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RESEARCH ARTICLE

PHYTOCHEMICAL SCREENING OF MUNG BEAN (VIGNA RADIATA (L.) WILCZEK) GENOTYPES FOR DUAL-PURPOSE BIOACTIVE AND ANTIOXIDANT TRAITS IN BURKINA FASO

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Abstract

Mung bean is an Asian-origin legume with significant agronomic and nutritional benefits, increasingly promoted in West Africa as a resilient crop to address food and nutritional security challenges. This study represents one of the first simultaneous evaluations of seed and leaves phytochemical profiles in mung bean genotypes cultivated under Sudanianagro-ecological conditions in Burkina Faso. It evaluated the biochemical composition and antioxidant activity of seeds and leaves from ten lines (nine introduced and one local) in Burkina Faso. Polyphenols and flavonoid contents, as well as antioxidant activity (DPPH, FRAP), were quantified in both organs. The results revealed a metabolic superiority of leaves over seeds regarding phenolic compounds. Lines VR-172, M34, and VR-114 were characterized by high antioxidant activity (DPPH > 3.4 µmol AAE/g in leaves). Furthermore, a significant positive correlation ($r = 0.48$; $p < 0.01$) was established between seed antioxidant activity and total polyphenols content. These genotypes (VR-172, M34, and VR-114) represent promising candidates for biofortification and food diversification programs. Our findings demonstrate the importance of considering both seeds and leaves when assessing the nutritional potential of mung bean germplasm.

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Introduction:-

Mung bean (Vigna radiata (L.) Wilczek) is a pulse crop widely cultivated in Asia and increasingly promoted in Africa due to its short growth cycle, adaptability to marginal environments, and high nutritional value (Kabré et al., 2022). Its seeds are rich in proteins, carbohydrates, vitamins, and minerals, making mung bean a vital component of

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plant-based diets(Tang et al., 2014; Hou et al., 2019). Beyond macronutrients, mung bean contains bioactive compounds such as phenolic acids and flavonoids, which contribute to its antioxidant properties(Hou et al., 2019; Narale et al., 2024; Elwahsh et al., 2025).While most studies focus on the nutritional quality of mung bean seeds, leaves are often overlooked, despite their traditional consumption in certain regions and their potential as functional foods. Legume leaf tissues are known to contain higher concentrations of phenolic compounds and antioxidants than seeds, owing to their metabolic activity and exposure to environmental stress(Lugumira et al., 2025). In Africa, the valorization of legume leaves could contribute to dietary diversification and micronutrient intake, particularly in rural communities.

The biochemical composition of mung bean is influenced by both genetic and environmental factors. Several studies have highlighted significant genotypic variation in protein content, phenolic concentration, and antioxidant activity among mung bean accessions (Iqbal et al., 2006; Tang et al., 2014).However, data on the biochemical characteristics of mung bean lines grown under Sudanianagro-ecological conditions remain limited, specifically regarding the comparative analysis of seeds and leaves. This study aims to compare the metabolic profiles of seeds and leaves from 10 mung bean genotypes to identify those with high nutritional and antioxidant density, suitable for future agronomic and nutritional valorization in Burkina Faso.

Materials and Methods:-

Materials:-

Study site:-

This study was conducted at the INERA (Institute of Environment and Agricultural Research) experimental station in Saria during the 2025 cropping season (12° 16′ N latitude, 2° 9′ W longitude, 300 m elevation). The climate is North-Sudanian, with an average annual rainfall of 800 mm. The average annual temperature is 28 °C, with monthly maximums reaching 40 °C in March and April (Sidibé et al., 2025). Saria soils are characterized by phosphorus deficiency, low organic matter content, and low cation exchange capacity. They are rapidly depleted under continuous cropping and the use of synthetic chemical fertilizers(Iseki et al., 2024).

Plant material:-

The plant material (Table I) consisted of nine (09) lines and one mung bean variety, "Beng-tigré," which is widely distributed in Burkina Faso and registered in the national catalog.

