

FORAGE YIELD AND NUTRITIONAL QUALITY OF PEARL MILLET GENOTYPES AS HAY AND SILAGE IN MEDITERRANEAN CONDITIONS

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ABSTRACT

Pearl millet *Pennisetum glaucum* (L.) R. Br.] exhibits drought tolerance and is increasingly used as essential feed. Nevertheless, limited studies have compared genotypes for hay and silage quality in semi-arid Mediterranean environments. Producers and breeders in Türkiye's Southeastern Anatolia (SA) Region region lack concurrent data linking biomass production with standardized feed-quality indices across various pearl millet [genotypes. This study addressed this gap by evaluating the qualitative attributes of hay and silage from 25 genotypes cultivated as a second crop during the summer season in Akçakale–Şanlıurfa (Mediterranean, semi-arid) in 2022. The primary objective was to identify high-performing candidate genotypes for semi-arid forage systems. Genotypes were evaluated for fodder and dry matter (DM) yield, as well as forage quality traits in pre-ensiled hay and silage produced after a 60-day fermentation period. Plants were harvested at the milk-dough stage, and forage yield, dry matter yield (DMY), and feed quality were assessed in both pre-ensiled and ensiled materials. Forage yield varied between 75.50 and 136.23 t ha⁻¹. Genotype 15836 had the maximum fodder production (136.23 t ha⁻¹), while genotypes 3642 and 1665 (75.50 and 75.55 t ha⁻¹, respectively) produced the lowest fodder yield. The DMY of tested genotypes varied between 24.70 and 45.14 t ha⁻¹. For hay and silage, crude protein ranged from 4.32% to 9.43% and 4.43% to 8.96%, respectively. Similarly, crude ash ranged from 6.44% to 10.80% and 5.29% to 9.89%. Likewise, neutral detergent fiber (NDF) ranged from 59.16% to 67.38% and 38.61% to 65.41%, whereas acid detergent fiber (ADF) ranged from 34.19% to 40.41% and 23.64% to 42.12%. In the same way, acid detergent lignin (ADL) ranged from 4.59% to 7.53% and 0.782% to 5.275%. Digestible dry matter (DDM) ranged from 57.42% to 62.17% for hay and from 56.09% to 70.49% for silage. Similarly, dry matter intake (DMI) varied between 1.791% and 2.028% and between 1.841% and 3.109%. Relative feed value (RFV) was between 79.99 and 96.42 and between 80.24 and 169.88. Silage materials demonstrated reduced fiber fractions and elevated DDM, DMI, and RFV across several genotypes, indicating improved intake potential and energy availability. Four genotypes (1566, 14522, 15836, 21438) consistently exhibited higher DM yield, although genotype 2346 produced the greatest silage RFV, with many others (1536, 1665, 7259, 8562) that also attained first-quality silage. These genotypes could reduce seasonal feed shortages and be used in the breeding programs for developing climate-resilient forage systems in semi-arid areas.

Keywords: Pearl Millet; Forage Yield; Feed Quality; Genotypes; Silage

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INTRODUCTION

Roughage feeds are crucial to ruminant nutrition and account for a significant portion of animal production costs. Roughages make up around 70% of overall expenditures in the animal production sector in Türkiye (Geren and Kavut, 2015). Ensuring a consistent supply of superior roughage is essential for economically viable and sustainable animal husbandry. Numerous regions

experience significant deficiencies in forage supply. Türkiye was projected to have a 27-million-ton shortfall of quality roughage in 2022, with around 8.3 million tons of that deficit occurring in Şanlıurfa province alone (Özer and Okant, 2025). This gap is expected to grow because of ongoing climate change and increasing livestock populations. These problems highlight the urgent need to enhance forage supplies and cultivate alternative feed crops suited to dry and semi-arid regions.

Summer-annual forage crops have attracted attention as alternate sources of roughage, particularly in hot and arid environments where conventional cool-season forages like maize may fail (Özer and Okant, 2025). Millets are known for their resilience to harsh environmental conditions. Millets, such as pearl millet and foxtail millet, are the sixth-largest grain crop globally by production and are known for their drought resistance. Millets are increasingly regarded as "climate-smart" crops due to their ability to withstand high temperatures and water scarcity while maintaining high yield and nutritional quality under harsh conditions (Kasule *et al.*, 2024). Furthermore, millets have multiple uses, functioning as food grains, animal feed, and biofuel sources, so increasing their importance in sustainable agriculture and food security. The varied characteristics of millets are an appealing option for areas such as Southeast Turkey, where crop diversification and fodder supply are essential goals (Yücel and Yücel, 2022).

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is a warm-season C4 cereal (Shrestha *et al.* 2023). It is an annual plant that grows upright to 3-4 m tall in semi-arid conditions typical of the Şanlıurfa region (Çiçek and Yücel, 2022; Saygıdar *et al.*, 2024). It has excellent resistance to drought and heat; yet it cannot thrive without a certain level of moisture availability. Pearl millet is well-suited to sandy or light-textured, low-fertility soils (optimal pH range of 6.2–7.7) and can grow under minimal input conditions. It is a short-day plant that generally requires a 12-hour photoperiod to initiate flowering and survives at average daily temperatures of approximately 28–30 °C. Pearl millet can grow to heights of 3–4 m and produce considerable biomass under optimal conditions (Çiçek and Yücel, 2022; Saygıdar *et al.*, 2024). This crop has high water-use efficiency, yielding an equivalent quantity of dry matter as maize but using around 30% less water. These characteristics highlight pearl millet's potential as a high-yield fodder in arid environments, where traditional crops such as maize may be economically or agronomically inefficient.

