Journal of Food, Nutrition and Agriculture 2025, 8: 19-26
https://doi.org/10.21839/jfna.2025.v8.9720

Research Article

Genotype by environment interaction and yield stability of common vetch (*Vicia sativa*) genotype in Bale Zone of Oromia, Southern Ethiopia

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(Received: September 15, 2025; Revised: December 03, 2025; Accepted: December 05, 2025; Published: December 26, 2025)

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ABSTRACT

Animal production faces a major challenge due to feed scarcity, both in quantity and quality, which calls for improvements in forage technology to fill the current feed gaps. This study aimed to identify high-yielding and stable genotypes of Common Vetch. Ten genotypes (LRI-5138, ILRI-5161, ILRI-5168, ILRI-5170, ILRI-5173, ILRI-5190, ILRI-5196, ILRI-5199, ILRI-5207, and ILRI-5209 were evaluated alongside a standard check (ICARD16509), organized in a Randomized Complete Block Design (RCBD) with three replications. Agronomic performance and yields varied significantly among genotypes, environments, and their interactions (G x E). The Additive Main effects and Multiplicative Interaction (AMMI) analysis indicated that the environment accounted for 68.19% of the total variation in dry biomass yield. In comparison, genotype and G x E interaction contributed 14.46% and 17.35%, respectively. The highest herbage dry matter yield was recorded for genotype ILRI-5209 (7.21 t ha^{-1}), followed by ILRI-5207 (6.93 t ha^{-1}) across various environments with dry matter yield advantages of 38.92% and 26.20% over the standard check, in that order. The analysis of chemical compositions showed significant differences ($p < 0.05$) among tested genotypes for all parameters. Crude protein (CP) content was highest for genotype ILRI-5207 (21.99%), followed by ILRI-5209 (21.09%), whereas the local genotype ILRI-5138 had the lowest CP content (16.13%). Therefore, given their high yield potential and nutritional quality, ILRI-5209 and ILRI-5207 are recommended for further verification and potential release in the highlands of Bale and similar agro-ecological areas.

Key words: AMMI, Dry matter yield, Genotypes, Stability, *Vicia sativa*

INTRODUCTION

Ethiopian has a sizable livestock population and diverse agro-ecological zones suitable for livestock production and for cultivating various food and fodder crops. However, livestock production in the country largely remains subsistence-oriented and is characterized by very low reproductive and production performance. This issue is primarily linked to the inadequate quality and quantity of available animal feed (Maleda, 2013) due to primary shortages of quality and quantity of animal feed (Maleda, 2013), which are further exacerbated by factors such as land degradation, land shortage, and poor soil fertility (Tewodros *et al.,* 2007). Additionally, the rapid increase human population has led to expansion in crop production while grazing areas are being reduced (Tolera, 2007). Nowadays livestock production systems are increasingly threatened by population pressure, climate change, recurrent droughts, and degradation of natural resources. These pressures are more acute in Bale Zone, where changes in land use from grazing land to arable land-pose major challenges. Addressing these issues is essential for improving sustainability, food security, and rural livelihoods through the cultivation of forage crops.

Forage legumes are recognized for their high nutritional quality, ability to thrive in marginal soil conditions, and capacity to enhance soil health via biological nitrogen fixation processes. Thus, they became an integral part of sustainable agricultural systems, providing quality feed; nectar, green manure, and soil cover (Sheaffer *et al.,* 2020). Furthermore, forage legumes adapt well to various climatic conditions, are ease to establish, exhibit high herbage productivity, and possess seed yield potential. Additionally, they contribute to soil erosion reduction and demonstrate resistance to pests and diseases (Tolera *et al.,* 2012). These attributes make forage legumes, particularly vetches, ideal candidate for improving livestock production. With their high protein content and relatively lower costs compared to feed concentrates, forage legumes are significant sources of nitrogen for livestock, especially in the context of developing nations (Kebede *et al.,* 2016).

