Seed Certification Center (TTSM, 2025). Border plants were excluded from harvest, and three plants per plot were removed as a subsample for quality analyses. The number of harvested plants per plot was recorded. The remaining net plot was then harvested for biomass, and green yield was calculated on a per-area basis using the net harvested area. Plots were harvested manually at the dough stage, and green weight was calculated on a plot-area basis and expressed as t ha^{-1} ; dry matter yield was computed as fresh yield $\times$ dry matter content. Nutrient composition traits were predicted by near-infrared reflectance spectroscopy (NIRS) using a

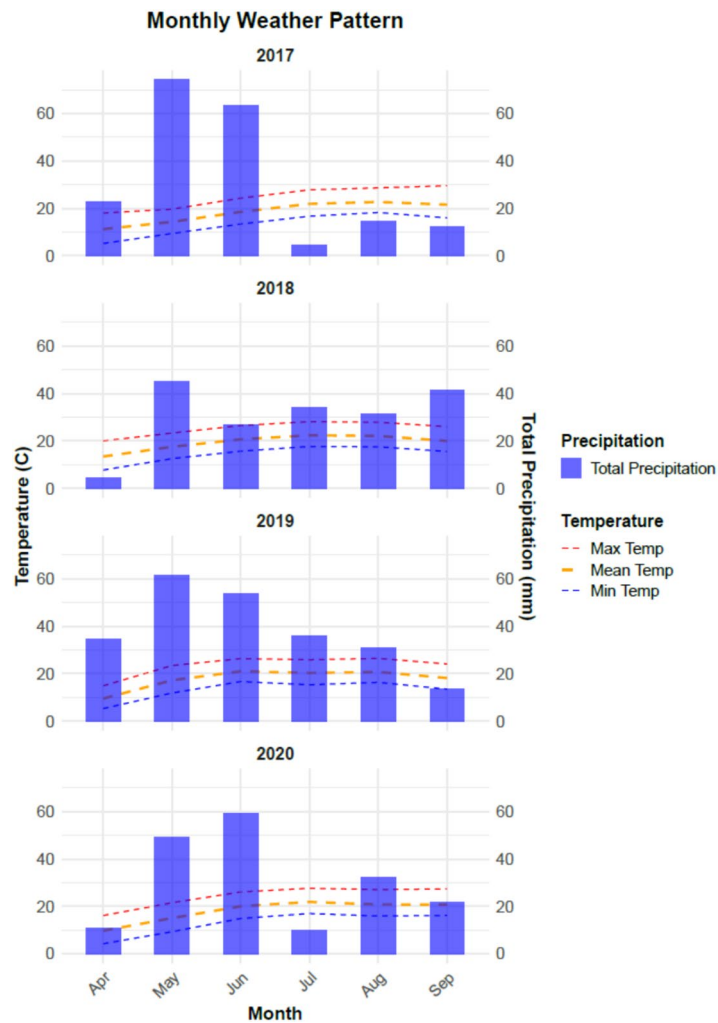


Fig. 2. Monthly weather patterns during the maize growing seasons of 2017–2020. Bar plots represent total monthly precipitation (mm), while dashed lines indicate minimum, mean, and maximum air temperatures (°C). Data illustrate interannual variation in climatic conditions across the main growth period (April–September).

FOSS NIR Systems 6500 scanning monochromator spectrometer (FOSS A/S, Hillerød, Denmark) operating over 1100–2498 nm (2-nm intervals) with the IC-0904FE calibration/software package. Dried and ground samples were scanned in duplicate. Calibration performance was assessed by cross-validation ($n = 312$) using R^2 , SEP, and RPD: ADF ($R^2 = 0.842$; SEP = 1.845; RPD = 2.642), dry matter (0.915; 0.724; 2.204), NDF (0.796; 2.105; 3.497), crude protein (0.902; 0.324; 3.642), crude fat (0.620; 0.684; 2.307), and crude cellulose (0.745; 0.540; 2.478).

Digestible energy (DE) (Eq. 1) and gross energy (GE) (Eq. 2) are calculated according to the formulas described by MAFF (Ministry of Agriculture, Fisheries and Food) 1975 (MAFF, 1975) and AAFCO (Association of American Feed Control Officials) 1997 (AAFCO, 1995), respectively.

For the GE (Mcal/kg DM) = Gross Energy in Mega-calories per kilogram of dry matter;

CP = Crude Protein (g/kg DM)

CF = Crude Fiber (g/kg DM)

EE = Ether Extract or Fat (g/kg DM)

NFE = Nitrogen-Free Extract (g/kg DM), which represents the remaining carbohydrates in the feed, excluding fiber (Eq. 3).

The factor 4.184 converts megacalories to megajoules. 1 Mcal = 4.184 MJ = 4184 kJ.

As for the DE (Mcal/kg DM) = Digestible Energy in Mega-calories per kilogram of dry matter;

CF = Crude Fiber content as g kg⁻¹ dry matter (g/kg DM).

87.9 is a constant related to the average energy digestibility in typical feeds.

0.88 is a factor that accounts for the influence of Crude Fiber (CF) on digestibility. As Crude Fiber increases, it tends to decrease the digestibility of the feed, and this formula reflects that relationship.

$$DE \text{ (Mcal/kg DM)} = \frac{(DE \times (87.9 - (0.88 \times CF)))}{100} \quad (1)$$

$$GE \text{ (Mcal/kg DM)} = \frac{(0.226 \times CP + 0.177 \times CF + 0.407 \times EE + 0.192 \times NFE)}{4.184} \quad (2)$$

$$NFE(\%) = CP(\%) + CF(\%) + Fat(\%) + Ash(\%) \quad (3)$$

Statistical analysis

Linear mixed-effects models were constructed for each trait using the lme4 package in R (Bates et al., 2015⁷²), with significant effects evaluated post hoc using the Tukey test. Genotype was specified as a fixed effect, while year, genotype $\times$ year interaction, and replication nested within year are specified as random effects.

$$y = \mu + G_i + E_j + R_r + (G \times E)_{ij} + \varepsilon \quad (4)$$

where: y : Phenotypic observation, μ : Overall mean, G_i : Fixed effect of the i -th genotype, E_j : Random effect of the j -th environment (year: 2017, 2018, 2019 and 2020), R_r : Random effect of the r -th replication (nested within environment (year)), $G \times E$: Random interaction effect between genotype and environment (year), ε : Residual error.

Heritability (H^2)

Broad-sense heritability (H^2) was calculated on an entry-mean basis across years using variance components estimated from the mixed-model analysis. Across-year H^2 was computed as:

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_{g \times y}^2 / n_Y + \sigma_e^2 / (n_Y \cdot r)} \quad (5)$$

where, $\sigma_g^2 = (MS_G - MS_{G \times Y}) / (n_Y \cdot r)$ is the genotypic variance, $\sigma_{g \times y}^2 = (MS_{G \times Y} - MS_E) / r$ is the genotype $\times$ year interaction variance, $\sigma_e^2 = MS_E$ is the residual variance, n_Y is the number of years, and r is the number of replications per year. Negative variance component estimates were constrained to zero.

Results

Correlation analysis

Correlations were computed using genotype BLUE values across years. The analysis revealed distinct relationships among morphological, yield-related, and nutritional-quality traits (Fig. 3). Morphological characteristics exhibited strong positive correlations with each other. Plant height showed a moderate positive correlation with ear height ($r = 0.55$, $p < 0.001$) and was positively associated with pollen-shedding time, indicating later anthesis in taller genotypes. Leaf-stem ratio was positively correlated with plant height and ear height (both $p < 0.001$).

A clear cluster of strong positive correlations was observed among biomass-related variables. Green weight was highly correlated with dry matter yield ($r \approx 0.89$, $p < 0.001$) and estimated milk yield per hectare ($r = 0.93$, $p < 0.001$). Dry matter yield also showed a very strong positive correlation with estimated milk yield ($r \approx 0.98$, $p < 0.001$).

