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Lie Liu
Yunnan Academy of Agricultural Sciences
Tingzhi Huang
Yunnan Academy of Agricultural Sciences
Xiangmei Qiao
Yunnan Academy of Agricultural Sciences
Jiasheng Cheng
Yunnan Academy of Agricultural Sciences
Xinliang Zhang
Yunnan Agricultural University
Ming Cai
Yunnan Academy of Grassland and Animal Science
Geng Cheng
Yunnan Academy of Agricultural Sciences
Zhiwei Wang
Yunnan Academy of Agricultural Sciences
Zhilong Wang
wzl@yaas.org.cn

Yunnan Academy of Agricultural Sciences

Article

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Posted Date: October 22nd, 2026

DOI: https://doi.org/10.21203/rs.3.rs-11101453/v1

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Additional Declarations: No competing interests reported.

Dry matter yield and interaction stability of forage barley across ten environments in Yunnan, China

Lie Liu[1]†, Tingzhi Huang[1]†, Xiangmei Qiao[1], Jiasheng Cheng[1], Xinliang Zhang[2], Ming Cai[3], Geng Cheng[1], Zhiwei Wang[1]*, Zhilong Wang[1]*

1. Food Crops Research Institute, Yunnan Academy of Agricultural Sciences, Kunming 650205, China

2. Department of Pratacultural Science, Faculty of Animal Science and Technology, Yunnan Agricultural University, Kunming 650201, China

3. Yunnan Academy of Grassland and Animal Science, Kunming 650212, China

†These authors contributed equally to this work: Lie Liu and Tingzhi Huang.

*Correspondence: Zhilong Wang (wzl@yaas.org.cn) and Zhiwei Wang (wzw0903@126.com)

Abstract

Selecting forage barley for heterogeneous production areas requires separating biomass production from genotype-by-environment response. We evaluated ten genotypes at five locations over two seasons in Yunnan, China (ten site–season environments; 300 plots). Dry matter yield (DMY) was the primary outcome. Genotype means and contrasts came from a fixed-effects model with environment-specific residual variances; AMMI and GGE analyses described interaction structure. Environment accounted for 88.19% of the genotype + environment + interaction sum of squares for DMY. G6 had the highest equally weighted DMY (17.81 t ha^{-1}; pointwise 95% confidence interval 17.14–18.48), followed by G1 (16.75 t ha^{-1}) and G8 (16.43 t ha^{-1}), although G6 did not differ from either after adjustment across 45 pairwise comparisons. G10 had the smallest all-axis weighted average of absolute AMMI scores, whereas G6 and G1 ranked first and second when yield and interaction stability received equal weight. G6 retained the highest mean after omission of each location and ranked first in 91.94% of intact-location resamples. The evidence supports G6 and G1 as candidates for expanded testing; nutritive value and performance in additional years remain to be established.

Keywords: AMMI; dry matter yield; forage barley; GGE biplot; genotype × environment interaction; multi-environment trial

Introduction

Whole-crop barley (*Hordeum vulgare* L.) is used as conserved forage in ruminant production systems, but its value depends on both the quantity and composition of harvested biomass [1,2]. A field study in south-central China found genotypic differences in forage yield and composition under sole-use and dual-use production, illustrating the need to evaluate barley for its intended end use [3]. Harvest management adds another dimension because cultivar-specific changes in dry matter concentration, starch accumulation and digestibility during grain filling can alter the balance between forage yield and quality [4]. Comparisons among winter cereal cultivars likewise show that biomass production, forage quality and a suitable harvest window are related but distinct objectives [5,6].

Regional cultivar evaluation must also account for variation among locations and growing seasons. Genotype × environment interaction (GEI) can change relative performance, so a high overall mean and a small interaction response describe different attributes of a cultivar [7,8]. Multi-environment trials provide the data needed to distinguish these attributes, but the statistical target must be stated. In particular, inference conditional on a defined

set of site–season environments is narrower than inference to an unsampled population of future locations and years.

AMMI separates genotype and environment main effects from their interaction, whereas GGE biplots display genotype effects together with GEI [9–13]. Weighted absolute AMMI scores can summarize the magnitude of interaction scores, and an explicitly weighted combination of yield and stability can support a declared selection preference [12]. Genotype comparisons also require an appropriate error model because trial precision can vary substantially among environments [14,15]. Treating such heterogeneity as absent may alter standard errors and pairwise conclusions.

Agronomic traits may help describe the phenotype associated with high biomass production, but multivariate axes are not themselves selection objectives. Principal component analysis (PCA), for example, is useful for displaying correlated genotype-mean traits but cannot establish causal trait effects or nutritional value [16]. Multiple testing also matters when correlations or many genotype contrasts are examined; adjusted inferences are needed to limit false-positive conclusions [17,18].

Here, ten forage barley entries were evaluated at five sites in Yunnan over two consecutive winter growing seasons. Our primary objective was to identify candidates with high milk-stage DMY and an acceptable interaction response within the ten tested environments. Secondary objectives were to describe associated agronomic variation and to assess the sensitivity of candidate rankings to AMMI axis choice, yield–stability weighting and omission or resampling of locations. The study addresses biomass production and agronomic performance; nutritional composition and ensiling performance were not measured.