The common vetch (*Vicia sativa* L., Tribe Viciae, Family Fabaceae) is one of the world's most economically important annual grain legumes, used as animal feed, as forage (grain, hay, and for silage production), and as a valuable grain legume, serving as an affordable source of high-quality protein and minerals with high digestibility and high energy content (Huang *et al.,* 2017; Parissi *et al.,* 2022). This species is particularly well adapted to the highland regions of Ethiopia (Getnet, 1999) and belongs to one of the world's leading legume families in terms of economic importance (Mikić *et al.,* 2009). Although the species originated from the arid regions of the Middle East (Ford *et al.,* 2008). It offers a low-cost, rich source of protein and minerals (Mao *et al.,* 2015). Additionally, V. sativa plays a significant role in human diets, especially during periods of food scarcity, and is valued by vegetarians (Akpinar *et al.,* 2001; Uzun *et al.,* 2011). Its remarkable nutritive value makes it an important protein supplement, while the grains serve as critical protein and energy sources in the diets of both ruminants and non-ruminants (Sadeghi *et al.,* 2009). Integrating forage legumes, such as common vetch, into local agricultural production systems can enhance livestock productivity by improving the quantity and quality of feed. This is achievable largely due to their ability to fix atmospheric nitrogen in symbiosis with root-nodule bacteria known as rhizobia (Tiruset, 2017). Research indicates that vetch associations can fix between 25 and 190 kg N ha^{-1}, effectively contributing to soil nitrogen enrichment (Ashworth *et al.,* 2017).

MATERIALS AND METHODS

Description of the study area

The study was conducted across four locations Sinana (on station), Agarfa and Adaba (sub-sites) and Goba (on farm) during two cropping seasons (2022/23 and 2023/24). The geographical locations and climatic conditions of the study areas are summarized in Table 1.

Treatments and eperimental materials

A total of 87 of vetch accessions were collected from International Livestock Research Institute (ILRI) to screen for superior genotypes during the breeding stage. Of these accessions, ten accessions: ILRI-5138, ILRI-5161, ILRI-5168, ILRI-5170, ILRI-5173, ILRI-5190, ILRI-5196, ILRI-5199, ILRI-5207, and ILRI-5209 were identified as superior genotypes and selected for further evaluation alongside with standard check (ICARD16509).

Experimental design and procedures

The experiment was set up using a randomized complete block design (RCBD) with three replications across the four locations. The size of each plot was 2.1 m x 2 m, with 1.5 m between blocks and 1 m between plots. Land preparation was carried out between May and June using a tractor, followed by harrowing and leveling to ensure an optimal seedbed before planting. A seed rate of 30 kg/ha was utilized, along with a fertilizer application at a rate of 100 kg/ha of NPS (Nitrogen, Phosphorus, and Sulfur) to provide essential nutrients for the growth of the vetch accessions.

Data collection and measurements

The date of flowering was recorded when 50% of plants reached flowering, while the date of maturity was recorded when plants reached 90% of the plants achieved physiological maturity. Data for plant height was taken from five randomly selected plants from inner row and the average height of these sampled plants was used. For herbage dry matter yield, the two middle rows of each plot were harvested at 50% flowering and the fresh weight of the cut biomass was measured using sensitive balance and recorded. Then sub-samples of 300 gm for herbage dry matter yields and 200 gm for leaf-to-stem ratio. These samples were then oven-dried at 65 °C for 72 hours until a constant weight was achieved. The dry biomass yield converted to tons per hectare using the formula (10 x TotFW x (DWss/HA x FWss)) (Tarawali *et al.,* 1995). Where; TotFW = total fresh weight from a plot (kg), DWss = dry weight of the sample in (grams), FWss= fresh weight of the sample (grams), HA=Harvest area (m^2) and, 10 = is a constant for conversion of yields in kg per m^2 to t ha^{-1}. For chemical analysis, a composite sample of the dry biomass was prepared for each genotype. The contents of dry matter (DM), ash, and crude protein (CP) were determined following AOAC (1990) procedures. Fiber components, including neutral detergent fiber (NDF), acid detergent fiber (ADF), and acid detergent lignin (ADL), were analyzed using the Van Soest method (Van Soest *et al.,* 1991) at Hawassa University.

Data analysis

For the combined analysis of variance (ANOVA), the location was considered as a random variable, while genotypes were considered as a fixed variable. Data analysis was performed using SAS software (version 9.0). The Genotype by Environment interaction was analyzed with GenStat (Version 18th). The Multiplicative interaction model AMMI (Additive Main effects and Multiplicative Interaction) proposed by Zobel *et al.* (1988) was used to compute genotype stability. In the AMMI model, the magnitude obtained in the first principal component (IPCA1) of each genotype was used as an indicator of stability. The lower absolute value of IPCA1 indicated a stable genotype.