Pearl millet provides nutritional and safety advantages for fodder purposes (Daduwal *et al.*, 2024). Unlike sorghum and Sudan grass, pearl millet doesn't produce hydrocyanic acid (prussic acid) (Hassan *et al.*, 2014), hence reducing the danger of prussic acid poisoning in cattle (Lauriault *et al.*, 2021). This indicates that farmers may graze or harvest pearl millet without the specific protections required for sorghum-family forages susceptible to cyanide leakage. Moreover, the nutritional value of pearl millet is equivalent to that of other prevalent forages (Daduwal *et al.*, 2024). It typically has high protein levels and digestible fiber, and lacks the presence of anti-nutritional elements commonly found in some sorghums. Previous studies indicated that pearl millet may match or exceed the nutritional quality of forage sorghum (Hassan *et al.*, 2014) and has been

proposed as an attractive alternative to maize silage in certain circumstances. In water-scarce regions, millet forages have been used to reduce dependence on maize silage without significantly affecting animal performance (Kheya *et al.*, 2023). The attributes of pearl millet provide it a viable alternative or supplement to conventional silage crops, especially in regions susceptible to drought stress (Yücel *et al.*, 2023).

Ensiling is an efficient method to prolong the use of pearl millet fodder beyond its growing season. Silage production facilitates the storage of high-moisture fodder in a fermented, stable state suitable for year-round feeding (da Silva *et al.*, 2025). The time of harvest is critical for producing high-quality silage. The optimum stage for silage harvest in cereals is often the soft-dough stage of the grain (Geren, 2014), when the plant's dry matter (DM) content is around 20–25% (Pinho *et al.*, 2014; Jacovetti *et al.*, 2018). The moisture level at this stage is ideal for fermentation. There is an increasing global interest in pearl millet as fodder, however, there are specific research gaps. Jukanti *et al.* (2016) highlighted the climatic resilience and nutritional benefits of millets, whereas Guimarães *et al.* (2014) demonstrated that pearl millet may provide high-quality silage from early harvests. Nevertheless, most of the current research mostly concentrates on a single cultivar or a limited selection of improved varieties. There is inadequate data on the heterogeneity among various genotypes of pearl millet regarding feed production and quality, particularly in evaluating their efficacy as fresh fodder compared to silage. This is especially true in Mediterranean and semi-arid regions such as Southeast Türkiye. Limited studies in Türkiye have assessed a wide range of pearl millet genotypes for dual-purpose applications (both as green forage/hay and silage) under local semi-arid conditions. Multi-genotype assessments are essential since they reveal genetic variations in variables like as protein content, fiber composition, and fermentability, hence guiding breeding programs and feeding decisions. In conclusion, assessing the nutritional content of several pearl millet genotypes before and after ensiling may facilitate the identification of the most acceptable genetic resources for fodder enhancement and application in dry locations.

The present study assessed pearl millet genotypes for forage quality at harvest (pre-silage) and after ensiling (post-fermentation) in arid/semi-arid environments of Şanlıurfa as a second-crop. The objectives were to (i) determine the dry matter yield potential of tested genotypes grown after the main crop (summer season); (ii) assess and compare the forage quality of these genotypes at harvest and after ensiling, including crude protein and fiber fraction analyses [neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL)] and calculation of indices like digestible dry matter (DDM), dry matter

intake (DMI), and relative feed value. It was hypothesized that genotype will exhibit significant variation in biomass production and feed quality. Ensiling was expected to reduce soluble carbohydrates and increase fiber concentrations owing to fermentation losses, while certain genotypes would retain high nutritional value in silage form. The results will help to identify the genotypes with high production and crude protein levels, reduced fiber content (enhanced digestibility), and better feed value.

MATERIALS AND METHODS

Experimental site and materials: The current study was conducted at GAP Agricultural Research Institute Talat Demirören Research Station Akçakale/Şanlıurfa (36° 54' 10" N and 38° 55' 23" E and 378 m altitude).

A total 25 different pearl millet [*Pennisetum glaucum* (L.) R. Br.] genotypes were included in the current study. Of these, 24 genotypes obtained from ICRISAT whereas control variety (Teafleaf III) was obtained from the USA.

Soil and climate characteristics of the experimental site: Soil samples were collected from 0-15 cm and 15-30 cm depths from the experimental area and analyzed for physical and chemical properties using standard methodologies. Soil had a clayey texture with 28-30% sand, 26-27% silt, and 44-45% clay. Soil analysis indicated a pH value ranging from 7.65 to 7.80, total salt content between 0.30% and 0.40%, nitrogen content from 0.05% to 0.08%, organic carbon levels of 0.34% to 0.55%, and phosphorus concentration at 0.039%. Lime (CaCO₃) content was 44.5-47.2%.

The average temperature of the experimental site during June-November 2022 varied between 15.89-32.86 °C, and the average temperatures of July, August, and the growing season were 32.86 °C, 31.76 °C and 26.16 °C, respectively. Average relative humidity for this period varied between 30.12-52.33% (Figure 1), with the highest and the lowest humidity observed in November and June, respectively. The experimental site is influenced by continental (dry and hot) and Mediterranean climates (humid and temperate) (Atalay and Mortan, 2006).