Fiber fractions (NDF, ADF, ADL, cellulose) formed a second distinct cluster. ADF was positively correlated with NDF ($r \approx 0.87$, $p < 0.001$) and ADL ($r \approx 0.84$, $p < 0.001$). ADL was positively correlated with both NDF and ADF ($p < 0.001$). In contrast, cellulose showed strong negative correlations with ADL (up to $r = -0.98$, $p < 0.001$).

Because DE and GE are derived traits calculated from forage composition variables, correlations involving DE/GE and their component traits should be interpreted cautiously, as they may reflect shared mathematical structure rather than independent biological relationships. Accordingly, the primary emphasis in the present study is placed on directly measured fiber fractions, particularly NDF, ADF, and ADL. Protein and oil were weakly correlated with most traits and did not cluster with either the morphological or fiber-related groups. Correlation coefficients describe associations and do not imply causality.

GGE biplot

The ASV ranking quantitatively supported these patterns (lower ASV = higher stability): the three most stable genotypes were TTM2016-22 (ASV = 2.232), TTM2016-20 (ASV = 3.282), and Kilowatt (St) (ASV = 3.59). In contrast, the least stable entries were AGA (st) (ASV = 14.685) and SAMADA-07(st) (ASV = 14.147), followed by TTM2016-23 (ASV = 13.615) and TTM2016-35 (ASV = 13.484).

Boxplots (Fig. 4C) further demonstrate the distribution of green weight across years for each genotype and confirm that the three highlighted genotypes (TTM2016-22, TTM2016-20, Kilowatt (St)) exhibit relatively consistent year-wise behavior.

Agronomic traits

For pollen DAP, the effects of genotype ($P = 0.005694$), year ($P = 0.01679$), and their interaction ($P < 0.0001$) were statistically significant. Days to flowering among genotypes ranged from 72.82 to 78.53 days. Burak was the latest-flowering genotype (78.53 days), whereas TTM2016-18 exhibited the earliest flowering (72.82 days). Yearly means across 2017–2020 were 78.61, 74.02, 73.11, and 75.71 days, respectively (Table 2).

Plant height was significantly affected by genotype ($P = 0.02862$), and genotype $\times$ year interaction ($P < 0.0001$), whereas the year effect was not significant ($P = 0.163$). Genotypic means varied from 286.94 to 324.70 cm. The tallest genotype was AGA (324.70 cm), followed by BURAK (323.88 cm) and TTM2016-19 (307.50 cm), while the shortest plants were observed in TTM2016-40 (286.94 cm). Yearly averages from 2017 to 2020 were 291.33, 309.90, 305.12, and 316.73 cm, respectively (Table 2).

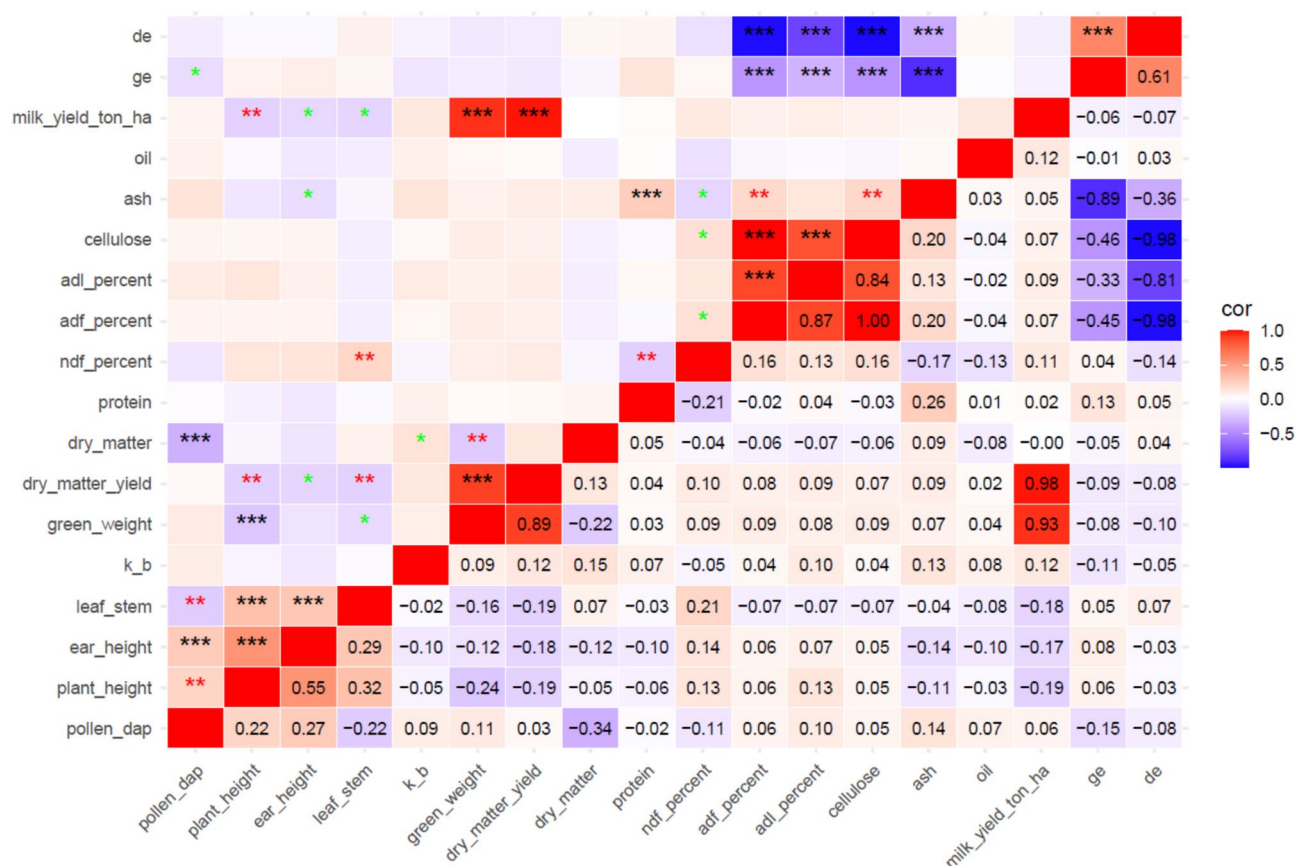


Fig. 3. Correlation matrix among agro-morphological, yield, quality, and energy-related traits of maize genotypes. The heatmap displays Pearson correlation coefficients, where red indicates positive correlations and blue indicates negative correlations. Color intensity represents the strength of the relationship. Significance levels are denoted by asterisks ($p < 0.05$, $p < 0.01$, $p < 0.001$). NDF (Neutral Detergent Fiber; %), ADF (Acid Detergent Fiber; %), ADL (Acid Detergent Lignin; %), DM (Dry Matter), GE (Gross Energy; Mcal kg⁻¹ DM), DE (Digestible Energy; Mcal kg⁻¹ DM), CP (Crude Protein, %), K/B (Cob/Plant Ratio (%)), MY (Milk yield, ton ha⁻¹).

Ear height was significantly affected by genotype ($P = 0.002982$), year ($P = 0.0003296$), and genotype $\times$ year interaction ($P = 0.0006$). Genotypic means ranged from 87.15 to 106.30 cm. The highest ear height was recorded for AGA (106.30 cm), followed by BURAK (103.29 cm) and TTM2016-20 (102.96 cm), whereas the lowest values were observed in TTM2016-35 (87.15 cm) and TTM2016-11 (87.72 cm). Yearly averages for 2017–2020 were 92.39, 91.35, 94.08, and 106.19 cm, respectively (Table 3).

Leaf-stem ratio was significantly affected by year ($P = 0.0012$) and the $G \times Y$ interaction ($P < 0.0001$), whereas the genotype main effect was not significant ($P = 0.125$). Genotypic means ranged from 38.69 to 50.24% (Table 3).