Materials and methods

Experimental environments and plant materials

Field trials were conducted during the 2021–2022 and 2022–2023 growing seasons at Longyang (Baoshan), Gucheng (Lijiang), Heqing (Dali), Songming (Kunming) and Yimen (Yuxi), Yunnan Province, China. Each location–season combination was treated as one test environment, giving ten environments (Table 1; Fig. 1). The sites ranged in reported elevation from 1,543 to 2,410 m. Growing-season weather observations were not available for this analysis; environmental effects were therefore interpreted as site–season differences rather than attributed to individual climatic variables.

The ten entries comprised released cultivars and breeding lines and were coded G1–G10 (Supplementary Table S1). Names, spike type, material type and source institution are reported in the Supplementary Information.

The released cultivars and breeding lines were provided by the institutions listed in Supplementary Table S1, and authorization was obtained from the respective material-holding institutions for their use in the field experiments and publication. All experimental research on plants complied with relevant institutional, national and international guidelines and legislation. No wild plant material was collected.

Table 1. Test environments.

Environment	Growing season	Location	Coordinates	Elevation (m)
E1-1	2021–2022	Longyang, Baoshan	25°19′ N, 99°22′ E	1,664
E1-2	2022–2023	Longyang, Baoshan	25°19′ N, 99°22′ E	1,664
E2-1	2021–2022	Gucheng, Lijiang	26°52′ N, 100°26′ E	2,410
E2-2	2022–2023	Gucheng, Lijiang	26°52′ N, 100°26′ E	2,410
E3-1	2021–2022	Heqing, Dali	26.5036° N, 100.1797° E	2,217

Environment	Growing season	Location	Coordinates	Elevation (m)
E3-2	2022–2023	Heqing, Dali	26.5036° N, 100.1797° E	2,217
E4-1	2021–2022	Songming, Kunming	25°21′ N, 103°06′ E	1,920
E4-2	2022–2023	Songming, Kunming	25°21′ N, 103°06′ E	1,920
E5-1	2021–2022	Yimen, Yuxi	24°39′ N, 102°17′ E	1,543
E5-2	2022–2023	Yimen, Yuxi	24°39′ N, 102°17′ E	1,543

Experimental design and crop management

Each trial used a randomized complete block design with three replicates. Each 10-m² plot contained 12 rows spaced 23 cm apart, and guard rows surrounded the experimental area. The target density was approximately 2.25 × 10^6 plants ha^{-1}, with seeding rates adjusted for germination percentage. Trials were sown from October to November according to local growing seasons. Fertilization, irrigation and pest management followed local agronomic practices and varied among locations and growing seasons. Previous crops and the documented irrigation practices are summarized in Supplementary Table S10. Accordingly, each environment represents a combination of location, season and local management, and is not attributable solely to climate.

Each genotype was harvested when it reached the milk stage. Above-ground biomass was cut approximately 5 cm above the soil surface and weighed immediately to obtain plot fresh biomass yield. An approximately 2-kg whole-plant subsample from each plot was heated at 105 °C for 2 h and then dried at 60 °C to constant mass. Dry matter yield was calculated as fresh biomass yield multiplied by dry matter fraction.

Plant height, effective tiller number and green leaves per plant were recorded one day before harvest. Plant height was measured on 30 randomly selected plants per plot from the plant base to the uppermost point in the natural standing position. Effective tillers were counted in the second and penultimate rows of each plot. The two row counts were summed and converted to tillers m^{-2} according to the surveyed row area. Green functional leaves were counted on 30 representative plants per plot.

Statistical analysis and scope of inference

The plot was the experimental unit. Each genotype was represented by three plots in each of ten environments. Genotype means were calculated by giving equal weight to each environment. The primary analysis was conditional on the ten environments and did not treat them as a random sample of all possible production environments. We fitted

$$Y_{ijk} = \mu + G_i + E_j + (GE)_{ij} + B_{k(j)} + \varepsilon_{ijk},$$

where Y_{ijk} is the plot observation, G_i is genotype, E_j is environment, $(GE)_{ij}$ is their interaction and $B_{k(j)}$ is block nested within environment. These terms were fitted as fixed effects. Plot errors were independent with an environment-specific variance, $\varepsilon_{ijk} \sim N(0, \sigma_j^2)$. For DMY, restricted maximum-likelihood generalized least squares was fitted with the nlme package [19]. In the balanced design, fitted marginal genotype means were identical to arithmetic means across the ten environments. Environment-specific residual variances were also obtained from the corresponding within-environment randomized-block analyses, each with 18 residual degrees of freedom, and were used to verify the generalized least-squares results.

For an equally weighted genotype mean, the estimated variance was $v = \sum_{e=1}^{10} s_e^2/(3 \times 10^2)$; for a difference between two genotype means it was $2v$, where s_e^2 is the residual variance in environment e. Approximate denominator degrees of freedom were obtained by Satterthwaite's method [17]. Equality of the ten genotype means

was tested with $F = \sum_g (\bar{y}_g - \bar{y})^2/(9v)$, using 9 numerator degrees of freedom and the Satterthwaite denominator degrees of freedom. Pointwise 95% confidence intervals are reported for genotype means. Pairwise tests were two-sided and adjusted by Holm's procedure across all 45 genotype pairs [18]. DMY was the principal outcome; analyses of other traits were exploratory.