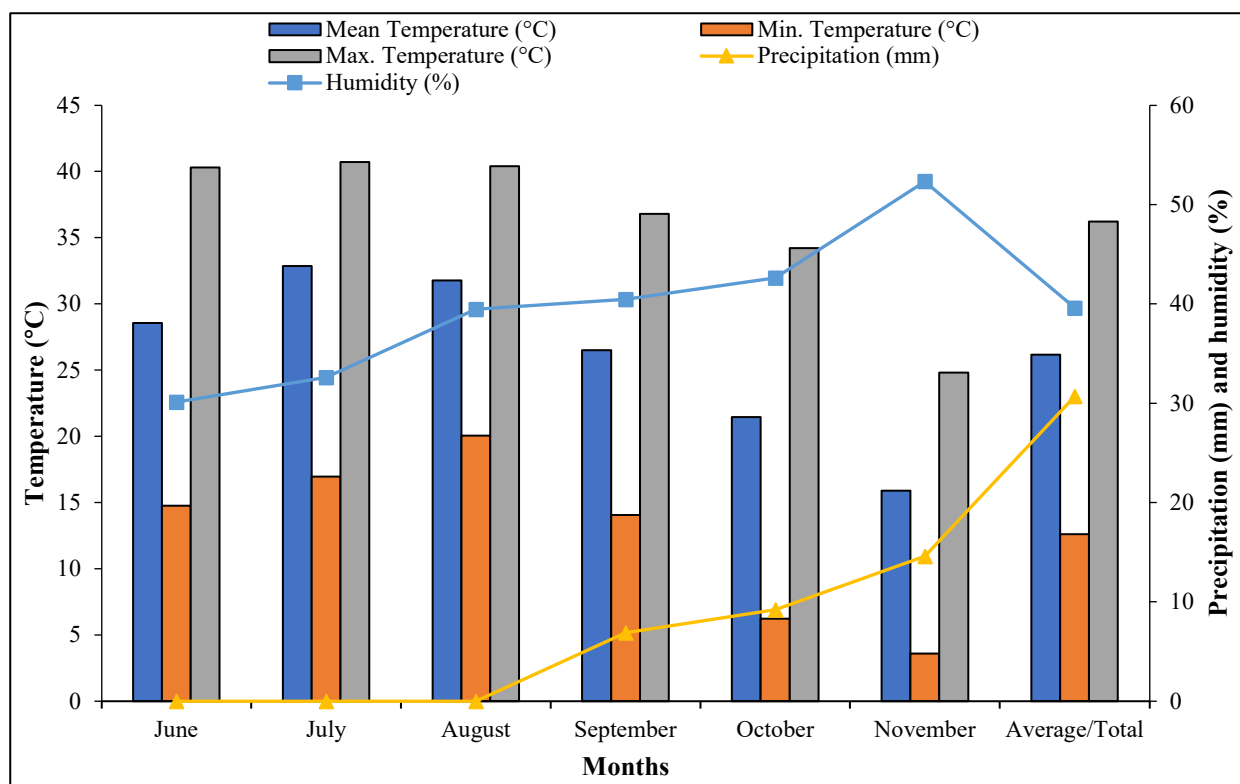


Figure 1. Weather data of the experimental site during the study period

The experiment was laid out according to randomized complete block design (RCBD) consisting of three blocks, with genotype as the fixed factor. Each genotype was sown manually in 4 rows, with 70 cm inter-row and 25 cm intra-row spacing. The net plot size was

3.5 m × 5 m = 17.5 m². Seeds were sown on 20 June after preparing a fine seedbed. Considering soil analyses, 20:20:0 compound fertilizer was used at the rate of 50 kg of pure N and 80 kg P per hectare (Mesquita and Pinto, 2000) before planting. Furthermore, 50 kg ha⁻¹ of pure N

was applied in the first week of August (knee height stage) using urea. Each plot was irrigated using sprinkler irrigation to ensure homogeneous emergence, and a total of four irrigations were applied. Weed control was carried out mechanically until knee height stage, and then manually as necessary. The plants were harvested at the milk-dough stage (70 days after sowing). Fresh forage samples, including stems, leaves, and bunches, were chopped, and a random sample was taken from each plot (1000 g). The samples were then dried in an oven at 60 °C until the weight stabilized. Afterwards, dry forage proportions were determined by weighing. Dry matter yields per hectare were determined by multiplying the hay ratios with the fresh hay yield. The collection and use of samples complied with all relevant institutional, national, and international guidelines and legislation.

Preparation of the dried plant samples before silage for analysis: The 1000 g fresh samples taken from each plot (3 replications) were dried, ground in a grinding mill, and then passed through a 2 mm sieve and subjected to quality analysis.