Cob/plant ratio was significantly influenced by genotype $\times$ year interaction ($P = 0.0001953$), whereas genotype ($P = 0.1229$) and year ($P = 0.7740$) were not significant. Genotypic means ranged from 38.09 to 42.11%. The highest cob/plant ratio occurred in TTM2016-20 (42.11%), followed by Kilowatt (41.01%) and TTM2016-22 (41.79%), whereas the lowest ratios were recorded for TTM2016-23 (38.77%) and BURAK (39.09%). Yearly averages for 2017–2020 were 41.01%, 41.43%, 40.17%, and 40.28%, respectively (Table 4).

Green weight was significantly affected by year and the $G \times Y$ interaction ($P < 0.0001$), whereas the genotype effect was marginal ($P = 0.0515$). Genotypic means ranged from 56.9 to 67.1 t ha⁻¹. The highest green weight was produced by TTM2015-22 (67.1 t ha⁻¹), followed by TTM2016-18 (65.9 t ha⁻¹), TTM2015-8 (65.8 t ha⁻¹), and TTM2016-38 (65.3 t ha⁻¹). The lowest values were recorded for TTM2016-22 (56.9 t ha⁻¹) and TTM2016-35 (57.1 t ha⁻¹). Annual means were 68.2, 56.2, 67.2, and 56.7 t ha⁻¹ from 2017 to 2020 (Table 4).

Dry matter yield was significantly influenced by year ($P < 0.0001$) and the $G \times Y$ interaction ($P < 0.0001$), whereas the genotype effect was not significant ($P = 0.3052$). Genotypic means ranged from 19.1 to 22.6 t ha⁻¹ (Table 5).

Dry matter was significantly affected by year ($P = 0.002344$) and the $G \times Y$ interaction ($P < 0.0001$), whereas genotype had no significant effect ($P = 0.2402$). Genotypic means ranged from 32.38 to 34.72% (Table 5).

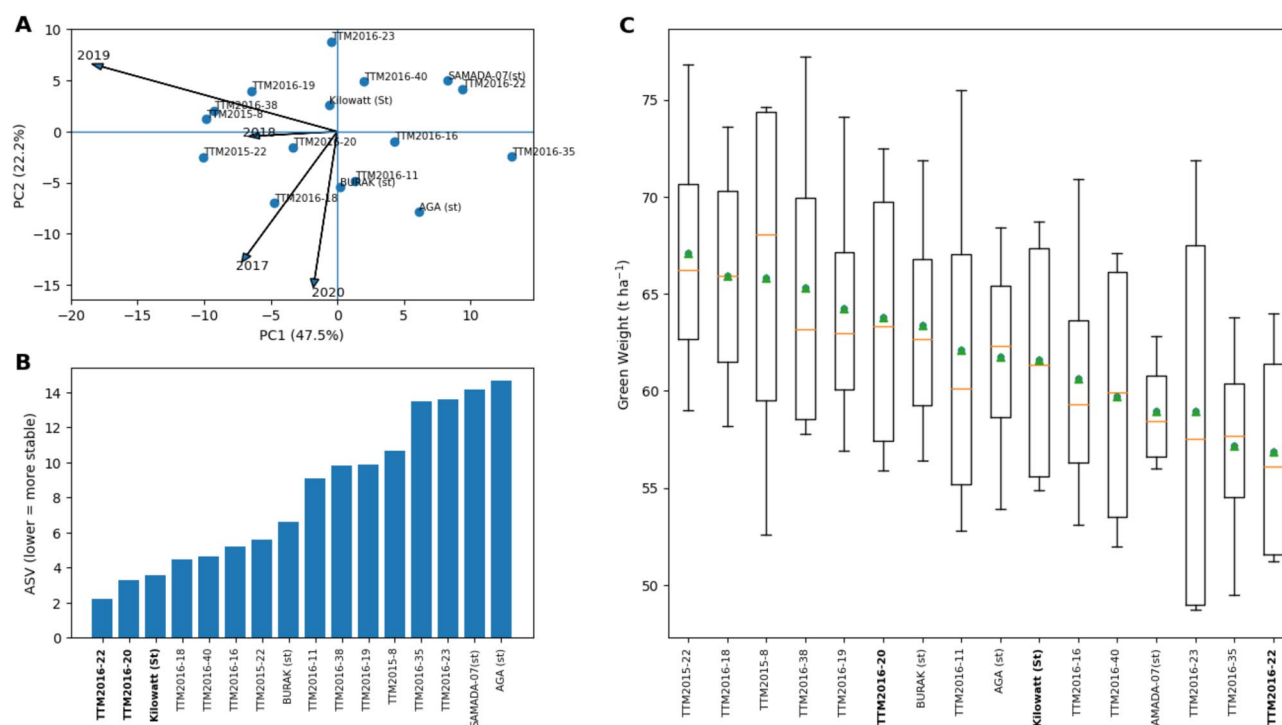


Fig. 4. Stability and year-wise performance of green weight in silage maize genotypes across four growing seasons (2017–2020), based on the genotype $\times$ year matrix of green weight (t ha⁻¹). **(A)** PCA biplot (GGE-style; environment-centered) showing genotype positions and year vectors. **(B)** AMMI Stability Value (ASV) for green weight; lower ASV indicates greater stability across years. **(C)** Boxplots of green weight across years for each genotype with genotype means overlaid. Highlighted genotypes represent the three most stable entries (lowest ASV).

Quality parameters

Neutral detergent fiber (NDF) was significantly influenced by year ($P < 0.0001$) and the $G \times Y$ interaction ($P < 0.0001$), whereas the genotype effect was not significant ($P = 0.9112$). Genotypic means ranged from 52.37 to 55.23% (Table 6).

Acid detergent fiber (ADF) was not significantly affected by genotype ($P = 0.4758$), year ($P = 0.6641$), or their interaction ($P = 0.3010$). Genotypic means ranged between 30.02% and 31.38% (Table 6).

Acid detergent lignin (ADL) showed no significant effects of genotype ($P = 0.2859$), year ($P = 1.0000$), or $G \times Y$ interaction ($P = 0.8287$). Genotypic means ranged from 3.18 to 3.35% (Table 7).

Ash content was unaffected by genotype ($P = 0.1501$), year ($P = 0.4050$), or the $G \times Y$ interaction ($P = 0.2266$). Genotypic means ranged from 3.87 to 4.29% (Table 7).

Oil content showed no significant effects of genotype ($P = 0.5618$) or year ($P = 0.3765$), although the $G \times Y$ interaction was significant ($P = 0.0362$). Genotypic means ranged from 3.01 to 3.52% (Table 8).

Protein content was unaffected by genotype ($P = 0.6586$), year ($P = 0.4379$), and the $G \times Y$ interaction ($P = 1.0000$). Genotypic means ranged between 8.58% and 9.19% (Table 8).

Cellulose content showed no significant effects of genotype ($P = 0.4885$), year ($P = 0.6333$), or interaction ($P = 0.2819$). Genotypic means ranged from 26.80 to 28.04% (Table 9).

Discussion

Across 2017–2020, biomass-related traits (green weight and dry matter yield) were strongly and positively associated with estimated milk yield per hectare, while fiber and lignin fractions were strongly interrelated, collectively indicating a yield–quality trade-off relevant to silage maize selection. Associations between structural and yield-related traits have been reported previously, with plant height and related morphological attributes often positively correlated with biomass accumulation^{39,40}. At the same time, negative relationships between yield indicators and fiber fractions (e.g., ADF and NDF) have been described in maize silage, emphasizing the need to balance biomass production with digestibility-related traits in genotype selection^{5,41}.