The data were analyzed with the model: Yijk = μ + Gi + Ej + (GE)ij + Bk(j) + e ijk; Where, Yijk = measured response

Table 1: Geographical locations of the study areas

Experimental sites	Geographical locations and temperatures				
	Distance from addis abeba (km)	Annual average RF (mm)	Altitude (m.a.s.l)	Latitude	Longitude
Sinana	463.3	905.13	2470	7° 5' 0"	40° 12' 0"
Goba	446	1000-1200	2500	6° 55' 0" N	40° 10' 0" E
Agarfa	420	800-1200	2450	7° 11' N to 7° 32' N	39° 40' E to 40° 5' E
Adaba	310	1000	2485	7° 00' 0.00" N	39° 29' 59.99" E

of genotype i in block k of environment j; μ = grand mean; Gi= effect of genotype i; Ej = effect of environment j; GEij= genotype and environment interaction; Bk (j) = effect of block k in environment j; eijk = random error effect of genotype i in block k of environment j.

RESULTS AND DISCUSSION

The results of the combined analysis of variance (ANOVA) for various agronomic parameters and yields of common vetch (*Vicia sativa*) genotypes are presented in Table 2. The analysis revealed that variations in genotypes, environment, and years have significant ($p<0.05$) effects on dry matter, seed yields, plant height, and thousands seed weight. Additionally, the interaction of genotypes with years and locations has a significant ($p<0.05$) effect on leaf-to-stem ratio (LSR), dry matter yield, and seed yield ($p<0.01$). These findings suggest that the genotypes displayed differential performance across the varied test environments and years, highlighting the genetic variability among the common vetch genotypes and the diversity of the tested locations and seasons (Figure 1).

Days to 50% flowering and maturity

Days to 50% flowering and maturity stage are presented in Table 3. Significant ($p<0.005$) variations were observed among the tested genotypes. The days to reach 50% flowering showed significant variations ($p<0.005$) when considering the interactions among genotypes, years, and locations. The mean values for days to 50% flowering across years and locations ranged from 111.87 to 115.5 days**.** The genotype ILRI-5196 recorded the longest duration to 50% flowering, with a mean of 115.5 days, followed closely by IRLI-5199, which had a mean of 114.50 days. In contrast, the standard check (ICARD61509) exhibited the shortest duration, taking 111.87 days to reach 50% flowering. Different scholars reported different dates of 50% flowering for different vetch varieties/or genotypes; for instance, Gezahagn *et al.* (2019) reported flowering durations ranging from 83.3 to 124.7 days, while Dawit *et al.* (2011) found values from 93 to 114 days for different vetch species, and Gezahagn *et al.* (2013) also reported values ranging from 101.04 to 111.95. The current study's findings are consistent with earlier research, notwithstanding minor discrepancies

Table 2: Mean squares of ANOVA for yields and yield components of Common vetch Genotypes

Source of variations	Mean squares							
	DF	Df (50%)	DM (90%)	PH (cm)	HDM yield (t/ha)	LSR	TSW (gm)	Seed yield (qun/ha)
Genotype (G)	11	24.93**	19.19**	1524.6**	11.322**	0.15395**	1216.45**	160.47**
Year (Y)	1	1005.85**	2241.25**	28007**	23.899**	0.54354**	925.29**	190.9**
Location (L)	3	215.41**	1468.18**	6945.5**	205.141**	0.9786**	364.03**	1906.87**
G*Y	11	23.81**	10.82**	430.5**	172.922*	0.08308*	70.94**	115.62*
G*L	33	11.57**	6.7**	105.5^{ns}	33.747*	0.06291*	22.27^{ns}	31.09**
Y*L	3	1007.87**	3013.08**	9495**	66.293**	1.28513**	306.24**	611.76*
G*Y*L	33	11.67**	6.02**	171.3*	3.203^{ns}	0.06371*	35.52*	13.96^{ns}
Error	190	4.49	1.6	113.2	2.782	0.04034	21.75	9.96

L=Location, G=Genotypes, DF=Degree of freedom, Df=days to 50% flowering, DM=Days to 90% maturity, PH=plant height in centimeters, HDM=herbage dry matter in tone per hectare, * = significant different (0.05), ** = highly significant different (0.01), TSW=Thousand seed weight, ns=none significant

Table 3: Dry matter yields (DMY ton ha^{-1}) of vetch genotypes across locations (Adaba, Goba, and Sinana) in 2022/23 and 2023/24, including combined means and yield advantage in percentage