A balanced analysis-of-variance decomposition was retained to describe the relative contributions of genotype, environment and GEI. For each trait, the descriptive percentage for source x was $100SS_x/(SS_G + SS_E + SS_{GE})$. These percentages are sums-of-squares shares and were not interpreted as random-effect variance components. A common residual variance and environment-specific residual variances were compared for DMY while retaining the same fixed-effects structure.

AMMI, GGE and multivariate descriptions

AMMI was applied to the 10 × 10 matrix of genotype-by-environment DMY means [10,11]. After removal of additive genotype and environment effects, the interaction matrix was decomposed by singular-value decomposition. Symmetric partitioning defined the genotype score on axis k as $\gamma_{gk} = u_{gk}\sqrt{d_k}$. The weighted average of absolute scores was

$$WAAS_g = \sum_{k=1}^{9} p_k|\gamma_{gk}|, p_k = d_k^2/\sum_{j=1}^{9} d_j^2.$$

All nine non-zero interaction axes were retained to describe the observed interaction matrix. Lower WAAS indicates a smaller interaction departure; it does not imply little absolute yield variation among environments. Because the index came from a fixed AMMI decomposition, it is denoted WAAS rather than WAASB [12]. Mean DMY and reversed WAAS were each rescaled from 0 to 100 and combined in WAASY with equal 0.5 weights. Sensitivity analyses used two or four axes, renormalized the retained-axis weights, and varied the yield weight from 0 to 1 in 0.05 increments. WAAS and WAASY ranks were treated as descriptive decision aids without standard errors or significance tests.

GGE analysis used environment-centred, unscaled DMY means with symmetric singular-value partitioning [9,13]. The first two components were used for which-won-where and average-environment-coordinate displays. Observed environment winners were tabulated separately because a winner from the two-axis approximation need not equal the highest observed mean.

PCA was applied to the exact across-environment means of fresh biomass yield, DMY, effective tiller number, plant height and green leaves per plant after centring and scaling each trait to unit variance [16]. Pearson correlations were calculated for the same ten genotype means; two-sided P values for the ten distinct trait pairs were adjusted by the Benjamini–Hochberg procedure [20]. These analyses were descriptive and were not converted into a composite genotype ranking.

Location-based sensitivity analyses

To avoid treating two seasons at the same location as independent locations, plot observations were averaged within each location and genotype. Paired genotype differences across five location means were summarized with t intervals and tests using four degrees of freedom, with Holm adjustment across 45 comparisons. Rankings were recalculated separately by season and after omission of each location. An intact-location bootstrap enumerated all $5^5 = 3{,}125$ ordered samples of five locations with replacement while retaining both seasons and all genotypes from each sampled location. Rank frequencies were used as internal sensitivity descriptions, not as estimates of performance in a wider population. An exact sign-flip analysis of the five paired location differences was also examined.

Analyses and figures were produced in R 4.6.1 [21]. The complete analysis code, source tables and session information are supplied with the article.

Code availability

R code reproducing the statistical analyses, tabulated results and figures is provided as Supplementary Code S1, with a master run script, individual-item scripts, dependency instructions and verification records. The external GADM 4.1 boundary files required for Figure 1 are identified in the code README and are not redistributed.

Use of generative AI

Codex (OpenAI) was used to assist with manuscript revision and statistical and plotting code development, with all AI-assisted content reviewed by the authors, who take full responsibility for the work.

Results

Biomass yield and heterogeneity among environments

The raw dataset contained 300 complete plot records (ten genotypes × ten environments × three blocks), with no missing genotype–environment–block combinations. Mean fresh biomass yield ranged from 40.84 t ha^{-1} for G5 to 50.70 t ha^{-1} for G6. Mean DMY ranged from 14.12 t ha^{-1} for G5 to 17.81 t ha^{-1} for G6 (Supplementary Table S2; Supplementary Fig. S6).

Average DMY differed among genotypes within the tested-environment set (approximate $F_{9,60.62} = 10.05$, $P = 2.87 \times 10^{-9}$). G6 had the highest equally weighted mean, 17.81 t ha^{-1} (pointwise 95% confidence interval 17.14–18.48), followed by G1 at 16.75 t ha^{-1} (16.08–17.42) and G8 at 16.43 t ha^{-1} (15.75–17.10; Table 3). After Holm adjustment across 45 DMY comparisons, G6 did not differ from G1 ($P_{Holm} = 0.682$) or G8 ($P_{Holm} = 0.149$). Its highest observed mean was therefore treated as a candidate-selection signal rather than proof of superiority to every other genotype.

Environment-specific residual variances were strongly supported over a common residual variance for DMY (AIC 967.89 versus 1117.28; restricted-likelihood-ratio statistic 167.40 with 9 df, approximate $P = 2.15 \times 10^{-31}$). Residual standard deviations also varied visibly among environments (Supplementary Fig. S3). This heterogeneity supports the use of environment-specific residual variances for genotype comparisons.

Descriptive partitioning of trial variation

Environment was the largest of the three modelled treatment sources for every trait (Table 2; Supplementary Fig. S2). For DMY, environment accounted for 88.19% of $SS_G + SS_E + SS_{GE}$, GEI for 8.12% and genotype for 3.69%. The corresponding environmental share was 90.97% for fresh biomass yield, 82.97% for effective tiller number, 75.11% for plant height and 87.14% for green leaves per plant. These percentages describe the observed dataset and do not identify the environmental causes.