As DE and GE are derived from proximate composition, their correlations with fiber/lignin may be partly mathematical; thus, we emphasize NDF/ADF/ADL as primary drivers and use DE/GE as summary indices. Accordingly, correlations involving DE and GE are interpreted cautiously and are secondary to directly measured fiber traits. The strong negative associations between lignin-related traits and digestible energy are consistent with the established role of lignification in limiting cell wall degradation and reducing energy availability to ruminants^{42,43}. This supports the view that improving silage quality can involve targeting lignin amount and/or composition, with implications for both livestock nutrition and broader biomass utilization⁴³. Environmental

Genotype	Pollen DAP (day)					Plant height (cm)				
	Year					Year				
	2017	2018	2019	2020	Mean	2017	2018	2019	2020	Mean
AGA (st)	77.98 ab	75.67 ab	75.00 ab	81.00 a	77.41	300.48 abc	335.00	303.33 ab	360.00 a	324.70
BURAK (st)	81.45 b	75.33 b	75.33 ab	82.00 a	78.53	295.52 bd	321.67	326.67 ac	351.67 ab	323.88
Kilowatt (St)	76.49 ab	75.33 acd	74.33 ab	75.00 bc	75.29	302.97 bc	305.00	323.33 ad	343.33 acd	318.66
SAMADA-07(st)	80.96 b	76.00 b	75.33 ab	78.00 d	77.57	307.93 b	318.33	311.67 ab	348.33 ad	321.57
TTM2015-22	79.17 ab	73.00 bde	70.33 ab	73.67 ce	74.04	283.10 ad	303.33	295.00 bcd	306.67 ef	297.02
TTM2015-8	80.16 ab	74.00 bd	70.33 ab	77.67 df	75.54	279.82 d	310.00	310.00 ab	335.00 acdg	308.71
TTM2016-11	80.96 b	73.00 b	77.17 b	78.00 d	77.28	288.07 cd	313.33	311.67 ab	281.67 eh	298.68
TTM2016-16	79.96 ab	73.33 bd	72.00 ab	78.33 d	75.91	302.97 bc	300.00	290.00 ab	328.33 bdf	305.32
TTM2016-18	79.96 ab	72.00 bd	68.00 a	71.33 e	72.82	288.07 cd	315.00	281.67 b	276.67 h	290.35
TTM2016-19	75.00 a	73.33 a	72.67 ab	75.33 bcf	74.08	291.67 bd	306.67	311.67 ab	320.00 cf	307.50
TTM2016-20	78.97 ab	75.00 ab	69.33 ac	74.33 bc	74.41	285.58 cd	308.33	296.67 bcd	328.33 bdf	304.73
TTM2016-22	76.52 ab	75.33 acd	74.93 ab	73.00 bc	74.95	286.00 cd	288.33	338.23 a	286.67 eh	299.81
TTM2016-23	75.49 ac	73.67 ae	71.00 ab	74.67 bd	73.71	285.58 cd	303.33	291.67 bcd	325.00 df	301.40
TTM2016-35	80.46 bc	75.00 bc	76.00 bc	76.33 bc	76.95	283.10 ad	323.33	308.33 ab	291.00 ehi	301.44
TTM2016-38	77.98 ab	73.33 ab	71.67 ab	74.00 g	74.24	288.07 cd	310.00	293.33 bcd	315.00 fgi	301.60
TTM2016-40	76.18 ab	71.00 ad	76.29 bc	68.67	73.04	292.38 bd	296.67	288.73 bd	270.00 h	286.94
Mean	78.61	74.02	73.11	75.71	75.36	291.33	309.90	305.12	316.73	305.77
G	0.005694 **					0.02862 *				
Y	0.01679 *					0.163				
G × Y	<.0001***					<.0001***				
CV (%)	2.52					3.73				

Table 2. Pollen DAP (days after planting) and plant height (cm) of maize (*Zea mays* L.) genotypes evaluated in the 2017, 2018, 2019, and 2020 growing seasons. Means followed by the same lowercase letters within rows and the same uppercase letters within columns indicate that, for the corresponding variable, no significant difference was detected according to the Scott–Knott test at the 5% significance level ($P < 0.05$). G = effect of genotype. Y = effect of year. G × Y = genotype-by-year interaction (reflecting the genotype–environment interaction). CV = coefficient of variation. The letters shown in the ‘Mean’ rows and columns represent comparisons of the isolated effects of year and genotype, respectively.

and management factors, including nitrogen supply, precipitation patterns, and planting density, may also influence protein and fiber fractions in silage maize, thereby contributing to seasonal variation^{5,44}.

Stability patterns identified by GGE biplot, AMMI2, and GGE-SI were consistent, supporting the complementarity of these models for evaluating genotype performance across environments (Yan & Kang, 2003⁷³; Gauch, 2013⁷⁴). The observation that phenological and structural traits tended to be more stable than nutritional traits agrees with previous reports indicating greater environmental sensitivity of fiber fractions in maize silage²⁰ (Ferraretto & Shaver, 2015⁷⁵). In this study, Kilowatt (st) and TTM2015-22 consistently ranked favorably across multivariate approaches, supporting their potential suitability for broad use under variable conditions, particularly when mean performance is considered together with stability, whereas genotypes with stronger GEI (e.g., BURAK (st) and TTM2016-40) may be better suited to specific environments or targeted production objectives.

Across years, stability reflects reduced GEI sensitivity but is not a proxy for genetic control. In this dataset, across-year broad-sense heritability (H^2) was moderate to high for phenology/morphology and biomass traits (e.g., ear height, pollen DAP, plant height, green weight), indicating repeatable between-genotype differences across seasons (Table 1). By contrast, H^2 was near zero for several compositional traits, showing that exploitable genetic variance was negligible relative to year-to-year, interaction, and residual variation in the current panel. Notably, for some compositional traits (e.g., protein and ADF), genotype, year, and G × Y effects were not statistically significant, consistent with strong genetic similarity among the evaluated genotypes and a narrow phenotypic range for these traits. In contrast, other compositional traits (e.g., NDF and oil) showed significant year and/or G × Y effects despite non-significant genotype main effects, suggesting that seasonal conditions altered trait expression and/or genotype ranking across years, thereby reducing across-year repeatability. Under this design and these environments, genetic differences for low- H^2 compositional traits are not repeatable enough to support efficient selection (Supplementary Tables 2 and 3). In addition, because compositional analyses were based on composite samples from only three plants per plot, limited sampling intensity may have increased residual variation and reduced the ability to detect genotype differences for traits such as NDF, ADF, and protein. Accordingly, the differences observed in these compositional traits appear to be mainly environmentally influenced and do not exhibit sufficient genetic consistency for reliable selection under the tested conditions. Therefore, apparent differences among genotypes for these traits should be interpreted carefully, and practical selection should be validated across a wider range of environments. Because the expected selection response

Genotype	Ear height (cm)					Leaf/stem ratio (%)				
	Year					Year				
	2017	2018	2019	2020	Mean	2017	2018	2019	2020	Mean
AGA (st)	96.85 abc	106.67	101.67 ab	120.00 ab	106.30	35.89 ab	44.19	48.27 ab	52.29 ab	45.16
BURAK (st)	109.27 a	111.67	106.67 b	128.33 a	113.98	30.30 c	43.56	48.36 ab	49.83 a	43.01
Kilowatt (St)	84.43 bde	88.33	93.33 ab	101.67 bcd	91.94	40.14 de	45.28	47.84 ab	48.78 b	45.51
SAMADA-07(st)	86.92 cde	96.67	100.00 ab	120.00 ab	100.90	42.72 df	39.95	45.63 bc	50.73 ab	44.76
TTM2015-22	77.78 d	88.33	90.00 ab	103.33 bcd	89.86	38.17 aeg	43.30	49.39 ab	58.01 acd	47.22
TTM2015-8	81.16 df	86.67	91.67 ab	116.67 ab	94.04	47.21 hi	45.44	47.89 ab	60.44 ad	50.24
TTM2016-11	91.88 cefg	66.67	101.67 ab	90.67 de	87.72	40.98 de	45.78	41.16 cd	41.97 b	42.47
TTM2016-16	94.37 cefg	81.67	90.00 ab	111.67 ad	94.42	33.18 bc	45.98	45.42 bc	60.77 a	46.34
TTM2016-18	89.40 cdeg	93.33	80.00 a	106.67 bcd	92.35	38.52 ae	41.94	45.37 bc	58.28 ad	46.03
TTM2016-19	106.67 ah	85.00	93.33 ab	111.67 ab	99.17	48.48 h	43.25	51.03 b	46.52 bd	47.32
TTM2016-20	96.85 abc	101.67	95.00 ab	118.33 ab	102.96	43.77 di	41.55	51.08 b	51.39 b	46.95
TTM2016-22	92.71 cefg	85.00	107.47 b	86.67 ce	92.96	39.24 aef	41.78	43.01 ac	41.75 b	41.44
TTM2016-23	96.85 ac	96.67	90.00 ab	110.00 ad	98.38	38.51 ae	40.91	48.67 ab	48.47 ab	44.14
TTM2016-35	81.95 de	88.33	86.67 ab	91.67 de	87.15	34.62 bg	43.87	40.88 cd	44.11 bc	40.87
TTM2016-38	101.82 ag	88.33	88.33 ab	101.67 bcd	95.04	34.71 bg	45.62	49.44 ab	52.91 ab	45.67
TTM2016-40	89.29 cde	96.67	89.51 ab	80.00 e	88.87	34.13 b	42.80	34.76 d	43.07 b	38.69
Mean	92.39	91.35	94.08	106.19	96.00	38.78	43.45	46.14	50.58	44.73
G	0.002982**					0.125				
Y	0.0003296***					0.0012**				
G × Y	0.0006***					<.0001***				
CV (%)	10.39					8.39				