Table 1: Name and origin of Vigna radiata genotypes evaluated in Saria (Burkina Faso)

Matériel vegetal	**Origine**
VR-75	World Vegetable Center
VR-77	World Vegetable Center
VR-114	World Vegetable Center
VR-157	World Vegetable Center
VR-172	World Vegetable Center
VR-207	World Vegetable Center
M8	Australia
M16	Australia
M34	Australia
Beng-tigré	India

Methods:-

Sample preparation:-

For each line, seeds and leaves were dried and ground into powder using a mortar and pestle. The resulting powders were sieved to ensure a homogeneous particle size before extraction.

Extraction of bioactive compounds:-

Phenolic and antioxidant compounds were extracted via maceration. For each line,three independent biological replicates of 500 mg of seed powder and 250 mg of leaf powder were mixed with 1 mL of 80% ethanol in Eppendorf tubes. The mixtures were vortexed and placed on a shaker for 24 hours. Subsequently, the tubes were centrifuged at 10,400 rpm for 14 minutes. The supernatants were collected and used for biochemical assays.

Phenolic compound assays:-

- **Total polyphenols content**

Total polyphenols were quantified according to the method described bySingletonet al.(1999)using Folin-Ciocalteu Reagent (FCR). In a microplate, 25 µL of extract and 125 µL of 0.2 N FCR were added to each well. After a 5-minute incubation, 100 µL of sodium carbonate (750 g/mL) was added. Following a 2-hour incubation, absorbance was measured at 760 nm. The concentration of total phenolics was calculated using the following formula :

$$X = \frac{C * D}{Ci} * 1000$$

where:

X = total phenolic content, expressed as mg gallic acid equivalents (GAE)/g dry weight (DW);
C = sample concentration read from the standard curve;
D = dilution factor of the sample used for analysis;
C_i = initial concentration of the sample solution to be analyzed (mg/mL).

- **Total flavonoidscontent:-**

Flavonoids were determined using the Dowd colorimetric method adapted byArvouet-Grand et al. (1994). In each well, 75 µL of 2% AlCl3 in 80% ethanol was added to 75 µL of extract. The mixture was incubated for 10 minutes in the dark at room temperature. Absorbance was then measured at 415 nm using a spectrophotometer against a blank consisting of 75 µL of extract and 75 µL of 80% ethanol

$$X = \frac{C * D}{Ci} * 1000$$

where:

X = total flavonoid content, expressed as mg quercetin equivalents (QE)/g dry weight (DW);
C = sample concentration read from the standard curve;
D = dilution factor of the sample used for analysis;
C_i = initial concentration of the sample solution to be analyzed (mg/mL).

Antioxidant activity assays:-

Antioxidant activity was determined using DPPH and FRAP methods.

- **DPPH radical scavenging activity:-**

This method is based on the decrease in absorbance at 517 nm when the stable free radical 2,2-diphenyl-1-picrylhydrazyl (DPPH) reacts with an antioxidant compound. Radical scavenging activity was evaluated according to the method of Velázquez et al. (2003). In each well of a microplate, 100 µL of sample solution (50 mg/mL) was mixed with 200 µL of DPPH solution. After a 15-minute incubation, absorbance was read at 517 nm against an ascorbic acid standard curve (0 to 10 mg/mL).

- **Ferric reducing antioxidant power (FRAP):-**

The FRAP method is based on the reduction of ferric ion (Fe^{3+}) to ferrous ion (Fe^{2+}). In a test tube containing 0.5 mL of sample solution (25 mg/mL for seeds and 5 mg/mL for leaves), the following were successively added: 1.25 mL of phosphate buffer (0.2 M, pH 6.6), 1.25 mL of 1% potassium hexacyanoferrate, and 125 µL of distilled water. The mixture was heated at 50 °C in a water bath for 30 minutes. Then, 1.25 mL of 10% trichloroacetic acid was added, and the mixture was centrifuged at 2000 rpm for 10 minutes. Three aliquots of 125 µL of the supernatant were transferred into a microplate, followed by 125 µL of distilled water and 25 µL of 0.1% FeCl3 in each well. A blank without sample was prepared under the same conditions. Absorbance was measured at 700 nm against an ascorbic acid standard curve (200 mg/L in distilled water).

$$X = \frac{c * D}{M * Ci} * 100$$

where:
X = concentration of reducing compounds, expressed as µmol AAE/g fresh leaves;
c = sample concentration read from the curve;
D = dilution factor of the crude extract solution;
C_i = concentration of the crude extract solution;
M = molar mass of ascorbic acid (176.1 g/mol).