Ensiling and preparation of samples for analysis:

Fresh plant samples taken from each plot during harvest were shredded using a 3-5 cm-sized stem-branch leaf grinding machine, placed in vacuum bags, and vacuum-packed by removing 95% of the air with a vacuum device. The forage samples were vacuum-sealed and ensiled under strictly anaerobic conditions for 60 days. Vacuum packaging was employed to ensure rapid oxygen exclusion and controlled, uniform fermentation, as described by Johnson *et al.* (2005) and Kaya *et al.* (2022). At the end of the fermentation period, a 250 g sample was taken from each silage, dried in an oven at 60°C, ground in the mill, and sieved through a 2 mm sieve for quality analysis. Laboratory analyses were performed in triplicate (n = 3) per sample. Nitrogen (N) content of pre- and post-silage samples was determined by the Kjeldahl method (AOAC, 1990). Crude protein ratios were calculated by multiplying the obtained values by the coefficient of 6.25. The neutral detergent fiber (NDF), acid detergent fiber (ADF), and acid detergent lignin (ADL) contents were determined using the ANKOM fiber analyzer, following the method described by Van Soest *et al.* (1991). Digestible dry matter (DDM) ratio, dry matter intake (DMI), and relative feed value (RFV) were calculated using the formula described by Schroeder (1994). Potential dry matter intake (DMI, % of body weight) was calculated from forage NDF content using equation 2 (Romero *et al.* 2014). This relationship is extensively used in computing Relative Feed Value and Relative Forage Quality indices, based on the principle that voluntary dry matter intake decreases when dietary neutral detergent fiber content increases.

$$\text{Digestible dry matter (DDM) ratio} = 88.9 - (0.779 \times \text{ADF}\%) \quad (1)$$

$$\text{Dry matter intake (DMI)} = 120 / \text{NDF}\% \quad (2)$$

$$\text{Relative feed value (RFV)} = (\text{DDMR}\% \times \text{DMI}\%) / 1.29 \quad (3)$$

Statistical analysis: The data were analysed by employing analysis of variance (ANOVA) using the model

$$Y_{ij} = \mu + B_i + G_j + \epsilon_{ij},$$

where Y_{ij} is the observation of the j^{th} genotype in the i^{th} block, μ is the overall mean, B_i is the random effect of block. G_j represents the fixed effect of genotype, and ϵ_{ij} is the residual error term (including the block \times genotype interaction) (Steel *et al.*, 1997). The data were analyzed using JMP Pro statistical software (SAS Institute). Normality (Shapiro–Wilk) and homoscedasticity (Levene) were checked prior to ANOVA which indicated no transformations were required. Genotype means were compared using Tukey's honestly significant difference ($\alpha = 0.05$) for each trait. The raw data has been provided as supplementary materials.

RESULTS

Trait-wise ANOVA revealed significant genotypic effects for most silage parameters. Tukey groups, F statistics and coefficients of variation are shown in Tables 1–3. Regarding fodder quality, ensiling generally decreased NDF and ADF, hence enhancing DMD, DMI, and RFV compared to hay.

Fodder yield exhibited significant differences among genotypes ($p < 0.05$), with a coefficient of variation of 12.12%, reflecting satisfactory experimental accuracy (Table 1). Forage yield varied between 75.50 and 136.23 t ha⁻¹. Genotype 15836 had the maximum fodder production (136.23 t ha⁻¹) and was statistically superior to most other genotypes. A limited group of high-yielding genotypes (21438, 14522, 6340, and 6133) produced fodder yields ranging from 99.07 to 108.11 t ha⁻¹, with no significant difference from genotype 15836. Most of the remaining genotypes comprised an intermediate-yield range, with fodder yields ranging from 78.81 to 94.61 t ha⁻¹. The lowest forage yields were recorded in genotypes 3642 and 1665 (75.50 and 75.55 t ha⁻¹, respectively), which were considerably inferior to the highest-yielding genotype 15836.

The dry matter (DM) production varied across genotypes, ranging from 24.7 to 45.1 t ha⁻¹ (mean: 31.4 t ha⁻¹), with four genotypes (1566, 14522, 15836, 21438) above 35 t ha⁻¹. Genotype 15836 produced the highest DM (45.14 t ha⁻¹), while the lowest yields were recorded for 3642 (24.70 t ha⁻¹), 2322 (26.44 t ha⁻¹), 1536 (26.75 t ha⁻¹) and 1665 (26.23 t ha⁻¹) (Table 1).

Crude protein (CP) concentrations differed among genotypes for both hay and silage. The mean CP

was similar across hay and silage (hay = 6.85% silage = 6.79%). The CP content in hay ranged from 4.32% to 9.43%, with a maximum of 9.43% in genotype 8562, followed by 8.91% in 4747 and 8.82% in 13760. The lowest values were recorded for genotypes 1566 and 2346. In silage, CP varied from 4.43% to 8.96%, with the highest value recorded for the genotype 5085 (8.96%) and followed by 9813 (8.36%) and 1665 (8.08%), while

the lowest values were noted for 14787 (4.43%) and 2346 (4.64%). The CP responses to ensiling were dependent on genotype, with increases observed for genotypes 1917, 6133, 6278, 6340, 9813, 1665, 21438, and 5085, while reductions were noted in genotypes including 13760, 15836, 4747, 8562, 13623, 13624, 14787, and 2346 (Table 1).