Table 2. Descriptive shares of genotype, environment and genotype × environment sums of squares.

Trait	Genotype (%)	Environment (%)	GEI (%)
Fresh biomass yield	3.81	90.97	5.22
Dry matter yield	3.69	88.19	8.12
Effective tiller number	7.15	82.97	9.88
Plant height	16.01	75.11	8.89
Green leaves per plant	2.47	87.14	10.39

Percentages use $SS_G + SS_E + SS_{GE}$ as the denominator. Blocks nested within environment and residual error are excluded.

AMMI stability and yield–stability sensitivity

The nine AMMI axes accounted for 100% of the observed DMY interaction sum of squares. The first and second axes accounted for 40.66% and 25.05%, respectively, and the first four axes accounted for 90.84% (Supplementary Table S4). Using all nine axes, G10 had the smallest WAAS (0.350), followed by G1 (0.442) and G6 (0.512). G9 had the largest WAAS (1.184; Table 3).

With equal weights for DMY and reversed WAAS, G6 ranked first for WAASY (90.32), followed by G1 (80.15) and G10 (66.94). G6 and G1 remained first and second when two or four AMMI axes were retained. Across two-, four- and nine-axis calculations, G6 ranked first once the yield weight reached 0.35, whereas G10 was preferred when stability dominated the weighting (Supplementary Fig. S4). Selection therefore depended on the stated balance between productivity and interaction magnitude.

Table 3. Dry matter yield estimates and all-axis AMMI summaries.

Genotype	Mean DMY (t ha^{-1})	Pointwise 95% CI	DMY rank	WAAS	WAAS rank	WAASY (50:50)	WAASY rank
G6	17.811	17.139–18.483	1	0.512	3	90.32	1
G1	16.752	16.080–17.424	2	0.442	2	80.15	2
G8	16.425	15.753–17.097	3	0.934	9	46.24	6
G9	16.106	15.434–16.778	4	1.184	10	26.93	10
G7	15.914	15.242–16.586	5	0.916	8	40.40	8
G10	15.369	14.697–16.041	6	0.350	1	66.94	3
G3	15.209	14.537–15.880	7	0.713	6	43.03	7
G4	15.078	14.406–15.750	8	0.529	4	52.30	4
G2	14.856	14.184–15.528	9	0.578	5	46.37	5
G5	14.117	13.446–14.789	10	0.727	7	27.42	9

Means are equally weighted over the ten tested environments. Confidence intervals use environment-specific residual variances and are pointwise. WAAS uses all nine interaction axes; lower values indicate smaller interaction departures. WAASY equally weights rescaled DMY and reversed WAAS; higher values indicate a preferred yield–stability combination.

GGE description and environment-specific winners

The first two GGE axes explained 36.59% and 25.46% of the environment-centred G + GE sum of squares, respectively (62.06% cumulatively; Figs. 2 and 3). The observed highest-mean genotypes were G8 in E1-1 and E1-2, G9 in E2-1 and E2-2, G6 in E3-1, E3-2, E4-2, E5-1 and E5-2, and G7 in E4-1 (Supplementary Table S5). The two-axis which-won-where approximation disagreed with the observed winner in E1-1 and E4-1, so sector membership was not used as a substitute for the observed environment means.

In the average-environment-coordinate display, G6 projected toward high mean performance, while G10 lay close to the average-environment axis. These properties are consistent with the separate mean and WAAS results. The first two axes omit 37.94% of G + GE variation, however, so the displayed perpendicular distance was not treated as a complete stability measure.

Agronomic trait profiles

Genotype means differed for all five traits in the conditional fixed-environment analysis (Supplementary Tables S2 and S3). G6 had the highest mean fresh biomass yield (50.70 t ha^{-1}), DMY, effective tiller density (739.59 tillers m^{-2}) and green leaves per plant (4.80), while G1 was tallest on average (108.40 cm) and had a similar tiller density.

PC1 and PC2 explained 78.93% and 9.90% of standardized variation among the ten genotype means, respectively (88.83% cumulatively; Fig. 4). All five trait vectors had positive PC1 loadings, and G6 and G1 had the largest positive PC1 scores. This configuration describes their joint agronomic profiles; it is not an independent confirmation of yield superiority because DMY and fresh biomass yield were included in the same PCA.

Fresh biomass yield correlated with DMY ($r = 0.948$, BH-adjusted $q = 0.00031$), effective tiller number ($r = 0.813$, $q = 0.0120$), plant height ($r = 0.743$, $q = 0.0277$) and green leaves per plant ($r = 0.707$, $q = 0.0369$). DMY correlated with effective tiller number ($r = 0.694$, $q = 0.0372$); its correlations with plant height ($q = 0.0631$) and green leaves per plant ($q = 0.0617$) did not pass the 0.05 adjusted threshold. These ten-genotype associations are descriptive and do not establish physiological effects.