Data analysis:-

Data were entered, cleaned, and coded using Excel 2021. Experimental results were expressed as mean ± standard deviation (SD). A one-way analysis of variance (ANOVA) was performed to compare the different lines for the studied parameters. When ANOVA indicated a significant difference, means were separated using the Student–Newman–Keuls post hoc test for multiple comparisons among lines. Differences were considered statistically significant at $p \leq 0.05$.

To examine relationships among the different biochemical parameters, correlation analysis was performed. Principal component analysis (PCA) was conductedusing the FactoMineR package (Lê et al., 2008)in R software version 4.4.1 to explore the structure of variability among variables and to visualize relationships between genotypes and biochemical traits. Finally, hierarchical cluster analysis (HCA) was carried out using Ward's method based on Euclidean distances to group lines with similar biochemical profiles.

Results:-

Biochemical composition of seeds:-

Significant differences ($p < 0.05$) were observed among mung bean lines for biochemical composition of seeds (Table 2).

Table 2.Metabolic profile and antioxidant potential of seeds in ten Vigna radiata genotypes

	FRAP	**Flavonoids**	**DPPH**	**Polyphenols**
Line code	**Mean±SD**	**Mean±SD**	**Mean±SD**	**Mean±SD**
B-T	0.14±0.05a	1.54±0.15a	0.24±0.04b	1.04±0.25abc
M16	0.07±0.07a	0.99±0.09cd	0.14±0d	0.54±0.02d
M34	0.16±0.06a	1.19±0.16bc	0.32±0.01a	1.14±0.38ab
M8	0.15±0.15a	0.96±0.15cd	0.2±0.02c	1.24±0.24a
VR-114	0.25±0.08a	1.14±0.17bc	0.31±0a	1.15±0.06ab
VR-157	0.16±0.04a	1±0.08cd	0.08±0.03^{e}	0.74±0.01bcd
VR-172	0.13±0.03a	1.39±0.18ab	0.15±0.01d	0.69±0.02cd
VR-207	0.17±0.09a	0.65±0.03e	0.24±0b	0.53±0.1d
VR-75	0.14±0.1a	0.74±0.1de	0.2±0.02c	0.69±0.03cd
VR-77	0.02±0.02a	1.34±0.11ab	0.19±0.01c	0.84±0abcd
P-value	**0.152**	**<0.0001**	**<0.0001**	**0.0001**

The FRAP values did not differ significantly among the lines studied ($p = 0.152$), indicating that the reducing power measured by this assay was broadly comparable across the seed samples analyzed.In contrast, antioxidant activity assessed by the DPPH test, as well as total flavonoid and total polyphenol contents, showed highly significant differences among the tested lines ($p < 0.0001$). These results indicate substantial biochemical variability among genotypes for these traits.Total flavonoid content ranged from 0.65 to 1.54, in VR-207 and B-T, respectively.
For DPPH antioxidant activity, the highest values were recorded in M34 (0.32) and VR-114 (0.31), indicating a strong free-radical scavenging capacity in these genotypes.The lines M8 (1.24), VR-114 (1.15), and M34 (1.14) showed the highest total polyphenol contents. In contrast, M16 (0.53) and VR-207 (0.54) had the lowest polyphenol concentrations.

Biochemical composition of leaves:-

Table 3 presents the biochemical analysis of the mung bean leaf samples. All biochemical parameters measured in leaves were highly significant ($p < 0.0001$).

Table 3.Metabolic profile and antioxidant capacity of leaf tissues in ten Vigna radiata genotypes

	DPPH	**Flavonoid**	**FRAP**	**Polyphenol**
Line code	**Mean±SD**	**Mean±SD**	**Mean±SD**	**Mean±SD**
B-T	3.78±0.05c	3.66±0.68de	15.72±0.49e	30.35±0.85d
M16	2.96±0.04^{e}	1.8±0.1f	16.5±0.26d	43.21±0.59b
M34	3.42±0.05d	10.08±1.21a	14.01±0.22f	26.01±0.17e
M8	1.77±0.07h	3.72±0.27de	7.58±0.25g	37.68±0.67c
VR-114	2.52±0.05g	4.04±2.03cde	21.07±0.18b	38.37±0.56c
VR-157	2.78±0.02f	5.44±0.13bcd	6.47±0.12h	18.85±0.55f
VR-172	3.94±0.05b	6.32±0.7b	20±0.13c	45.55±0.6a
VR-207	4.05±0a	5.68±0.38bc	14.24±0.38f	37.7±1.33c
VR-75	3.41±0.02d	2.9±0.36ef	22.25±0.28a	17.92±1.12f
VR-77	4.03±0.05a	1.68±0.15f	13.81±0.09f	25.68±1.21^{e}
P-value	**<0.0001**	**<0.0001**	**<0.0001**	**<0.0001**