Genotypes	Year 1 (2022/23)				Year 2 (2023/24)				Combined mean	Yield advantages
	Adaba	Agarfa	Goba	Sinana	Adaba	Agarfa	Goba	Sinana		DMY
ILRI-5138	5.63^{abcd}	4.90^{ab}	8.66^{a}	6.38	3.29^{d}	1.70^{d}	9.34^{abc}	4.40^{cde}	5.54b^{cde}	
ILRI-5161	6.26^{abc}	5.56^{ab}	5.97^{bc}	8.58	4.67^{abcd}	3.42^{abcd}	11.08^{ab}	6.91^{ab}	6.56^{abcde}	
ILRI-5168	3.79^{de}	4.90^{ab}	8.32^{a}	7.51	3.85^{cd}	1.95^{cd}	6.68^{c}	5.61^{abcd}	5.33^{de}	
ILRI-5170	4.27^{de}	7.11^{a}	8.76^{a}	8.86	4.77^{abcd}	4.40^{ab}	10.51^{abc}	5.36^{abcd}	6.76^{abc}	
ILRI-5173	6.73^{ab}	6.05^{ab}	8.51$_{a}$	8.04	4.60^{bcd}	3.31^{abcd}	11.76$_{a}$	3.63^{de}	6.58^{abcde}	
ILRI-5190	6.38^{abc}	4.83^{ab}	6.62^{abc}	7.46	6.60^{ab}	4.68^{a}	9.42^{abc}	7.50^{a}	6.69^{abcd}	
ILRI-5196	2.89^{e}	6.14^{ab}	8.5^{a}	4.97	5.60^{abcd}	2.62^{bcd}	8.43^{abc}	2.09^{e}	5.35^{cde}	
ILRI-5199	4.15^{de}	5.25^{ab}	5.94^{bc}	7.88	4.43^{bcd}	4.25^{ab}	8.17^{abc}	6.26^{abc}	5.89^{abcde}	
ILRI-5207	5.57^{abcd}	6.93^{ab}	7.51^{ab}	8.11	5.89^{abc}	2.63^{bcd}	10.83^{abc}	7.30^{a}	6.90^{ab}	26.20
ILRI-5209	6.99^{a}	6.21^{ab}	8.10^{ab}	8.58	7.13^{a}	3.77^{abc}	10.70^{abc}	7.17^{a}	7.21^{a}	38.72
ICARD61509	4.68^{cde}	4.16^{b}	8.05^{ab}	5.93	5.56^{abcd}	3.28^{abcd}	7.11^{bc}	5.98^{abcd}	5.19^{e}	
LSD (0.05)	1.985	2.90	2.412	ns	2.55	1.86	4.11	1.503	1.51	
CV %	22.36	30.19	19.54	24.53	29.21	29.21	25.51	16.10	26.46	
F-value	0.0043	0.05	0.0022	0.5901	0.01	0.041	0.01	<0.001	0.01	

that are most likely the consequence of seasonal and varietal variances.

The main impacts of year, location, and genotype did not significantly alter physiological maturity ($p>0.01$), and no significant interaction was observed. The physiological maturity for the genotypes ranged from 169.09 to 172.09 days, aligning with findings by Dawit *et al.* (2011) and Gezahagn *et al.* (2019).

Plant height

Plant height emerged as a critical factor that influenced herbage dry matter yield. Significant ($p<0.05$) variations in plant height were observed among genotypes at the 50% flowering stage. The grand mean plant height for the vetch genotypes was 81.04 cm, with mean values ranging from 72.0 to 91.38 cm. Among locations, the highest plant height was obtained from Goba site during the 2022/23 cropping season, while the minimum plant height was recorded at Agarfa subsite in 2023/24 cropping season. The tallest genotype was ILRI-5161, measuring 91.38 cm, whereas the shortest was ILRI-5196, at 72.0 cm. The present finding was similar ranges with the finding of Gezahagn *et al.* (2019). Variations in plant height could be attributed to differences in location, variety, and seasonal conditions.

Dry matter yields

V. sativa genotypes were evaluated along with Vetch variety (ICARD61509) as standard check across years and locations. Significant differences ($p<0.05$) were observed among genotypes in the mean dry matter yields across years and locations (Table 3). The highest herbage dry matter yield was obtained from genotypes ILRI-5209 (7.21 ton ha^{-1}), followed by ILRI-5170 (6.90 ton ha^{-1}). Conversely, the lowest dry matter yield was recorded from the standard check ICARD61509 (5.19 ton ha^{-1}). Moreover, herbage dry matter yield exhibited significant variations across locations and years. The maximum mean dry matter yield was recorded from Goba location (8.35 ton ha^{-1}) the Agarfa sub-site recorded the lowest yield (4.46 ton ha^{-1}).