Table 3. Ear height (cm) and leaf/stem ratio (%) of maize (*Zea mays* L.) genotypes evaluated in the 2017, 2018, 2019, and 2020 growing seasons. Means followed by the same lowercase letters within rows and the same uppercase letters within columns indicate that, for the corresponding variable, no significant difference was detected according to the Scott–Knott test at the 5% significance level ($P < 0.05$). G = effect of genotype. Y = effect of year. G × Y = genotype-by-year interaction (reflecting the genotype–environment interaction). CV = coefficient of variation. The letters shown in the ‘Mean’ rows and columns represent comparisons of the isolated effects of year and genotype, respectively.

is proportional to heritability and selection differential ($R = h^2S$), selection should be most efficient for traits with higher H^2 and consistent rankings, whereas improvement of low- H^2 compositional traits likely requires expanded multi-year/multi-environment testing (more environments/years/replications) and/or index-based selection to increase repeatability and progress under Black Sea conditions (Tables 10 and 11).

GGE biplot Multivariate stability of green weight ($t\ ha^{-1}$) across four growing seasons (2017–2020) was assessed using a GGE-style (environment-centered) PCA biplot (Fig. 4A) and the AMMI Stability Value (ASV) (Fig. 4B), with genotype-wise boxplots (Fig. 4C) used to visualize year-to-year dispersion and mean performance. In the PCA biplot, the first two components accounted for 47.5% (PC1) and 22.2% (PC2) of the variance. Genotypes located closer to the origin—notably TTM2016-20 and Kilowatt (St)—showed comparatively smaller genotype × year interaction, whereas genotypes positioned farther from the origin (e.g., TTM2016-23, TTM2016-35, AGA (st), and SAMADA-07(st)) exhibited more pronounced year-associated responses (Table 11). Significant year-to-year variability for several agronomic and yield traits, together with significant G × Y effects for key outcomes, indicates that interannual environmental variation contributed to differential genotype responses across 2017–2020. Such patterns are consistent with prior reports that phenology and plant stature can shift substantially among seasons and environments^{1,38}. Comparisons with previous studies show that the ranges observed here for flowering time, plant height, and ear height fall within the breadth reported under diverse production settings, though differences among studies likely reflect environmental conditions, genotype composition, and management practices^{45–49}.

For cob/plant ratio and biomass traits, the values obtained were broadly comparable to those reported across different regions and management regimes, while deviations among studies likely reflect maturity group, climate, and agronomic inputs^{50–59}. Similarly, dry matter yield variability aligns with previous findings and may reflect differences in planting density, irrigation, fertilization, and genotype potential^{60,61}.

Quality trait values (e.g., ADF, NDF, ADL) were within the ranges reported in the literature, although differences among studies are expected due to maturity stage at harvest, environmental conditions, and genotype differences^{51,62–70}. Overall, the combined evidence from trait correlations and stability analyses indicates that selection for silage maize improvement should integrate biomass productivity with digestibility-related fiber traits to optimize feeding value and performance under variable seasonal conditions.

Genotype	Cob/plant ratio (%)					Green weight (t ha ⁻¹)				
	Year					Year				
	2017	2018	2019	2020	Mean	2017	2018	2019	2020	Mean
AGA (st)	37.65 ab	41.05	39.14 ab	41.43	39.82	68.4 ab	53.9 ab	60.2 ab	64.4 ab	61.7
BURAK (st)	38.24 ac	40.47	38.54 b	39.10	39.09	71.9 ab	56.4 ab	65.1 bc	60.2 ab	63.4
Kilowatt (St)	41.42 bcd	42.15	41.38 ab	39.07	41.01	66.9 ab	55.8 ab	68.7 bc	54.9 cde	61.6
SAMADA-07(st)	39.93 ace	41.57	39.83 ab	39.58	40.23	56.0 c	62.8 b	60.1 ab	56.8 bde	58.9
TTM2015-22	40.63 bcd	40.96	40.24 ab	41.59	40.85	68.6 ab	59.0 ab	76.8 c	63.9 af	67.1
TTM2015-8	41.72 bcd	42.91	40.42 b	39.58	41.16	74.6 ad	61.8 b	74.3 ac	52.6 eg	65.8
TTM2016-11	45.00 de	43.11	36.62 ab	37.85	40.65	75.5 a	52.8 ab	64.2 bc	56.0 eg	62.1
TTM2016-16	40.73 bcd	39.03	39.81 ab	39.62	39.80	70.9 ac	57.4 ab	61.2 ab	53.1 a	60.7
TTM2016-18	40.03 bce	40.82	39.17 ab	41.00	40.26	73.6 ab	58.2 ab	69.2 bc	62.6 af	65.9
TTM2016-19	40.51 bcd	42.68	42.50 ab	38.98	41.17	64.8 ab	61.1 b	74.1 ac	56.9 be	64.2
TTM2016-20	45.49 d	42.06	40.29 ab	40.61	42.11	72.5 ab	57.9 ab	68.8 bc	55.9 bde	63.8
TTM2016-22	42.32 bcd	41.25	42.19 ab	41.39	41.79	64.0 bcd	51.2 ab	60.5 ab	51.7 dg	56.9
TTM2016-23	34.67 a	41.58	39.83 ab	39.01	38.77	66.0 ac	49.1 a	71.9 ac	48.7 g	58.9
TTM2016-35	40.33 bcd	41.60	38.26 b	42.04	40.56	63.8 bc	49.5 a	56.2 b	59.2 bcf	57.1
TTM2016-38	44.20 de	39.85	39.70 ab	40.44	41.05	67.5 ab	57.8 ab	77.2 c	58.8 fg	65.3
TTM2016-40	43.31 cd	41.72	44.80 a	43.12	43.24	65.8 ac	54.0 ab	67.1 bc	52.0 eg	59.7
Mean	41.01	41.43	40.17	40.28	40.72	68.2	56.2	67.2	56.7	62.1
G	0.1229					0.0515				
Y	0.774					<.0001***				
G × Y	0.0001953***					<.0001***				
CV (%)	4.90					6.55				

Table 4. Cob/plant ratio (%) and green weight (t ha⁻¹) of maize (*Zea mays* L.) genotypes evaluated in the 2017, 2018, 2019, and 2020 growing seasons. Means followed by the same lowercase letters within rows and the same uppercase letters within columns indicate that, for the corresponding variable, no significant difference was detected according to the Scott–Knott test at the 5% significance level ($P < 0.05$). G = effect of genotype. Y = effect of year. G × Y = genotype-by-year interaction (reflecting the genotype–environment interaction). CV = coefficient of variation. The letters shown in the ‘Mean’ rows and columns represent comparisons of the isolated effects of year and genotype, respectively.