Table 1. Fodder and dry matter yield, crude protein ratio, and ash contents in hay and silage of pearl millet genotypes grown in Mediterranean climatic conditions

Genotype No	Fodder yield (t ha ⁻¹)	Dry Matter Yield (t ha ⁻¹)	Crude Protein (%)		Ash Content (%)	
			Hay	Silage	Hay	Silage
1566	90.26 b+	35.57 ab	4.32 d	5.81 cde	6.85 cd	6.91 ab
2761	81.86 b	31.22 ab	5.79 bcd	5.78 cde	6.44 d	7.70 ab
7422	83.34 b	29.18 ab	6.30 a-d	6.12 b-e	10.04 ab	9.58 a
13760	83.66 b	29.03 ab	8.82 ab	6.66 a-e	9.98 abc	8.65 ab
14522	103.38 ab	35.29 ab	7.51 a-d	7.62 a-d	7.88 a-d	7.92 ab
15836	136.23 a	45.14 a	7.81 abc	6.47 b-e	7.77 a-d	7.46 ab
Teafleaf III	80.85 b	30.40 ab	7.41 a-d	7.36 a-d	9.48 a-d	6.26 ab
1536	86.19 b	26.75 b	6.69 a-d	7.14 a-d	9.06 a-d	7.24 ab
1917	86.11 b	32.10 ab	5.74 bcd	7.75 a-d	8.82 a-d	7.35 ab
2322	78.81 b	26.44 b	6.65 a-d	6.87 a-d	10.32 ab	7.97 ab
3642	75.50 b	24.70 b	6.78 a-d	5.83 cde	8.86 a-d	6.11 ab
4747	94.61 b	29.67 ab	8.91 ab	5.79 cde	10.80 a	7.30 ab
6133	99.07 ab	31.52 ab	6.67 a-d	8.09 abc	8.40 a-d	9.89 a
6278	92.57 b	30.94 ab	6.24 a-d	7.47 a-d	8.14 a-d	8.24 ab
6340	101.05 ab	33.87 ab	6.95 a-d	7.31 ad	8.86 a-d	8.49 ab
7259	89.49 b	29.60 ab	6.39 a-d	5.40 de	8.78 a-d	8.76 ab
8562	90.94 b	33.57 ab	9.43 a	7.30 a-d	8.75 a-d	7.41 ab
9813	88.60 b	29.15 ab	6.16 a-d	8.36 ab	8.95 a-d	8.77 ab
1665	75.55 b	26.23 b	7.09 a-d	8.08 abc	10.34 ab	8.48 ab
13623	93.88 b	32.60 ab	7.41 a-d	6.18 b-e	9.33 a-d	8.07 ab
13624	96.75 b	33.07 ab	7.56 a-d	6.58 a-e	8.43 a-d	7.66 ab
14787	85.36 b	28.84 b	5.85 bcd	4.43 e	7.53 bcd	6.47 ab
21438	108.11 ab	38.07 ab	5.69 bcd	7.68 a-d	9.46 a-d	7.71 ab
2346	93.04 b	30.35 ab	5.05 cd	4.64 e	7.23 bcd	5.29 b
5085	90.40 b	31.06 ab	7.96 abc	8.96 a	8.54 a-d	7.41 ab
CV (%)	12.12	16.30	15.52	21.97	11.29	16.52
F	*	*	**	*	**	*

+) The means shown with different letters are statistically different from each other within P≤0.05 error limits according to the Tukey multiple comparison test.

Ash content exhibited considerable variation across genotypes in both hay and silage. The average ash content decreased post-ensiling (hay 8.76% vs. silage 7.96%), exhibiting less variability in hay (CV = 11.29%) compared to silage (CV = 16.52%). In hay, ash content varied from 6.44% to 10.80%, with the greatest level seen in 4747 (10.80%), followed by 1665 (10.34%) and 7422 (10.04%), while 2761 exhibited the lowest value. In silage, values varied from 5.29% to 9.89%, with the highest (9.89%) value recorded for 6113 and followed by 7422 (9.58%) and 9813 (8.77%). The lowest ash content in silage was recorded for genotype 2346 (Table 1).

Neutral detergent fiber (NDF) varied across genotypes in both hay and silage. The mean NDF

decreased from hay to silage (62.77% compared to 52.86%). NDF in hay varied from 59.16% to 67.38%, being lowest in 1536 and highest in 14787, with 13624 also exhibiting a high value of 66.96%. NDF in silage ranged from 38.61% to 65.41%, with the lowest value in 2346 and the highest in 4747 (Table 2).

Acid detergent fiber (ADF) exhibited no genotypic variations in hay but indicated variations in silage. On average, ADF decreased after ensiling (36.78% to 31.41%). Hay ADF ranged from 34.19% (13760) to 40.41% (13624). The ADF of silage varied from 23.64% to 42.12%, with the lowest and the highest values recorded for 2346 and 4747 genotypes, respectively (Table 2).

Acid detergent lignin (ADL) exhibited no variation across genotypes in hay but showed genotype dependency in silage. The mean ADL was reduced by almost half with ensiling, decreasing from 5.90% to 3.04%. In hay, the ADL varied from 4.59% to 7.53% (lowest in 13760 and highest in 6278). In silage, ADL varied from 1.61% to 5.27% (14787 being the lowest and 1566 the highest). Significantly, whereas most genotypes showed decreased fiber fractions post-ensiling, many (e.g., 4747 for NDF and ADF; 7422 and 6340 for ADF) displayed elevated silage values compared to hay, highlighting significant genotypic variations (Table 2).