Location-based sensitivity of candidate rankings

G6 had the highest mean DMY in separate summaries of both seasons and after omission of each of the five locations. In the 3,125 intact-location resamples, G6 ranked first in 91.94% and among the first three in all resamples; G8 and G9 ranked first in 5.79% and 2.27%, respectively (Table 4). In the paired five-location analysis, the G6–G1 difference was 1.06 t ha^{-1}, but it did not remain significant after Holm adjustment ($P = 0.802$). Only G6 versus G5 remained significant after the 45-comparison adjustment ($P = 0.0334$). No contrast reached $P < 0.05$ in the exact sign-flip check; with five pairs, the smallest attainable two-sided P value was 0.0625.

Table 4. Internal sensitivity of selected dry matter yield rankings.

Genotype	Full-data DMY rank	Rank after omitting one location	Rank 1 in location resamples (%)	Top 3 in location resamples (%)
G6	1	1–1	91.94	100.00
G1	2	2–3	0.00	91.14
G8	3	2–5	5.79	55.07
G9	4	3–5	2.27	40.10
G10	6	5–9	0.00	0.64

Resampling retained both seasons and all genotypes at each sampled location. Frequencies are internal ranking-sensitivity summaries and are not probabilities of future superiority.

Discussion

Environment, precision and the target of inference

Site–season environment was the dominant observed treatment source for DMY and the other agronomic traits. This finding supports multi-environment evaluation but does not identify the cause of the differences. Temperature, rainfall, soil conditions, crop development and management can jointly influence whole-crop barley, and process-based studies need explicit weather, management and compositional data to separate these influences [22]. Because the present dataset contained neither growing-season meteorological measurements nor soil covariates, causal climatic explanations and agroecological zoning would exceed the evidence.

Trial precision also differed substantially among environments. Modelling an environment-specific residual variance produced a much better DMY fit than assuming one pooled variance, consistent with previous demonstrations that heterogeneous error can affect genotype comparisons in multi-location trials [14,15]. The equal-weighted estimand used here gives each of the ten tested environments the same influence on genotype means while allowing their plot-level uncertainties to differ. Its confidence intervals quantify experimental error within this defined environment set; they do not include uncertainty from sampling future years, locations or management systems.

Candidate selection and its limits

G6 had the highest mean DMY, retained that rank in both seasons and in every leave-one-location-out analysis, and ranked first in most intact-location resamples. G1 combined the second-highest mean with the second-lowest all-axis WAAS. These convergent summaries justify advancing G6 and G1 to larger regional trials. They do not establish that G6 is uniformly superior: its adjusted contrasts with G1 and G8 were not significant, and the site-paired G6–G1 comparison was also non-significant after multiplicity adjustment.

The priority given to G6 and G1 concerns whole-crop biomass at the harvest stage evaluated here. It does not demonstrate an advantage in crude protein, fibre, digestibility, fermentation quality or animal performance. Cereal forage studies have shown that later maturity may increase DMY while changing protein, fibre, starch and digestibility [4–6]. Cultivar-specific grain-filling dynamics also mean that a common calendar date need not represent equivalent physiological development [4]. Subsequent evaluation should record phenological stage consistently and combine yield with nutritive and ensiling measurements.

G6 and G1 were the only two two-row entries in the panel, but row type is completely confounded with genotype subgroup in a set containing two two-row and eight six-row entries. Their performance therefore cannot be attributed to row type. A separate Chinese forage-barley study found higher forage yield for six-row entries in its population and production context [3], reinforcing the need to evaluate individual entries rather than generalize from the present imbalance.

Stability depends on the statistic and selection preference

G10 illustrates why stability and productivity must be separated. It had the smallest WAAS, indicating the weakest weighted interaction departure, but ranked sixth for mean DMY. Moreover, its across-environment coefficient of variation was not the smallest because WAAS removes additive environmental effects before describing interaction. A low WAAS therefore does not mean constant absolute yield.

WAASY made the selection preference explicit. G6 ranked first once yield received at least 35% weight under the tested axis choices, whereas G10 was preferred at low yield weights. G6 and G1 remained first and second under equal weights with two, four or all nine axes. These checks show that their priority is robust within a reasonable productivity-oriented decision rule, while also showing that no yield–stability rank is assumption-free. Similar weight sensitivity has been used in forage-oriented multi-environment studies to make the decision criterion visible [23,24].

The GGE plots provided a useful graphical view of response structure, but the first two axes represented 62.06% of G + GE variation and did not reproduce every observed winner. We therefore interpret their sectors and average-environment coordinates as two-dimensional descriptions, together with observed means and all-axis AMMI summaries. Agreement among AMMI, GGE and resampling analyses derived from the same observations is consistency, not external validation.

Agronomic associations and future work

The PCA and correlations showed that higher DMY in this small panel accompanied a generally high-biomass trait profile, particularly higher fresh biomass yield and effective tiller density. Because the analysis used only ten genotype means, included DMY itself in the PCA and did not control genetic relatedness, these results cannot identify causal mechanisms or independently validate genotype ranking.

The study contains only five locations, two consecutive seasons and three plots per genotype–environment combination. The conditional model assumes independent, approximately Gaussian plot errors and a common variance across genotypes within each environment. The location-level checks have limited small-sample resolution, and the bootstrap resamples only the five observed locations. More locations and years, verified phenology and site metadata, and direct forage-quality measurements are needed before recommendations for broad cultivation or specific adaptation.