Conclusion

Over four years (2017–2020) under Central Black Sea conditions of Türkiye, year effects and genotype × year interactions were major drivers of variation in silage performance. Genotype main effects were statistically supported mainly for phenology and plant architecture traits, whereas biomass and several quality-related traits showed stronger year dependence. For green weight, we therefore integrated mean performance with stability analysis; the AMMI-based ASV approach summarizes both productivity and year-to-year consistency. Among the evaluated materials, TTM2015-22 stood out for forage yield, with the highest fresh biomass productivity (67.1 t ha⁻¹) and one of the highest dry matter yields (22.6 t ha⁻¹). In addition, TTM2016-22, TTM2016-20, and Kilowatt (St) showed favorable stability for green weight across years. However, several compositional traits were strongly influenced by seasonal conditions; therefore, nutritional-quality recommendations require validation across a broader range of environments. Overall, the study’s key strength is the multi-year, stability-integrated evaluation, providing a practical basis for selecting genotypes according to production goals while accounting for seasonal variability.

Genotype	Dry matter yield (t ha ⁻¹)					Dry matter ratio (%)				
	Year					Year				
	2017	2018	2019	2020	Mean	2017	2018	2019	2020	Mean
AGA (st)	20.8 ab	19.4 ab	20.3 ab	20.6 ab	20.3	30.35 ab	36.05	33.67	32.00 ab	33.02
BURAK (st)	21.7 bc	19.2 ab	21.7 bc	19.3 bcde	20.5	30.23 a	33.97	33.33	32.00 ab	32.38
Kilowatt (St)	22.0 b	20.2 ab	23.3 bc	17.2 cf	20.7	32.95 cd	36.33	34.00	31.33 a	33.65
SAMADA-07(st)	17.9 b	22.4 a	20.4 ab	18.4 def	19.8	32.01 ce	35.67	34.00	32.33 ab	33.50
TTM2015-22	21.7 bc	20.8 ab	26.1 c	21.7 a	22.6	31.64 bc	35.33	34.00	34.00 ab	33.74
TTM2015-8	25.0 ac	21.4 ab	25.2 ac	18.2 def	22.5	33.50 df	34.33	34.00	34.67 b	34.13
TTM2016-11	24.9 ac	18.3 ab	21.4 bc	18.5 bcde	20.8	33.00 cd	34.67	33.33	33.00 ab	33.50
TTM2016-16	24.6 ac	20.6 ab	20.8 ab	17.7 ef	20.9	34.76 f.	35.89	34.00	33.33 ab	34.50
TTM2016-18	25.4 c	20.8 ab	23.3 ac	13.5 g	20.7	34.56 fg	35.72	33.67	33.00 ab	34.24
TTM2016-19	21.7 bc	20.4 ab	25.2 ac	19.2 bcde	21.6	33.33 deg	33.33	34.00	33.67 ab	33.58
TTM2016-20	24.0 ac	20.1 ab	23.4 bc	19.2 bcde	21.7	33.11 de	34.73	34.00	34.33 ab	34.04
TTM2016-22	21.2 bc	17.9 ab	19.7 ab	17.7 ef	19.1	33.07 de	34.97	32.53	34.33 ab	33.73
TTM2016-23	21.2 ab	17.0 ab	24.7 bc	16.2 f.	19.8	32.16 cd	34.67	34.33	33.33 ab	33.62
TTM2016-35	20.7 b	16.8 b	19.6 b	19.7 bcde	19.2	32.50 cd	34.00	35.00	33.33	33.71
TTM2016-38	21.7 c	19.1 ab	26.0 c	20.4 ad	21.8	32.22 cd	32.97	33.67	34.67 b	33.38
TTM2016-40	22.1 bc	19.6 ab	22.8 bc	18.2 def	20.7	33.50 df	36.39	34.00	35.00 ab	34.72
Mean	22.3	19.6	22.7	18.5	20.8	32.68	34.94	33.85	33.40 b	33.72
G	0.3052					0.2402				
Y	<.0001***					0.002344**				
G x Y	<.0001***					<.0001***				
CV (%)	7.53					3.05				

Table 5. Dry matter yield (t ha⁻¹) and dry matter ratio (%) of maize (*Zea mays* L.) genotypes evaluated in the 2017, 2018, 2019, and 2020 growing seasons. Means followed by the same lowercase letters within rows and the same uppercase letters within columns indicate that, for the corresponding variable, no significant difference was detected according to the Scott–Knott test at the 5% significance level ($P < 0.05$). G = effect of genotype. Y = effect of year. G × Y = genotype-by-year interaction (reflecting the genotype–environment interaction). CV = coefficient of variation. The letters shown in the ‘Mean’ rows and columns represent comparisons of the isolated effects of year and genotype, respectively.

Genotype	NDF (%)					ADF (%)				
	Year					Year				
	2017	2018	2019	2020	Mean	2017	2018	2019	2020	Mean
AGA (st)	51.57	50.72 ab	55.91 abc	56.81 a	53.75	30.91	31.61	31.18	31.10	31.20
BURAK (st)	51.51	48.55 a	56.81 bc	56.73 a	53.40	32.03	30.42	31.10	31.11	31.16
Kilowatt (St)	50.92	49.99 ab	56.73 bc	56.44 acd	53.52	30.12	28.63	31.11	30.24	30.02
SAMADA-07(st)	51.79	53.57 ab	56.44 bc	55.08 ab	54.22	30.61	30.30	30.24	30.63	30.44
TTM2015-22	51.66	51.82 ab	55.08 cd	56.28 acd	53.71	30.24	31.53	30.63	30.07	30.62
TTM2015-8	50.38	50.72 ab	56.28 ac	52.11 bde	52.37	30.84	31.61	30.07	29.82	30.58
TTM2016-11	51.91	52.35 ab	55.82 abc	56.12 ad	54.05	30.61	29.57	30.08	30.18	30.11
TTM2016-16	52.53	52.04 ab	55.35 abc	51.99 de	52.98	30.18	29.93	32.31	29.62	30.51
TTM2016-18	53.78	50.67 ab	57.52 c	51.46 ce	53.36	30.44	29.79	31.23	30.36	30.46
TTM2016-19	53.33	50.80 ab	57.38 c	50.03 e	52.89	30.97	29.51	32.37	28.76	30.40
TTM2016-20	52.60	52.26 ab	56.83 bc	55.66 acd	54.34	30.06	30.94	31.07	31.24	30.83
TTM2016-22	51.10	51.75 ab	55.64 abc	55.53 acd	53.51	30.34	31.92	31.67	31.59	31.38
TTM2016-23	52.35	53.51 ab	53.02 bd	55.84 ad	53.68	31.30	30.87	30.05	31.16	30.85
TTM2016-35	54.60	50.72 ab	51.96 ad	55.33 acd	53.15	30.87	31.62	30.21	30.37	30.77
TTM2016-38	51.85	50.34 ab	50.86 d	57.58 ad	52.66	30.57	29.66	31.06	30.27	30.39
TTM2016-40	50.68	55.20 b	57.29 bc	57.75 a	55.23	30.21	31.01	30.79	30.18	30.55
Mean	52.04	51.56	55.56	55.05	53.55	30.64	30.56	30.95	30.42	30.64
G	0.9112					0.4758				
Y	<.0001***					0.6641				
G x Y	<.0001***					0.3010				
CV (%)	3.33					3.76				

Table 6. Neutral detergent fiber (NDF, %) and acid detergent fiber (ADF, %) of maize (*Zea mays* L.) genotypes evaluated in the 2017, 2018, 2019, and 2020 growing seasons. Means followed by the same lowercase letters within rows and the same uppercase letters within columns indicate that, for the corresponding variable, no significant difference was detected according to the Scott–Knott test at the 5% significance level ($P < 0.05$). G = effect of genotype. Y = effect of year. G × Y = genotype-by-year interaction (reflecting the genotype–environment interaction). CV = coefficient of variation. The letters shown in the ‘Mean’ rows and columns represent comparisons of the isolated effects of year and genotype, respectively.