Dry matter digestibility (DDM), dry matter intake (DMI), and relative feed value (RFV) exhibited no genotypic variation in hay but were significantly influenced by genotype in silage. Ensiling improved all three indicators. Mean DDM increased from 60.25% to 64.43%, DMI from 1.92% to 2.31%, and RFV from 89.6 to 116.3, with increased between-genotype variability post-ensiling (CV increased from 3.13 to 4.47% for DDM, 4.2 to 8.43% for DMI, 6.8 to 11.7% for RFV)

(Table 3). Silage performance revealed unique top performers, i.e., genotype 2346 had the highest DDM (70.49%), DMI (3.109%), and RFV (169.9). Similar performances were noted for 1536 (DDM 69.10%; DMI 2.663%; RFV 142.9), 1665 (68.10%; 2.621%; 138.4), and 7259 (67.52%; 2.562% BW; 134.1). Conversely, genotype 4747 consistently exhibited the lowest values in silage (DDM 56.09%; DMI 1.841%; RFV 80.2) (Table 3).

Despite the differences being non-significant among genotypes, quantitatively, genotype 1536 had the highest hay RFV (96.4) and DMI (2.028% BW), while 13624 and 14787 recorded the lowest values (RFV 80.0–80.4; DMI 1.791–1.794%). The significant genotypic differentiation post-ensiling, especially the dominance of 2346 and the consistently elevated values of 1536, 1665, and 7259 demonstrates marked genotype × preservation-form interactions that correspond with the fiber reductions noted in silage (decreased NDF/ADF/ADL), resulting in significantly improved intake and feeding value (Table 3).

Table 2. Neutral detergent fiber, acid detergent fiber and acid detergent lignin in hay and silage of pearl millet genotypes grown in Mediterranean climatic conditions.

Genotype No	Neutral Detergent Fiber (%)		Acid Detergent Fiber (%)		Acid Detergent Lignin (%)	
	Hay	Silage	Hay	Silage	Hay	Silage
1566	63.78 a-f†	56.86 a-c	37.97	35.42 abc	6.60	5.27 a
2761	60.21 fg	53.07 a-d	35.42	29.34 bcd	4.81	2.64 bc
7422	63.90 a-f	60.62 ab	37.08	37.74 ab	5.19	3.84 abc
13760	60.36 efg	56.12 abc	34.19	32.87 a-d	4.59	3.16 abc
14522	61.91 c-g	51.29 a-d	36.20	30.42 a-d	4.76	2.74 bc
15836	63.22 a-g	49.74 bcd	37.95	29.13 bcd	5.96	2.33 bc
Teafleaf III	60.99 d-g	49.65 bcd	35.41	28.61 bcd	6.19	3.08 abc
1536	59.16 g	45.21 cd	35.41	25.41 cd	5.55	2.18 c
1917	64.98 a-d	52.93 a-d	38.05	31.77 a-d	5.84	3.27 abc
2322	61.80 c-g	57.46 abc	36.62	35.17 a-d	6.29	3.05 abc
3642	62.19 c-g	57.14 abc	35.92	35.77 abc	4.99	3.51 abc
4747	61.00 d-g	65.41 a	35.40	42.12 a	5.70	4.60 ab
6133	61.65 d-g	57.00 abc	36.24	34.53 a-d	6.18	2.460bc
6278	62.48 c-g	54.69 abc	38.88	32.89 a-d	7.53	3.65 abc
6340	60.58 efg	60.44 cb	35.19	36.73 abc	5.96	2.24 c
7259	61.82 c-g	46.86 b-d	35.85	27.45 bcd	6.37	3.20 abc
8562	62.85 b-g	52.65 a-d	35.31	27.22 bcd	5.69	2.87 bc
9813	63.81 a-f	50.64 bcd	37.77	29.87 bcd	6.18	3.35 abc
1665	62.13 c-g	45.79 cd	36.10	26.70 bcd	6.49	2.96 bc
13623	64.52 a-e	49.12 bcd	37.50	29.36 bcd	5.60	3.43 abc
13624	66.96 ab	50.67 bcd	40.41	30.11 bcd	6.01	3.62 abc
14787	67.38 a	55.92 abc	39.37	34.32 a-d	6.32	1.61 cd
21438	60.98 d-g	49.77 bcd	34.31	29.94 bcd	5.88	2.03 c
2346	66.03 abc	38.61 d	38.96	23.64 d	6.49	2.96 bc
5085	64.45 a-f	53.73 abc	38.14	28.77 bcd	6.26	2.21 c
CV (%)	4.18	8.74	6.59	11.78	16.60	23.58
F	*	**	NS	**	NS	**

+) The means shown with different letters are statistically different from each other within $P \leq 0.05$ error limits according to the Tukey multiple comparison test.

Table 3. Dry matter digestibility, dry matter intake and relative feed value of hay and silage obtained from pearl millet genotypes grown in Mediterranean climatic conditions.