DPPH antioxidant activity differed markedly among genotypes. VR-207 (4.05), VR-77 (4.03), and VR-172 (3.94) exhibited the highest antioxidant activities, indicating strong radical scavenging capacity. By contrast, M8 (1.77) showed the lowest value, suggesting much weaker antioxidant activity.For flavonoid content, determined by the total flavonoid colorimetric method, M34 stood out clearly with a value of 10.08, far higher than the other genotypes. Relatively high values were also observed in VR-172 (6.32) and VR-207 (5.68). In contrast, M16 and VR-77 showed the lowest values, indicating more limited accumulation of these secondary phenolic compounds.FRAP analysis showed that VR-75 (22.25) and VR-114 (21.07) had the highest reducing power among all samples studied. At the other extreme, VR-157 (6.47) and M8 (7.58) displayed the lowest values.Finally, total polyphenol analysis using the Folin–Ciocalteu method showed that VR-172 (45.55) and M16 (43.21) had the highest phenolic contents. VR-75 and VR-157 were characterized by the lowest polyphenol levels.

Relationships among biochemical traits:-

The correlation analysis, presented in Table 4, revealed significant positive relationships between total phenolic content and antioxidant activity, particularly in leaves

Table 4.Pearson correlation matrix between biochemical parameters and antioxidant activities in seeds and leaves of 10 Vigna radiata genotypes

	DPPH.L	**DPPH.S**	**FRAP.L**	**FRAP.S**	**LPC**	**SPC**	**LFC**	**SFC**
DPPH.L	-	0.848	**0.040**	0.214	0.669	**0.012**	0.523	0.236
DPPH.S	0.04	-	**0.078**	0.173	0.675	**0.007**	0.063	0.567
FRAP.L	**0.38**	**0.33**	-	0.664	0.256	0.346	0.516	0.684
FRAP.S	-0.23	0.26	0.08	-	0.820	0.069	0.109	0.185
LPC	-0.08	0.08	0.21	0.04	-	0.712	0.823	0.506
SPC	**-0.45**	**0.48**	-0.18	0.34	-0.07	-	0.225	0.076
LFC	0.12	0.34	-0.12	0.3	-0.04	0.23	-	0.814
SFC	0.22	0.11	0.08	-0.25	0.13	0.33	0.04	-

Legend.DPPH.L:leaves DPPH; DPPH.S :seeds DPPH; FRAP.L :leaves FRAP; LPC:leaves total polyphenols content; SPC: seeds total polyphenols content; LFC : leaves flavonoids content; SFC: seeds flavonoids conten.A significant negative correlation was observed between DPPH.L and SPC (r = -0.45; p = 0.012). This indicates that higher leaf antioxidant activity tended to be associated with lower total polyphenols content in seeds.Conversely, a significant positive correlation was found between DPPH.S and SPC (r = 0.48; p = 0.007). This suggests that samples with higher antioxidant activity in seeds also tended to have higher total polyphenols concentration in the same organ.