Genotype	ADL (%)					ASH (%)				
	Year					Year				
	2017	2018	2019	2020	Mean	2017	2018	2019	2020	Mean
AGA (st)	3.27	3.34	3.28	3.35	3.31	4.28	4.21	3.85	4.01	4.08
BURAK (st)	3.38	3.28	3.35	3.36	3.34	3.86	3.74	4.01	3.89	3.87
Kilowatt (St)	3.26	3.10	3.36	3.20	3.23	4.04	4.09	3.89	3.88	3.97
SAMADA-07(st)	3.31	3.21	3.20	3.23	3.24	4.31	4.20	3.88	4.13	4.13
TTM2015-22	3.20	3.40	3.23	3.18	3.25	3.88	4.44	4.13	4.15	4.15
TTM2015-8	3.33	3.34	3.18	3.23	3.27	4.35	4.21	4.15	4.31	4.26
TTM2016-11	3.24	3.13	3.18	3.18	3.19	4.31	4.33	4.16	4.34	4.29
TTM2016-16	3.20	3.18	3.39	3.20	3.24	4.28	4.34	4.13	4.29	4.26
TTM2016-18	3.22	3.09	3.29	3.11	3.18	4.18	3.99	4.04	4.14	4.09
TTM2016-19	3.28	3.12	3.49	3.05	3.24	4.28	4.02	4.29	3.82	4.10
TTM2016-20	3.25	3.27	3.36	3.30	3.30	4.28	4.07	3.74	4.19	4.07
TTM2016-22	3.27	3.38	3.34	3.40	3.35	4.37	4.44	4.11	4.21	4.28
TTM2016-23	3.27	3.27	3.18	3.36	3.27	4.02	4.12	4.13	3.98	4.06
TTM2016-35	3.21	3.34	3.20	3.21	3.24	4.16	4.21	4.14	4.15	4.17
TTM2016-38	3.30	3.14	3.29	3.27	3.25	4.40	3.79	4.37	3.59	4.04
TTM2016-40	3.20	3.28	3.25	3.26	3.25	4.09	4.22	4.46	3.69	4.11
Mean	3.26	3.24	3.29	3.24	3.26	4.19	4.15	4.09	4.05	4.12
G	0.2859					0.1501				
Y	1.0000					0.4050				
G x Y	0.8287					0.2266				
CV (%)	4.43					6.76				

Table 7. ADL (%) and ASH (%) of maize (*Zea mays* L.) genotypes evaluated in the 2017, 2018, 2019, and 2020 growing seasons. Means followed by the same lowercase letters within rows and the same uppercase letters within columns indicate that, for the corresponding variable, no significant difference was detected according to the Scott–Knott test at the 5% significance level ($P < 0.05$). G = effect of genotype. Y = effect of year. G × Y = genotype-by-year interaction (reflecting the genotype–environment interaction). CV = coefficient of variation. The letters shown in the ‘Mean’ rows and columns represent comparisons of the isolated effects of year and genotype, respectively.

Genotype	OIL (%)					Protein (%)				
	Year					Year				
	2017	2018	2019	2020	Mean	2017	2018	2019	2020	Mean
AGA (st)	3.51	2.85 ab	2.78	2.91	3.01	9.04	8.83	9.08	8.49	8.86
BURAK (st)	3.67	3.32 ab	2.83	3.89	3.43	8.37	8.77	8.49	8.67	8.58
Kilowatt (St)	3.43	3.74 b	2.96	3.64	3.44	8.92	8.65	8.67	9.52	8.94
SAMADA-07(st)	3.21	3.85 b	3.28	3.16	3.38	8.93	9.17	9.52	8.52	9.03
TTM2015-22	3.32	3.67 ab	3.14	3.06	3.29	8.80	9.47	8.52	8.14	8.73
TTM2015-8	3.52	3.18 ab	3.66	3.34	3.43	8.99	8.83	8.14	9.01	8.74
TTM2016-11	3.18	3.51 ab	3.10	2.83	3.15	9.10	9.00	8.76	8.00	8.72
TTM2016-16	3.12	3.50 ab	3.41	3.51	3.39	8.98	8.87	9.19	8.90	8.98
TTM2016-18	3.33	3.62 ab	2.85	3.18	3.24	9.37	8.75	8.75	8.95	8.95
TTM2016-19	3.51	3.30 ab	3.75	3.51	3.52	8.98	8.74	9.06	8.66	8.86
TTM2016-20	3.44	3.44 ab	3.36	3.58	3.46	8.96	8.46	8.78	8.14	8.59
TTM2016-22	3.04	3.51 ab	2.84	3.32	3.18	8.80	9.19	8.77	9.00	8.94
TTM2016-23	3.31	2.91 ab	3.38	2.91	3.13	8.66	8.72	9.98	9.38	9.19
TTM2016-35	3.33	3.29 ab	3.52	3.26	3.35	8.74	8.84	8.98	9.31	8.97
TTM2016-38	3.60	3.22 ab	3.01	3.21	3.26	9.64	8.77	9.02	8.52	8.99
TTM2016-40	3.82	2.69 a	3.29	3.68	3.37	9.02	8.80	8.16	8.50	8.62
Mean	3.40	3.35	3.20	3.31	3.31	8.96	8.86	8.87	8.73	8.85
G	0.5618					0.6586				
Y	0.9011					1.0000				
G x Y	0.0362*					1.0000				
CV (%)	11.96					7.69				

Table 8. OIL (%) and protein (%) contents of maize (*Zea mays* L.) genotypes evaluated in the 2017, 2018, 2019, and 2020 growing seasons. Means followed by the same lowercase letters within rows and the same uppercase letters within columns indicate that, for the corresponding variable, no significant difference was detected according to the Scott–Knott test at the 5% significance level ($P < 0.05$). G = effect of genotype. Y = effect of year. G $\times$ Y = genotype-by-year interaction (reflecting the genotype–environment interaction). CV = coefficient of variation. The letters shown in the ‘Mean’ rows and columns represent comparisons of the isolated effects of year and genotype, respectively.

Genotype	Cellulose (%)					Estimated milk yield (t ha ⁻¹)				
	Year					Year				
	2017	2018	2019	2020	Mean	2017	2018	2019	2020	Mean
AGA (st)	27.64	28.27	27.90	27.75	27.89	33.05 ab	24.96 ab	29.69 a	31.74 ab	29.86
BURAK (st)	28.64	27.14	27.75	27.75	27.82	36.48 ab	27.23 ab	34.26 ab	29.67 bcd	31.91
Kilowatt (St)	26.87	25.53	27.75	27.04	26.80	36.97 ab	29.15 ab	39.53 ab	23.26 ef	32.23
SAMADA-07(st)	27.30	27.09	27.04	27.40	27.21	24.22 a	36.17 a	30.90 ab	25.23 def	29.13
TTM2015-22	27.04	28.12	27.40	26.89	27.36	36.45 ab	30.58 ab	49.23 b	33.89 b	37.54
TTM2015-8	27.50	28.27	26.89	26.59	27.31	46.40 b	32.77 ab	47.55 ac	23.72 cef	37.61
TTM2016-11	27.37	26.44	26.89	27.00	26.92	45.91 b	24.03 ab	33.40 ab	24.69 def	32.01
TTM2016-16	26.98	26.74	28.92	26.42	27.27	42.65 ab	29.47 ab	31.60 ac	23.27 ef	31.75
TTM2016-18	27.22	26.70	27.95	27.26	27.28	46.41 ab	31.10 ab	39.14 bc	13.55 g	32.55
TTM2016-19	27.69	26.38	28.88	25.72	27.17	35.98 ab	31.07 ab	47.20 bc	27.78 adfh	35.51
TTM2016-20	26.81	27.67	27.71	27.94	27.53	43.07 ab	29.74 ab	40.85 ab	27.44 adf	35.28
TTM2016-22	27.07	28.55	28.33	28.20	28.04	32.50 ab	22.40 ab	28.86 a	22.56 eh	26.58
TTM2016-23	28.04	27.61	26.87	27.80	27.58	34.62 ab	20.11 b	44.08 ab	19.42 eg	29.56
TTM2016-35	27.66	28.28	27.01	27.16	27.53	32.66 ab	20.48 b	27.74 a	28.72 bcf	27.40
TTM2016-38	27.27	26.52	27.78	27.00	27.14	36.14 ab	27.65 ab	48.96 b	30.42 bd	35.79
TTM2016-40	27.01	27.73	27.55	26.92	27.30	37.07 ab	25.09 ab	37.39 ab	24.62 def	31.04
Mean	27.38	27.31	27.66	27.18	27.38	37.54	27.63	38.15	25.62	32.23
G	0.4885					0.1658				
Y	0.6333					<.0001***				
G × Y	0.2819					<.0001***				
CV (%)	3.76					15.00				