Genotype No	Dry Matter Digestibility Ratio (%)		Dry Matter Intake (%)		Relative Feed Value	
	Hay	Silage	Hay	Silage	Hay	Silage
1566	59.32	61.31 bcd+	1.882	2.161 bcd	86.5	103.8 b-e
2761	61.30	66.04 abc	1.993	2.265 bcd	94.8	116.0 b-e
7422	60.02	59.50 cd	1.879	1.980 cd	87.5	91.3 de
13760	62.27	63.30 a-d	1.989	2.185 bcd	96.0	108.0 b-e
14522	60.70	65.21 a-d	1.939	2.346 bcd	91.3	118.7 b-e
15836	59.33	66.21 abc	1.899	2.453 bcd	87.4	126.5 bcd
Teafleaf III	61.32	66.61 abc	1.973	2.418 bcd	93.9	124.9 bcd
1536	61.32	69.10 ab	2.028	2.663 ab	96.4	142.9 ab
1917	59.26	64.15 a-d	1.851	2.283 bcd	85.2	113.8 b-e
2322	60.37	61.50 a-d	1.943	2.093 bcd	90.9	100.0 b-e
3642	60.92	61.03 bcd	1.938	2.100 bcd	91.7	99.4 cde
4747	61.33	56.09 d	1.969	1.841 d	93.6	80.2 e
6133	60.67	62.00 a-d	1.950	2.114 bcd	91.8	101.8 b-e
6278	58.61	63.28 a-d	1.927	2.197 bcd	87.6	107.8 b-e
6340	61.49	60.29 bcd	1.982	1.986 cd	94.5	92.8 de
7259	60.97	67.52 abc	1.945	2.562 abc	92.0	134.1 a-d
8562	61.62	67.69 ac	1.912	2.390 bcd	92.0	125.1 bcd
9813	59.47	65.63 abc	1.884	2.372 bcd	87.0	120.7 b-e
1665	60.78	68.10 abc	1.932	2.621 ab	91.0	138.4 abc
13623	59.69	66.03 abc	1.864	2.454 bcd	86.3	125.8 bcd
13624	57.42	65.45 abc	1.794	2.380 bcd	80.0	121.0 b-e
14787	58.23	62.16 a-d	1.791	2.150bcd	80.4	103.7 b-e
21438	62.17	65.57 abc	1.969	2.447 bcd	94.9	125.0 bcd
2346	58.55	70.49 a	1.818	3.109 a	82.5	169.9 a
5085	59.19	66.49 abc	1.862	2.247 bcd	85.4	116.1 b-e
CV(%)	3.13	4.47	4.2	8.43	6.8	11.70
F	NS	**	NS	**	NS	**

+) The means shown with different letters are statistically different from each other within $P \leq 0.05$ error limits according to the Tukey multiple comparison test.

DISCUSSION

Pearl millet genotypes exhibited significant variation in DM yield, ranging from 24.70 to 45.14 t ha⁻¹, indicating substantial genetic variety available for utilization under semi-arid, second-crop situations. The top performers regarding yield, i.e., 15836 (45.14 t ha⁻¹), 21438 (38.07 t ha⁻¹), 1566 (35.57 t ha⁻¹), and 14522 (35.29 t ha⁻¹) outperformed; nevertheless, their nutritional profiles varied, indicating the traditional yield-quality trade-off in C₄ forages (Liebert *et al.*, 2023). For example, 1566 exhibited high yield with the lowest hay crude protein (4.32%), while 15836 demonstrated superior production with excellent silage quality (DMD = 66.21%, RFV = 126.5). These variations suggest that multi-trait selection, rather than yield alone, will be crucial for breeding and cultivar recommendations in Mediterranean and semi-arid environments. Several earlier studies have reported significant genotypic variations in yield of pearl millet

genotypes in various geographic regions of the world (Hassan *et al.*, 2014; Morales *et al.*, 2015; Medici *et al.*, 2018; Salama *et al.*, 2020; Saygıdar *et al.*, 2024).

The CP varied from 4.32% to 9.43% in hay and from 4.43% to 8.96% in silage, indicating an expected reduction post-ensiling. The decrease aligns with proteolysis that occurs during fermentation and losses of effluent/N, especially when whole-plant dry matter is low at the time of chopping (Albrecht and Muck, 1991; Winters *et al.*, 2000). Ensiling dynamics are influenced by crop dry matter, soluble carbohydrates, and acidification kinetics (Santos *et al.*, 2020). High-moisture forages are susceptible to unfavourable fermentations and effluent losses unless regulated with wilting/absorbents or efficient inoculation, which ultimately affects nitrogen retention and fiber solubilization (Bao *et al.*, 2022). These processes correspond with the observed pattern, i.e., genotypes exhibiting reduced post-ensiling CP were often those demonstrating greater fiber reductions, indicating increased fermentation and possible nitrogen

losses in cell wall structure (de Moura Zanine *et al.*, 2020; Muck *et al.*, 2020; Venturini *et al.*, 2024). The CP ratio determines the nutritional content of forages, should be within the range of 6-7% in diets for livestock (Van Soest, 2018). The CP ratios observed in the research exceed the 6-7% threshold in several genotypes. The findings of the study on the crude protein ratio in pearl millet align with those of many studies studying similar crops (Rasnake *et al.*, 1981; El-Lattief, 2011; Makarana *et al.*, 2018), yet they are below to the results reported by certain researchers (Shrestha *et al.*, 2023; Morales *et al.*, 2015).

The mineral (ash) content exhibited significant genotypic variation, ranging from 6.44% to 10.34% for hay and from 5.29% to 9.89% for silage. The significantly elevated silage ash content in 6113 (9.89%) compared to the moderate hay ash suggests either true mineral concentration (e.g., dry matter loss concentrating minerals) or contamination during field or harvest. The latter is a known risk in chopped forages and may reduce energy density. In contrast, numerous genotypes (e.g., 6133, 7422, 1665) exhibited sufficiently high ash content with acceptable protein levels, indicating their potential for mineral supply without compromising quality. Emmanuel *et al.* (2022) indicated that the concentration of macro and micronutrients in feeds may have increased as a result of the increasing ash content. Furthermore, the elevated levels of raw ash enhance the quality of the feed, hence a high concentration of this component is preferred in the feed formulation.