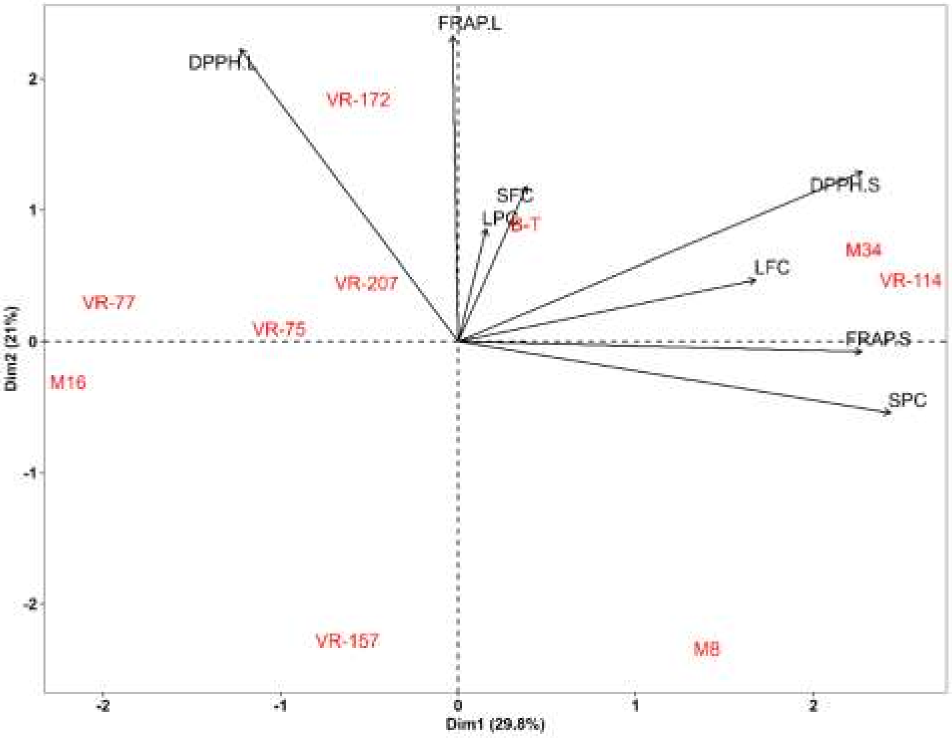

Figure 1. Principal Component Analysis (PCA) illustrating the structure of biochemical variability and the positioning of Vigna radiata genotypes on the factorial plane (Dim1 × Dim2).

The PCA highlighted the structure of the variability in the studied variables across the first two factorial axes. The first axis (Dim1) explained 29.8% of the total variance and clearly separated two groups of variables. On the positive side of this axis were projected DPPH.S, FRAP.S, SPC, and LFC, reflecting a profile characterized by high antioxidant activity associated with high levels of soluble metabolites. In contrast, the negative side of this axis was dominated by DPPH.L, indicating opposition between leaf antioxidant activity and the other variables grouped on the positive side.The second axis (Dim2) explained 21% of the total variance and was strongly associated with FRAP.L and DPPH.L, both projecting in the positive direction of this axis. This axis therefore mainly reflected variation in leaf antioxidant activity, as revealed by the DPPH and FRAP assays.

Inspection of genotype projection on the factorial plane made it possible to distinguish several groups. M34 and VR-114 were located on the positive side of Dim1, indicating their association with high DPPH.S and FRAP.S values, and therefore with a marked antioxidant profile in the corresponding samples. VR-172 projected mainly toward the positive side of Dim2, suggesting association with high leaf antioxidant activity, especially for DPPH.L and FRAP.L.By contrast, VR-157 and M8 occupied a negative position in the factorial space, indicating a weak contribution to the main axes characterizing antioxidant activity. VR-77 and VR-75 also appeared on the opposite side of the pole defined by SPC and FRAP.S, suggesting lower values for these variables.

The Euclidean distance matrix (Table V) was used to assess the overall level of dissimilarity among genotypes based on all measured variables. A low distance indicates strong similarity between two lines, whereas a high distance reflects substantial divergence in their biochemical profiles.

Table 5. Euclidean distance matrix reflecting the overall biochemical dissimilarity among ten Vigna radiata genotypes

	B-T	M16	M34	M8	VR-114	VR-157	VR-172	VR-207	VR-75	VR-77
B-T	0									
M16	3,80	0								
M34	3,14	5,35	0							
M8	3,90	4,00	4,17	0						
VR-114	3,24	4,69	3,59	3,58	0					
VR-157	4,08	3,94	4,45	3,54	5,14	0				
VR-172	2,81	3,01	4,09	4,80	4,12	4,44	0			
VR-207	3,90	3,36	3,92	4,50	4,15	3,95	3,31	0		
VR-75	3,70	3,41	4,45	4,67	4,07	3,78	4,04	3,07	0	
VR-77	2,60	3,07	4,67	4,60	5,20	4,05	3,61	4,25	3,59	0

The distances among genotypes ranged approximately from 2.60 to 5.35, indicating moderate to relatively high inter-genotypic variability.The smallest distance was observed between B-T and VR-77 (2.60), showing that these two lines had very similar biochemical profiles for the variables analyzed. A relatively close relationship was also observed between B-T and VR-172 (2.81), suggesting that these two genotypes shared comparable antioxidant characteristics.