Genotypes ILRI-5209 (7.21 ton ha^{-1}) and ILRI-5207 (6. 90 ton ha^{-1}) are recommended as candidate varieties due to their yield advantages of 38.92% and 26.20%, respectively, over the standard check ICARD61509 (5.19 ton ha^{-1}). The herbage dry matter yields in the current study are comparable to the findings of Gezahagn *et al.* (2019), who reported values ranging from 5.05-6.79 ton ha^{-1}, Conversely, the yields observed here are higher than those documented by Dawit *et al.* (2011), who reported an average yield of 4.70 ton ha^{-1} for Gebisa variety of *V. sative's* species.

Leaf to steam ratio

The leaf to steam ratio is a crucial indicator of forage quality, influencing parameters such as digestibility and feed conversion efficiency. The present study revealed that the tested genotypes were varied significantly ($p<0.01$) in the leaf-steam-ratio across locations and years. The highest leaf to steam ratio was obtained from ICARD61509 (0.91), followed closely by ILRI-5209 (0.87), while the lowest leaf-to-steam ratio was obtained from ILRI-5196 (0.64).

Seed yield and thousand seed weight

Vicia sativa genotypes were evaluated along with standard check across years and locations. The result shows significant differences ($p<0.05$) among genotypes in the mean seed yields across years and locations (Table 4). The highest seed yields were obtained from genotypes ILRI-5161 (13.92 qunt/ha) and ILRI-5209 (12.92 qunt/ha), followed closely by ILRI-5170 (12.21 qut/ha) and ILRI-5170 (12.07 qunt/ha). In contrast, the lowest seed yield was recorded from ILRI-5196 (3.99 qunt/ha). Also, seed yields significantly varied across locations and years. Average seed yield was reported from Gobasite (14.11 qunt/ha) and Sinana site (13.48 qunt/ha), while seed yield was recorded from Agarfa sub-site (2.81 qunt/ha). The data indicates that both location and the cropping season significantly affect the seed yields of these vetch genotypes.

Genotypes ILRI-5209 and ILRI-5207 produced optimum seed yields of 12.96 qunt/ha) and 12.07 qunt/ha, respectively, were selected as potential candidates showcasing seed yield advantages 36.34% and 26.79%, in that order, over the standard check ICARD61509 (9.52 qunt/ha). The seed yield obtained in the current study was partially agreed with the findings of Gezahagn *et al.* (2019), who reported values ranging from 0.4 to 0.8 ton ha^{-1} (mean of 0.6 ton ha^{-1}) at Holetta and 2.0 to 2.9 ton ha^{-1} (mean of 2.4 ton ha^{-1}) at Ginchi. Similarly Dawit *et al.* (2011) reported an average seed yield of 1.96 ton ha^{-1} recorded for Gebisa variety of *V. sative* species. However, in some extent the ranges reported by these authors were higher than the findings of the present study.

The thousand seed weight of the tested vetch genotypes also showed significant differences ($p<0.05$) across locations. The weight ranged from 29.87 g (ICARD61509) to 53.81 g (ILRI-5168), with a mean of 47.74 g (Table 5). The highest mean thousand seed weight was recorded from genotype ILRI-51.68 (53.81 gm) whereas the lowest mean thousand seed weight was recorded from the standard check ICARD61509 (29.87 g). This highlights the potential of selecting vetch genotypes with improved seed weight and yields, essential for overall agronomic performance.

Pests and diseases

Diseases cause losses in quality and yield of common vetch crops include; viral, bacterial, and fungal infections, as well as, insect, spider, and nematode pests (Renzi & Cantamutto, 2013). Many of the insects that infest forage legumes can attack vetches, including beetles, flies, and aphids, promoting direct injuries or causing indirect damages by being vectors of virus transmission. The herbivorous beetle vetch weevil (*Bruchus rufipes* Herbst.) is an important pest for legumes, including vetches. Their larvae feed the grains, reducing the germination capacity of the seeds. The beetle *Sitona lineatus* L. is also a common pest of *V. sativa*. However, during the

Table 4: The combined mean of herbage dry matter (t/ha), seed yield (qunt/ha) and agronomic parameters of common vetch genotypes across locations and years