Conclusion

Within ten tested Yunnan site–season environments, G6 had the highest mean DMY and a favorable yield–interaction-stability balance, while G1 combined high mean DMY with a smaller AMMI interaction score. G10 was the most interaction-stable genotype by WAAS but had only moderate mean yield. Heterogeneous trial precision, multiplicity-adjusted comparisons and location-based sensitivity analyses all argue for treating G6 and G1 as candidates for expanded evaluation rather than as established broadly adapted cultivars. Further trials should extend the number of years and environments and measure forage nutritive value.

Data availability

The complete plot-level data are provided in Supplementary Data S1 as a CSV file, with variable definitions and genotype–environment codes in the accompanying README and Supplementary Table S1.

Author contributions

Zhilong Wang conceived and designed the study. Geng Cheng and Ming Cai conducted the field experiments. Lie Liu and Tingzhi Huang performed the data analysis and wrote the original manuscript. Xiangmei Qiao, Jiasheng Cheng and Xinliang Zhang prepared the figures and tables. Zhilong Wang and Zhiwei Wang reviewed the manuscript and supervised the project. Lie Liu and Tingzhi Huang contributed equally to this work. All authors reviewed and approved the final manuscript.

Funding

This work was supported by the Yunnan Provincial Major Science and Technology Special Program (202502AE090011), the 2026 Yunnan Provincial Crop Variety Promotion Post-subsidy Project (2610609000333), the Expert Workstation Project of Lijiang City (Ljgzz2025-09),and the Major Special Project of the Yunnan Provincial Department of Finance Budget (530000210000000013809).

The funders had no role in study design, data collection, analysis, interpretation of results or the decision to submit the manuscript for publication.

Competing interests

The authors declare no competing interests.

Figure legends



(a) MNR standard map GS(2019)1676; (b) GADM 4.1 and author-confirmed site coordinates.

Figure 1. Geographic distribution of the five trial locations. (a) Location of Yunnan within China, shown using a standard map from the Ministry of Natural Resources of China (map approval No. GS(2019)1676), including the original South China Sea islands inset. The Yunnan arrow indicates the study province, rather than an individual trial site. The base-map boundaries and inset were retained. (b) Author-confirmed trial-field locations in Yunnan; red circles identify E1–E5, each evaluated in two growing seasons. Site coordinates and reported elevations correspond to Table 1. Boundaries in panel (b) are from the author-held GADM version 4.1 dataset (https://gadm.org). The scale bar in panel (b) is approximate at 25° N.