Table 9. Cellulose (%) and estimated milk yield (t ha⁻¹) of maize (*Zea mays* L.) genotypes evaluated in the 2017, 2018, 2019, and 2020 growing seasons. Means followed by the same lowercase letters within rows and the same uppercase letters within columns indicate that, for the corresponding variable, no significant difference was detected according to the Scott–Knott test at the 5% significance level ($P < 0.05$). G = effect of genotype. Y = effect of year. G × Y = genotype-by-year interaction (reflecting the genotype–environment interaction). CV = coefficient of variation. The letters shown in the ‘Mean’ rows and columns represent comparisons of the isolated effects of year and genotype, respectively.

Trait	2017	2018	2019	2020
Pollen DAP (day)	0.85	0.45	0.65	0.98
Plant height (cm)	0.81	0.43	0.76	0.96
Ear height (cm)	0.92	0.27	0.51	0.89
Leaf/stem ratio (%)	0.85	0	0.90	0.79
Cob/plant ratio (%)	0.84	0	0.57	0.44
Green weight (t ha ⁻¹)	0.80	0.67	0.76	0.95
Dry matter yield (t ha ⁻¹)	0.80	0.53	0.77	0.94
Dry matter (%)	0.95	0.38	0.08	0.66
Protein (%)	0	0	0	0
NDF (%)	0	0.55	0.79	0.85
ADF (%)	0	0.60	0	0.41
ADL (%)	0	0.50	0.14	0.36
Cellulose (%)	0	0.59	0	0.39
Ash (%)	0.14	0.31	0.07	0.56
OIL (%)	0	0.54	0.47	0.41

Table 1. Within-year broad-sense heritability (H^2) estimates for agronomic and quality traits of silage maize genotypes across the 2017–2020 growing seasons. Within-year H^2 was calculated for each year separately using plot-level data from the randomized complete block design (RCBD), based on the mixed-model-derived variance components. DAP, days after planting; NDF, neutral detergent fiber; ADF, acid detergent fiber; ADL, acid detergent lignin.

Genotype	Gross energy (GE = Mcal/kg DM)					Digestible energy (DE, Mcal/kg DM)				
	Year					Year				
	2017	2018	2019	2020	Mean	2017	2018	2019	2020	Mean
AGA (st)	4.51	4.51	4.53	4.52	4.52	2.87	2.84	2.87	2.87	2.86
BURAK (st)	4.52	4.53	4.52	4.52	4.52	2.83	2.90	2.87	2.87	2.87
Kilowatt (St)	4.52	4.52	4.52	4.53	4.53	2.91	2.96	2.87	2.91	2.91
SAMADA-07(st)	4.51	4.52	4.53	4.51	4.52	2.88	2.89	2.91	2.88	2.89
TTM2015-22	4.53	4.50	4.51	4.51	4.51	2.90	2.84	2.88	2.90	2.88
TTM2015-8	4.51	4.51	4.51	4.51	4.51	2.87	2.84	2.90	2.91	2.88
TTM2016-11	4.51	4.51	4.52	4.50	4.51	2.88	2.92	2.90	2.89	2.90
TTM2016-16	4.51	4.51	4.51	4.51	4.51	2.89	2.90	2.82	2.92	2.88
TTM2016-18	4.52	4.52	4.52	4.52	4.52	2.89	2.91	2.86	2.89	2.89
TTM2016-19	4.51	4.52	4.50	4.53	4.52	2.86	2.93	2.81	2.96	2.89
TTM2016-20	4.51	4.51	4.53	4.50	4.52	2.90	2.87	2.88	2.85	2.88
TTM2016-22	4.51	4.50	4.51	4.51	4.51	2.89	2.82	2.84	2.85	2.85
TTM2016-23	4.52	4.51	4.53	4.52	4.52	2.86	2.87	2.91	2.87	2.88
TTM2016-35	4.51	4.51	4.52	4.52	4.51	2.87	2.84	2.90	2.89	2.87
TTM2016-38	4.51	4.53	4.50	4.54	4.52	2.88	2.93	2.86	2.91	2.89
TTM2016-40	4.52	4.51	4.49	4.53	4.51	2.90	2.86	2.86	2.91	2.88
Mean	4.51	4.51	4.52	4.52	4.52	2.88	2.88	2.87	2.89	2.88
G	0.2557					0.5430				
Y	1.0000					0.7104				
G × Y	0.1335					0.3230				
CV (%)	0.30					1.60				

Table 10. Gross energy (GE, Mcal kg⁻¹ DM) and digestible energy (DE, Mcal kg⁻¹ DM) of maize (*Zea mays* L.) genotypes evaluated during the 2017–2020 growing seasons. Means followed by the same lowercase letters within rows and the same uppercase letters within columns indicate that, for the corresponding variable, no significant difference was detected according to the Scott–Knott test at the 5% significance level ($P < 0.05$). G = effect of genotype. Y = effect of year. G × Y = genotype-by-year interaction (reflecting the genotype–environment interaction). CV = coefficient of variation. The letters shown in the ‘Mean’ rows and columns represent comparisons of the isolated effects of year and genotype, respectively.

Trait	Genotype	Mean value*	Mean rank	GGE-SI	Stability rank	Integrated rank
Green weight	BURAK (st)	63.4	7	0.504	2	9
Green weight	TTM2016-20	63.8	6	0.852	4	10
Green weight	TTM2016-18	65.9	2	1.406	9	11
Green weight	Kilowatt (St)	61.6	10	0.312	1	11
Green weight	TTM2015-22	67.1	1	2.004	11	12
Dry matter yield	TTM2016-20	21.7	4	0.725	4	8
Dry matter yield	TTM2016-40	20.7	8	0.036	1	9
Dry matter yield	Kilowatt (St)	20.7	8	0.492	2	10
Dry matter yield	TTM2016-38	21.8	3	1.326	9	12
Dry matter yield	TTM2016-16	20.9	6	1.086	6	12
Estimated milk yield	Kilowatt (St)	32.23	7	0.356	1	8
Estimated milk yield	TTM2016-20	35.28	5	0.913	5	10
Estimated milk yield	TTM2016-38	35.79	3	1.417	8	11
Estimated milk yield	BURAK (st)	31.91	9	0.792	3	12
Estimated milk yield	TTM2016-19	35.51	4	1.439	9	13

Table 11. Integrated summary of mean performance and stability for green weight, dry matter yield, and estimated milk yield traits in 16 silage maize genotypes evaluated across 2017–2020. Mean values were taken from the across-year genotype means in the main results tables, and stability ranks were derived from the GGE-SI spreadsheet. Lower GGE-SI and lower stability rank indicate greater stability. Integrated rank was calculated as mean rank + stability rank; lower values indicate a more favorable balance between performance and stability.

Data availability

Data available on request from the corresponding author.

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Declarations

Competing interests

The authors declare no competing interests.

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Consent to publication

Authors read the manuscript and showed his willingness to publish this study.

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