The largest distance was observed between M16 and M34 (5.35), suggesting strongly contrasting biochemical profiles. Large divergences were also observed between VR-114 and VR-77 (5.20) and between VR-114 and VR-157 (5.14). These high values indicate marked differences among these genotypes in terms of antioxidant activity and phenolic composition.The dendrogram obtained from hierarchical clustering of the biochemical parameters of thedifferent tested lines is shown in Figure 2.

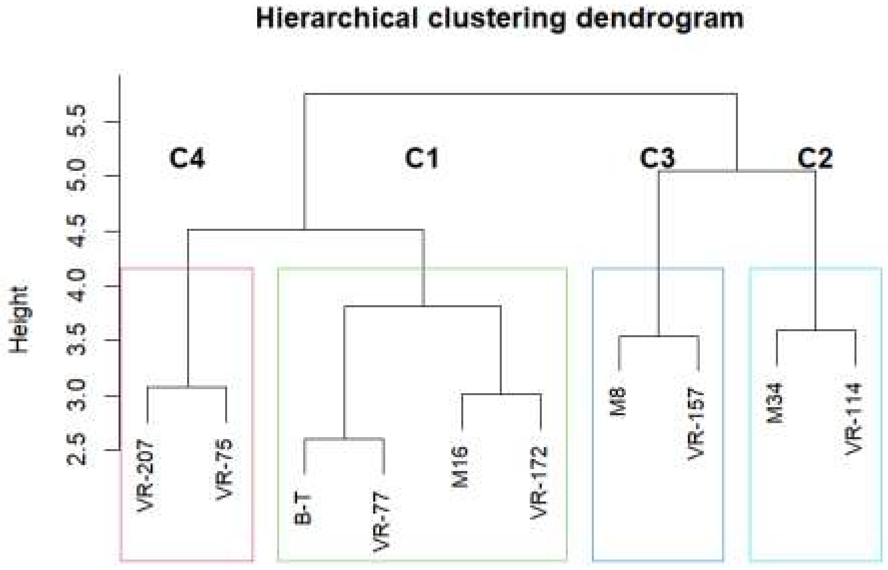

Figure 2. Hierarchical clustering dendrogram grouping the ten Vigna radiata genotypes according to their nutritional and antioxidant profiles

Hierarchical clustering identified four major genotype groups with distinct biochemical profiles:-

The first group (C1) included B-T, VR-77, M16, and VR-172. These genotypes generally showed intermediate to relatively high levels of flavonoids and total polyphenols, although their FRAP-based antioxidant capacity remained fairly heterogeneous. This internal variability suggests that, despite comparable phenolic accumulation, the effectiveness of reducing power differed among genotypes within this group.

The second group (C2) comprised M34 and VR-114. This cluster was particularly cohesive and stood out for its high overall antioxidant activity. The genotypes in this group were strongly associated with DPPH.S and FRAP.S in the PCA (Figure 1). This indicates strong radical scavenging capacity and high reducing power. These lines can therefore be considered the genotypes with the most favorable antioxidant profiles in the study. The third group (C3) consisted of M8 and VR-157. These genotypes were characterized by poor antioxidant performance, especially for leaf FRAP activity. Their clustering confirmed the results of the factor analysis, where these lines also appeared to contribute weakly to the main antioxidant-related axes. The fourth group (C4) included VR-207 and VR-75, which showed a specific and contrasting biochemical profile. VR-207 was mainly distinguished by high leaf DPPH activity, whereas VR-75 was characterized by particularly strong leaf reducing power as measured by FRAP. This cluster therefore reflects differentiated biochemical strategies for the accumulation or expression of antioxidant compounds.