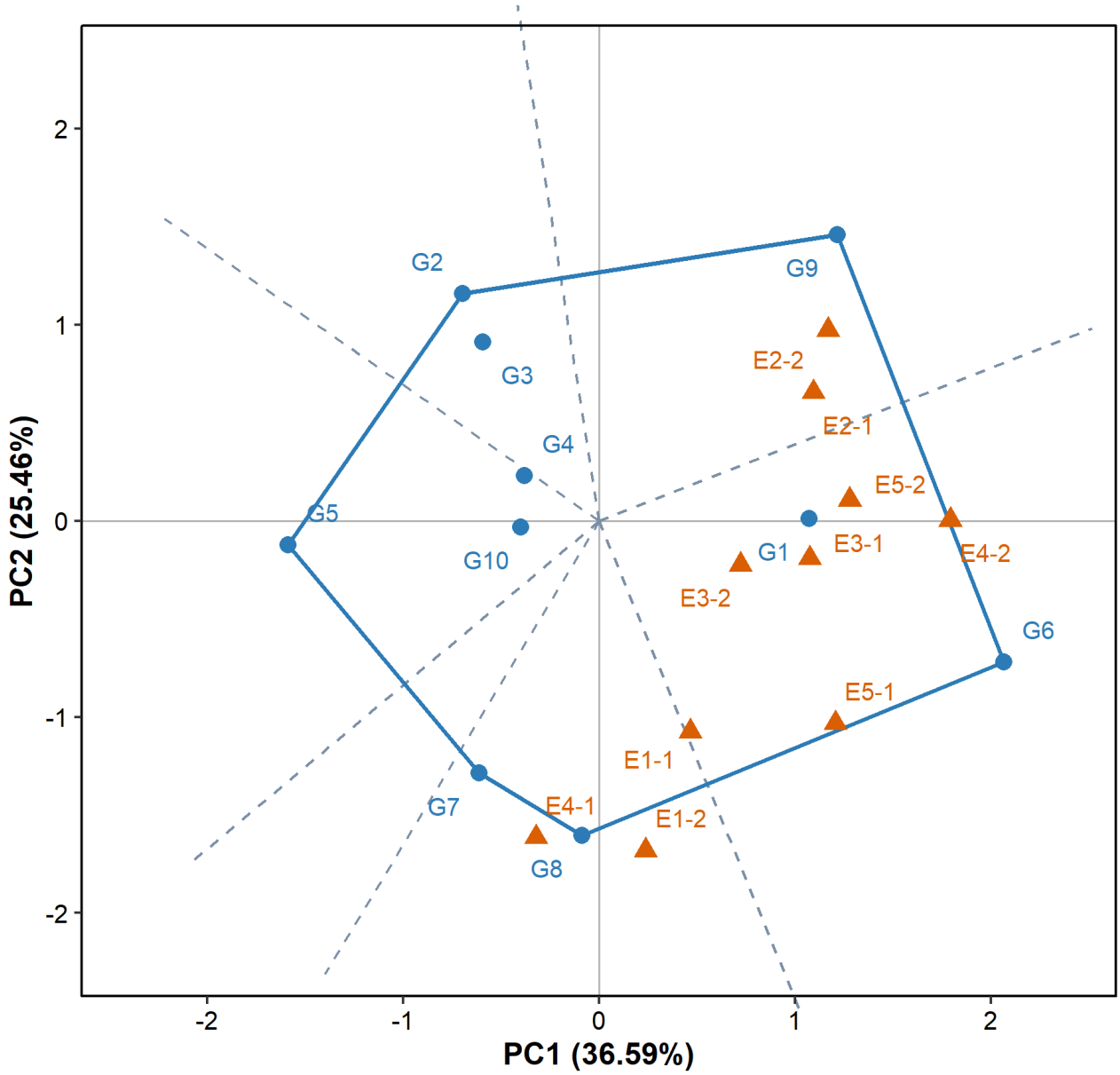


Figure 2. Which-won-where GGE biplot for dry matter yield. The input comprises 10 genotype × 10 environment means, each based on three replicate plots. Environment means were subtracted without variance scaling. Genotype and environment coordinates use symmetric singular-value partitioning. PC1 and PC2 explain 36.59% and 25.46% of G + GE sum of squares. Circles identify genotypes, triangles identify environments and the polygon joins vertex genotypes. Dashed rays delimit sectors of the two-axis approximation. Sector winners need not equal the highest observed means; observed and predicted winners differ in E1-1 and E4-1.