	Parameters						
Genotypes	**Days to (50%) flowering**	**Days to maturing**	**Plant ht. (cm)**	**Dry biomass Yield (ton/ha)**	**Leaf-to-steam ratio**	**1000 seed wt (g)**	**Seed yield (qunt/ha)**
ILRI-5138	112.92^{cde}	169.84	85.79^{abc}	5.54^{cd}	0.765^{bcde}	49.59^{bcd}	10.19^{bcd}
ILRI-5161	113.13^{cde}	170.64	91.38^{a}	6.56^{abc}	0.82^{abc}	52.33^{ab}	13.92^{a}
ILRI-5168	112.58^{cde}	170.8	89.00^{ab}	5.33^{d}	0.724^{cde}	53.81^{a}	8.97^{d}
ILRI-5170	112.21^{de}	170.14	88.50^{ab}	6.76^{ab}	0.82^{abc}	51.41^{abc}	12.21^{ab}
ILRI-5173	113.70^{bc}	171.13	78.31^{cde}	6.58^{abc}	0.797^{abcd}	51.90^{abc}	9.74^{bcd}
ILRI-5190	114.75^{ab}	171.68	72.78^{e}	6.60^{abc}	0.656^{de}	43.05^{e}	9.29^{d}
ILRI-5196	115.17^{a}	172.09	72.00^{e}	5.31^{d}	0.638^{e}	39.22^{f}	3.99^{e}
ILRI-5199	114.78^{ab}	171.59	76.00^{de}	5.90^{bcd}	0.750^{bcde}	48.98^{cd}	9.32^{d}
ILRI-5207	113.58^{bcd}	171.73	81.71^{bcd}	6.90^{ab}	0.785^{abcd}	48.03^{d}	12.07^{abc}
ILRI-5209	113.46^{bcd}	171.04	80.33^{bcde}	7.21^{a}	0.87^{ab}	50.05^{bcd}	12.96^{a}
ICARD61509	111.88^{e}	169.09	75.25^{de}	5.19^{d}	0.91^{a}	29.87^{g}	9.52^{cd}
GM	113.47	170.94	81.04	6.173	0.78	47.737	10.308
LSD (5%)	1.2314	NS	8.69	1.15	0.14	3.04	2.584
C.V (%)	2.14	0.9	13.55	26.46	26.55	11.17	33.46
Adaba	111.97^{c}	165.46^{d}	74.22^{b}	5.17^{c}	0.941^{a}	49.682^{a}	10.39^{b}
Agarfa	113.76^{b}	176.52^{a}	70.70^{b}	4.46^{d}	0.729$_{b}$	43.995^{c}	2.81^{c}
Goba	112.08^{c}	169.50^{c}	91.86^{a}	8.35^{a}	0.680^{b}	47.006^{b}	14.11^{a}
Sinana	115.71^{a}	172.08^{b}	87.24^{a}	6.63^{b}	0.754^{b}	47.769$_{b}$	13.48^{a}
LSD (5%)	1.47	2.11	5.24	0.69	0.09	1.83	1.56
2022/23	111.48^{b}	168.03^{b}	91.15^{a}	6.43^{a}	0.726^{b}	48.82^{a}	10.94^{a}
2023/24	115.28^{a}	173.74$_{a}$	70.86^{b}	5.88^{b}	0.826^{a}	45.41^{b}	9.46^{b}
LSD (5%)	0.99	1.5	3.72	0.49	0.061	1.29	1.09

Table 5: Combined mean chemical compositions of Common Vetch genotypes tested in locations (Sinana, Adaba, Agarfa and Goba, 2022/23)

Entry	**DM%**	**Ash**	**CP%**	**NDF**	**ADF**	**ADL**
ILRI-5138	91.10^{b}	8.865^{c}	16.13^{e}	36.115^{d}	26.005^{c}	6.035^{c}
ILRI-5161	91.035^{b}	9.235^{c}	20.79^{b}	31.77^{f}	22.115^{g}	4.825^{d}
ILRI-5168	90.87^{b}	8.915^{c}	18.00^{c}	34.005^{e}	24.175^{e}	5.000^{d}
ILRI-5170	91.045^{b}	10.140^{b}	16.90^{d}	33.990^{e}	23.805^{e}	4.760^{d}
ILRI-5173	91.225^{b}	9.030^{c}	17.87^{c}	39.090^{b}	28.105^{b}	6.795^{b}
ILRI-5190	91.815^{a}	9.850^{b}	20.84^{b}	39.065^{b}	27.835^{b}	6.840^{b}
ILRI-5196	91.11^{b}	9.100^{c}	16.86^{d}	39.895^{a}	27.775^{b}	6.090^{c}
ILRI-5199	90.02^{c}	9.120^{c}	18.22^{c}	34.135^{e}	23.185^{f}	4.960^{d}
ILRI-5207	90.93^{b}	10.160^{b}	21.99^{a}	35.905^{d}	25.755^{cd}	5.205^{d}
ILRI-5209	92.085^{a}	10.940^{a}	21.09^{b}	36.760^{c}	25.215^{d}	5.925^{c}
ICARD61509	91.2^{b}	10.135^{b}	17.11^{d}	39.100^{b}	28.775^{a}	9.110^{a}
GM	91.13	9.59	18.492	36.110	25.485	5.8850
CV (%)	0.02	0.2	0.09	0.04	0.09	0.36
LSD (0.05)	0.0209	0.0193	0.0172	0.0157	0.0234	0.0210