Discussion:-

Biochemical composition of seeds and leaves in mung bean lines:-

The results of this study highlight substantial variability in antioxidant activity and phenolic content among the Vigna radiata's lines evaluated. Some lines showed particularly high antioxidant activity, notably VR-207, VR-77, and VR-172, whereas others, especially M8, displayed much lower performance. This variability confirms the presence of significant biochemical diversity within the genetic material studied. A high level of biochemical diversity was also reported by Desta et al. (2024)in a set of 136 mung bean accessions. According to those authors, this variability was mainly linked to genetic differences affecting the metabolic pathways involved in phenolic biosynthesis. Similarly, a multivariate analysis by Wang et al. (2021)on 24 mung bean genotypes showed that the genotypes could be separated into several groups based on their polyphenol, flavonoid, and antioxidant activity profiles.

In seeds, DPPH antioxidant activity varied significantly among lines, with some genotypes, such as M34 and VR-114, showing clearly higher values. This variation reflects differences in the ability of the extracts to neutralize free radicals. Similar observations have been reported in several studies on mung bean. Tang et al. (2014)showed that the antioxidant activity of mung bean seeds varies greatly depending on genotype and growing conditions, confirming a strong genetic component in the expression of this trait. Likewise, flavonoid contents showed marked variation among the tested lines. This differential flavonoid accumulation may partly explain the observed differences in antioxidant activity. Comparable results were reported byDesta et al. (2024), who showed that mung bean seeds contain major flavonoids such as vitexin and isovitexin, which contribute significantly to extract antioxidant activity. According toZhou et al. (2023) , these flavonoid compounds can neutralize reactive oxygen species through their hydroxyl groups, reinforcing their protective role against oxidative stress.

Total polyphenol concentrations also differed significantly among the studied lines. This richness in polyphenols may contribute to strengthening the overall antioxidant activity of the extracts. Indeed, authors such asNarale et al. (2024),Elwahsh et al. (2025)identified compounds such as gallic acid, chlorogenic acid, ferulic acid, and ellagic acid in mung bean seeds. These molecules have chemical structures rich in hydroxyl groups, which confer strong radical-scavenging capacity and the ability to inhibit oxidation reactions.

Relationships among the biochemical parameters studied:-

The correlation analyses indicate that the relationship between polyphenol content and antioxidant activity is not consistently strong or significant for all the variables studied. This suggests that overall antioxidant activity does not depend solely on the total concentration of phenolic compounds. Other bioactive compounds may also contribute to modulating the antioxidant activity of the extracts. Comparable results were reported by(Zhang et al., 2024),), who showed that the correlation between total polyphenols and antioxidant activity can vary depending on the analytical methods used and the nature of the compounds present in the extract. This hypothesis is supported byWu et al. (2026), who showed that polysaccharides present in the seed coat of mung bean can act synergistically with polyphenols to enhance the overall antioxidant capacity of plant extracts.

Our results showed important differences between seeds and leaves for several biochemical parameters. This observation is consistent with plant physiology. Leaves are the main site of synthesis of secondary metabolites involved in defense mechanisms against environmental stress (Narale et al., 2024). These findings are also consistent with those reported by Wang et al. (2021)andPuyanda et al. (2022), who showed that vegetative tissues, especially leaves and young shoots, often contain higher concentrations of phenolic compounds than seeds.

The PCA performed in this study shows that the first two axes explain a substantial proportion of the total variance. Variables associated with phenolic compounds and antioxidant activity contributed strongly to the structure of these axes. A similar pattern was previously observed by Wang et al. (2021)in an analysis of 24 genotypes, where the first two PCA axes explained more than 66% of the total variability, allowing clear separation of genotypes according to their metabolic profiles.

Overall, the results suggest that some lines have high levels of phenolic compounds and strong antioxidant activity, others show intermediate concentrations, and some present relatively low values across the studied parameters.
The variability observed in this study represents a valuable genetic resource for mung bean improvement programs. Lines with high levels of bioactive compounds could be used as parents in breeding programs aimed at improving the nutritional quality of cultivated varieties.

Conclusion:-

This study demonstrated significant genotypic variability in the biochemical composition and antioxidant potential of seeds and leaves of mung bean cultivated in Burkina Faso. Leaves were particularly rich in phenolic compounds and showed strong antioxidant activity. Certain lines, such as M34 and VR-114, combined favourable biochemical traits in both seeds and leaves, making them promising candidates for inclusion in breeding programs in Burkina Faso because of their balanced polyphenol and antioxidant profiles. Future work should evaluate the stability of these traits under water stress.

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