The fiber fractions exhibited the most significant relationship between hay and silage of different genotype. On average, NDF decreased from 62.77% (hay) to 52.86% (silage) and ADF declined from 36.78% to 31.41%, exhibiting extremely significant genotypic effects in silage. These changes align with hemicellulose solubilization and partial cell-wall modification during fermentation, which generally enhance digestibility and intake potential. Nonetheless, reactions were particular to the genotype. Genotype 2346 exhibited a significant enhancement (NDF 66.03 decreased to 38.61%; ADF 38.96 decreased to 23.64%), resulting in the greatest silage DMD (70.49%), DMI (3.10%), and RFV (169.9). Conversely, genotype 4747 had a distinct trend (NDF 61.00 → 65.41%; ADF 35.40 → 42.12%), resulting in the lowest silage DMD (56.09), DMI (1.841), and RFV (80.2). This variance indicates underlying genetic variations in the availability of water-soluble carbohydrates (WSC), buffering capability, and the ecology of epiphytic lactic acid bacteria (LAB), which combined influence fermentation intensity, pH reduction, and fiber solubilization. Comparable genotype-dependent silage quality trends have been seen in pearl millet and other tropical C₄ forages (de Pinho Costa *et al.*, 2012; Costa *et al.*, 2018).

The NDF content indicates the quantity of feed that animals are able to ingest (Eskandari *et al.*, 2009). Higher cell wall constituents make the plant more fibrous and less digestible, leading to increased NDF levels. A reduced fiber content in feed enhances both intake and digestibility, hence demonstrating a correlation between NDF and consumption (Van Soest, 2018). Silage enhances anaerobic and lactic acid bacterial populations. This reduces NDF in cell walls (Bolsen *et al.*, 1996). The DM and NDF decrease throughout silage, but non-fiber carbohydrates linearly increase (Naeini *et al.*, 2014). Feed depends on cell wall constituents (NDF and ADF) as well as CP concentrations, particularly in terms of digestibility. Consequently, genotypes with low NDF and ADF are selected. The investigation revealed comparable NDF content to Buso *et al.* (2014), although it was lower to that reported in the majority of studies on similar plants (Rasnake *et al.*, 1981; Makarana *et al.*, 2018; Dağtekin, 2019; Salama *et al.*, 2020). This may result from studies involving diverse ecologies, purposes, and genotypes. Negative correlations are observed among RFV, NDF, and ADF. Numerous studies have demonstrated similar findings (Van Soest, 2018; Yücel, 2020; Yücel and Erkan, 2020; Yücel *et al.*, 2023). Rohweder *et al.* (1978) classified silages as follows: RFV > 151 as top grade, 125–151 as 1st quality (very good), 103–124 as 2nd quality (excellent), 87–102 as 3rd quality (medium), and 75–86 as 4th quality (bad). Genotype 2346 has the greatest silage RFV values, as seen in Table 3. Genotypes 15836, 1536, 7259, 8562, 1665, 13623, and 21438 are classified as 1st quality, but 4747 is considered poor, and the other genotypes are mostly 2nd quality. RFV could be increased due to decreased ADF and NDF values. This aligns with the results of Yücel *et al.* (2018) and Yücel (2020). The RFV findings align with a few studies (De Medeiros *et al.*, 2022; Erten and Koç, 2023) who concluded that the silage process decreases the nutritional value of silages, although contrast with other studies that reported no significant impact.

From a selection perspective, several genotype “archetypes” emerged in the current study. “Balanced” genotypes coupling high yield with good silage value include 15836 (top yield; silage NDF 49.74%, DMD 66.21, RFV 126.5), 21438 (DMD 65.57, RFV 125.0) and 14522 (DMD 65.21, RFV 118.7). These are major candidate genotypes where production and aerobic-stable silage are priorities. “Quality-first” genotypes such as 2346 and 1536 produce exceptional silage energy/voluntary intake (RFV 169.9 and 142.9) but carry lower CP (notably 2346: silage CP 4.64%). These can be used with protein supplements (e.g., alfalfa hay, oilseed meals). For protein supply, 5085 had the highest silage CP (8.96%) and competitive RFV (116.1), and 8562 offers the highest hay CP (9.43%) with strong silage value (RFV 125.1). Conversely, 4747 is a clear “avoid” for silage due to its fiber increases and depressed

functional indices. These genotype-level insights provide concrete, environment-specific options for both breeders (as parents/candidate releases) and farmers (as purpose-fit cultivars).

The study was carried out over one year at a single site in Mediterranean and semi-arid conditions, without any moisture adjustment prior to ensiling. To ensure stability and expand the suggestions, it is essential to do investigations that extend over many years and various locations. Nevertheless, results support the use of certain pearl millet genotypes into semi-arid forage rotations to enhance the summer roughage supply, suggesting for harvest at the milk-dough stage and immediate ensiling under regulated circumstances to optimize nutritional value.

Conclusion: The results revealed significant, actionable genotypic variation for yield and feed quality. For semi-arid Mediterranean environments, we propose 15836, 21438, and 14522 for reliable silage production, 5085 for improved silage protein, and 2346 or 1536 for optimum energy/voluntary intake, in conjunction with protein supplements. Genotype 4747 should not be used for silage until management measures clearly address its fermentation and fiber characteristics. These results provide practical direction for cultivar development and specific objectives for breeding initiatives aimed at climate-resilient, high-value roughage.

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