study, no pests or diseases of common vetch (*V. sativa)* were observed.

Nutritional quality analysis

The nutritional analysis of various common vetch genotypes is presented in Table 5. The crude protein (CP), ash, Neutral detergent fiber (NDF), Acid detergent fiber (ADF), and Acid detergent lignin (ADL) were significantly ($p<0.05$) different among the genotypes. The CP content ranged from 16.13 to 21.99%, indicating that *V. sativa's* potential to satisfy ruminant livestock's protein requirements. This range is consistent with the findings of Dawit *et al.* (2011), who reported the highest CP value at 20.80%, and Gezahagn *et al.* (2019), who reported a CP value of 21.5% for *V. sativa*. The high CP levels obtained indicate that the vetch genotypes can effectively complement natural pastures and other low-quality roughages.

Additive main effects and multiplicative interaction (AMMI) analysis

The results of the AMMI model analysis of variance for dry biomass and seed yields (Table 6). The analysis revealed the presence of highly significant ($p<0.001$) differences among genotypes and environment and statistically significant due

Table 6: ANOVA of AMMI model for DMY of common vetch genotypes

Source	d.f.	s.s.	m.s.	Total variation	% SS Explained	F pr
Total	263	1749.5	6.65			
Treatments	43	862.2	20.05	5.16		<0.001
Genotypes	10	124.7	12.47	3.21	14.46	<0.001
Environments	3	587.9	195.96	24.68	68.19	<0.001
Block	8	63.5	7.94	2.04		0.0428
Interactions	30	149.6	4.99	1.28	17.35	0.1586
IPCA 1	12	98.9	8.24	2.12	66.11	0.0168
IPCA 2	10	35.8	3.58	0.92	23.93	0.5148
Residuals	8	14.9	1.87	0.48		0.8691
Error	212	823.8	3.89			

Table 7: ANOVA of AMMI model for Seed yield of Common Vetch genotypes

Source	d.f.	s.s.	m.s.	Total variation	% SS Explained	F pr
Total	263	12321	46.8			
Treatments	43	8016	186.4	10.06		<0.001
Genotypes	10	1713	171.3	9.25	21.37	<0.001
Environments	3	5321	1773.6	37.59	66.38	<0.001
Block	8	377	47.2	2.55		0.0114
Interactions	30	982	32.7	1.77	12.25	0.0115
IPCA 1	12	672	56	3.02	68.43	<0.001
IPCA 2	10	277	27.7	1.5	28.21	0.1423
Residuals	8	32	4.1	0.22		0.9873
Error	212	3928	18.5			

to genotype-by-environment interaction for dry matter yield. The total treatment sum of squares of variations observed for dry matter yield was largely due to environment (68.19%) followed by Genotypes (14.46%) and genotype by environment interaction (17.35%). The large yield variation explained by environment and followed genotypes indicated the existence of genetic variability among the tested genotypes. This also indicated the existence of a considerable amount of differential discriminating ability in the test environments and the differential response among the evaluated common vetch genotypes to changes in growing environments. Substantial percentages (17.35%) of G x E interaction were explained by IPCA-1(66.11%) followed by IPCA-2 (23.93%) and therefore, used to plot a two-dimensional GGE biplot.

The seed yield of the AMMI model analysis of variance (Table 7). The analysis revealed the presence of highly significant (p<0.001) differences among genotypes and environment and statistically significant due to genotype-by-environment interaction for seed yield. The total treatment sum of squares of variations observed for seed yield was largely due to environment (66.38%) followed by Genotypes (21.37%) and genotype by environment interaction (12.25%). The large yield variation explained by environment and followed genotypes indicated the existence of genetic variability among the tested genotypes.