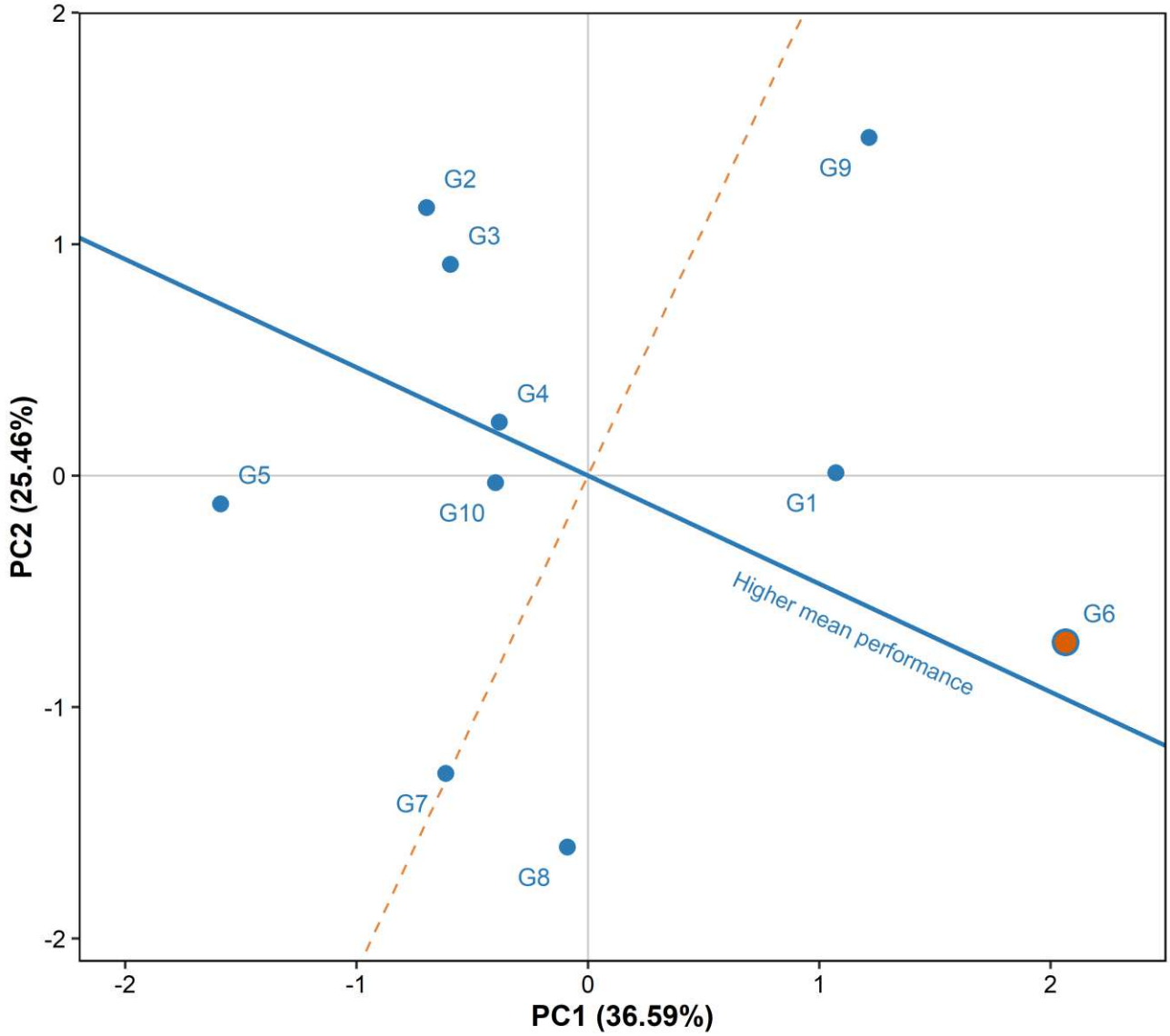


Figure 3. Average-environment-coordinate view of the dry matter yield GGE biplot. Preprocessing and explained percentages are as in Fig. 2. Points identify genotypes, with G6 highlighted. The blue solid line is the average-environment axis, with the direction of higher mean performance labelled; the orange dashed line is perpendicular to that axis. A smaller perpendicular distance from a genotype to the blue axis indicates less interaction represented by the displayed axes and does not establish stability on omitted axes or in new environments.

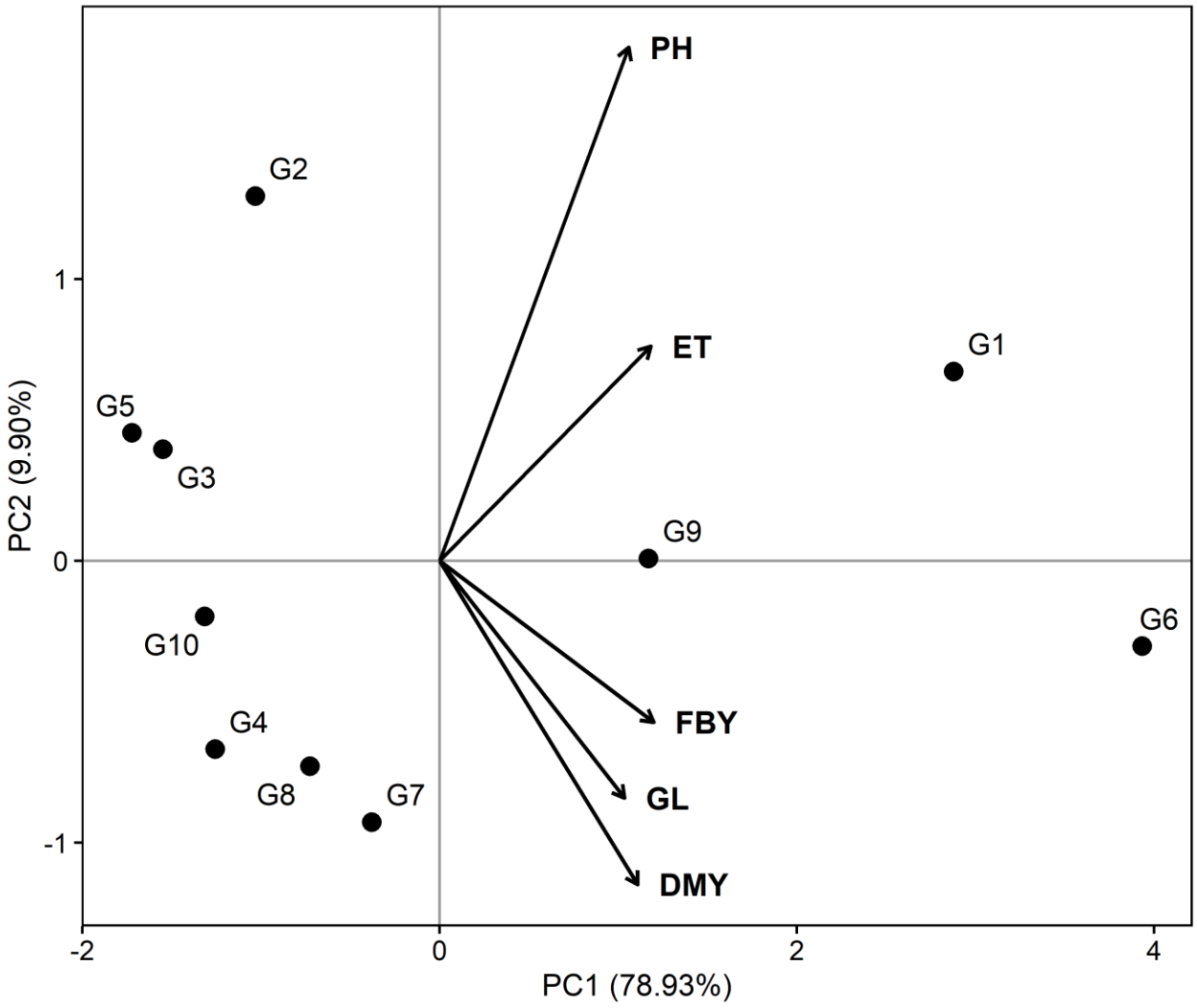


Figure 4. Descriptive PCA biplot of five agronomic traits. PCA used exact across-environment genotype means after centring and scaling each trait to unit variance. Points show raw principal component scores; arrows show eigenvector loadings multiplied by 2.5 for display. The signs of both axes were reversed consistently for points and arrows. PC1 and PC2 account for 78.93% and 9.90% of standardized variation. Arrow lengths are display-scaled loadings, not trait–PC correlations. FBY, fresh biomass yield; DMY, dry matter yield; ET, effective tiller number; PH, plant height; GL, green leaves per plant.

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