Genotypes and genotypes by environment interaction (GGE) biplot analysis

Based on the "Which-won-where pattern" of biplot analysis, the lines from the biplot's origin perpendicular to the polygon's sides divided the polygon into four sectors, as shown in Figure 2. Results indicated that genotypes ILRI-5168, ILRI-5190, ILRI-5209, ILRI-5170, ILRI-5196, ILRI-5138 and standard check (ICARD61509) were vertex genotypes, and the rest were located in the polygon. A genotype and test environment located near the origin of the biplot with two IPCA scores of almost zero was stable. Based on the result genotypes ILRI-5209, ILRI-5161, and ILRI-5207 were slightly closer to the origin, illustrating the stability and greater mean grand value of dry biomass yield, which presented good stability. On the other hand, ILRI-5196, ILRI-5138, ILRI-5168 and standard check (ICARD61509) were located far away from the origin of the polygon, indicating less stabile genotypes.

Figure 1: Photo shown field performances of common vetch

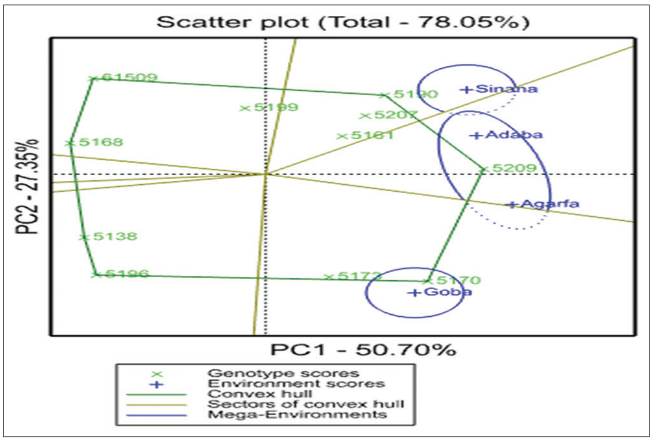

Figure 2: Scatter biplot of genotypes and four environments for dry biomass yield

The results indicated in Figure 3. The genotypes, ILRI-5196, ILRI-5190 ILRI-5209, ILRI-5161, ILRI-5207, and standard check (ICARD61509) were vertex genotypes, and the rest were located in the polygon. A genotype and test environment located near the origin of the biplot with two IPCA scores of almost zero was stable. Based on the result genotypes ILRI-5209, ILRI-5170, and ILRI-5207 were slightly closer to

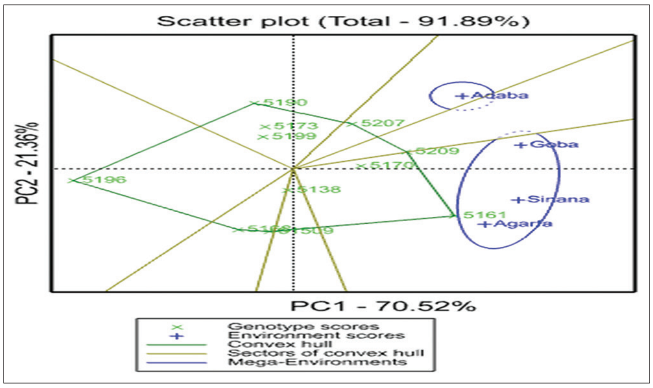

Figure 3: Scatter plot of genotypes and four environments for seed yield

the origin, illustrating the stability and greater mean grand value of seed yield, which presented good stability. Whereas ILRI-5196 and ILRI-5190 and standard check (ICARD61509) far from the origin thus indicate that less stabile genotypes.

CONCLUSIONS AND RECOMMENDATION

Significant variations were observed among the tested common vetch genotypes evaluated in the four environments for two consecutive years. There was also substantial genotype-by-environment interactions for most of the traits evaluated, indicating that the test genotypes had differential performances in diverse locations. Among stability parameters, IPCA1, IPC2, AMMI stability value, and GGE biplot further confirmed and identified high yielding and stable genotypes. Accordingly, genotypes ILRI-5209 and ILRI-5207 revealed the highest dry biomass, seed yields and highest CP and were most stable in the tested environments. Therefore, ILRI-5209 and ILRI-5207, because of their yield potential and stability in the testing environments, were selected as candidate genotypes and were recommended for cultivation and release as a variety in the tested locations and with similar agro-ecologies.

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