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**Original Research Article**

# Principal Component Analysis and Genetic Divergence Studies for Yield and Yield-Related Trait of Groundnut (*Arachis hypogaea* L.) Genotypes at Pawe North Western Ethiopia

Desalegn Nigatu Habite[1*]

[1]Ethiopian Institute of Agricultural Research (EIAR), Pawe Agricultural Research Center (PARC)

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**Abstract:** A study was conducted on sixty-four (64) groundnut genotypes at Pawe northwestern part of Ethiopia. And the analysis of variance revealed the existence of significant variation among the tested groundnut genotypes. Cluster analysis showed the existence of five (5) divergent groups and the maximum inter-cluster distance was observed between cluster (II) and cluster (V) D2=1419.77 and the shortest inter-cluster squared distance was found between cluster (I) and Cluster (III) $D^2$=247.23. The first four principal components for (PCs) accounted for 70.03% of the total variation. Overall, the results of the current study depicted the presence of sufficient genetic diversity existed among tested groundnut genotypes for further use in breeding programs. However, a one-season experiment will not realize variability because quantitative traits are polygenic and highly influenced by the environment. So, further experiments must be conducted over location and seasons.

**Keywords:** Variability, genetic divergence, cluster.



## INTRODUCTION

Groundnut (*Arachis hypogaea* L..) is a self-pollinated, annual, herbaceous, allotetraploid legume having genome AABB and somatic chromosome number (2n = 4x = 40), which belongs to the family Leguminoceae and sub-family Papilionaceae (Stalker and Wilson, 2015).One of the main legume crops grown worldwide, it is primarily grown in tropical, subtropical, and warm temperate climates. It was first domesticated in the Eastern Foothills of the Andes, Southern Bolivia, and Northern Argentina (Hampannavar and Khan, 2019). Groundnut oil is the most important product made from the crop, used for both domestic and commercial purposes, with many advantages including having easily digestible proteins, high-quality oils, and important elements such as iron and zinc that are important, especially in children. Groundnut is typically produced for food, cash earnings, and animal feed. Its halves and leaves serve as a rich source of cattle feed (Francisco and Resurreccion, 2008;Pasupuleti *et al.,* 2013; Jibrin *et al.,* 2016). It also fixes atmospheric nitrogen also boosts soil fertility and productivity (Hamidou *et al.,* 2018).According to the CSA (2021), Ethiopia's groundnut production for the 2021 growing season will span 113,514 ha, with a productivity of 1.8 t/ha and a total production of 2050.6 tons. Oromia (57,721 ha) and Benshangul-Gumuz (28,898 ha), regional states, are the main groundnut-producing regions in Ethiopia, with average national productivity of 1.8 t/ha (CSA, 2021) respectively. Groundnuts were grown on 24,355 ha of land in the Metekel zone, producing 1.9 t/ha on average (CSA, 2021).The average national productivity was typically lower than the global yield due to various production constraints, including a lack of improved varieties, a limited genetic potential of released varieties, poor soil fertility, pre-harvest diseases, the use of low-yielding varieties, and the limited availability of improved varieties (Abady *et al.,* 2019b).The need for oil crop output, on the other hand, is rising as a result of rising urbanization, agro-processing companies, and population increase(Hagos and Bekele, 2018). The research area's farmers have a strong need for cultivars with desired characteristics, such as high yield, greater adaptability, and resistance to biotic and abiotic stress. So, to improve the yield of groundnut, plant breeders should have a better understanding of the genetic variability of yield and its components and development of high-yielding cultivars as breeding programs depend on the amount of variability available in the population (Vinithashri *et al.,* 2019).This suggested that testing and identification of widely and specifically adapted genotypes in the study area is important to fill the research gap.

***Corresponding Author:** Desalegn Nigatu Habite
Ethiopian Institute of Agricultural Research (EIAR), Pawe Agricultural Research Center (PARC)

## OBJECTIVE

- To determine relationships among genotypes based on genetic divergence.

## MATERIALS AND METHODS

### Description of Experimental Sites

The experiment was conducted at Pawe Agricultural Research Center (PARC) on station during the main cropping season of 2021. PARC is geographically located between 110 15′ North latitude and 360 30′ East longitudes with altitude of 1150 m.a.s.l in Benshangul-Gumuz Regional state, Metekel Zone, Ethiopia. It is located 570 km away from Addis Ababa, the capital city of Ethiopia (Figure 1). The site receives 1586mm rainfall annually. The mean annual maximum and minimum temperatures are 32.6℃ and 16.5℃, respectively. The soils types of Pawe district are characterized as dark 60%, red 31%, and blended 9%. Whereas the soil type of Pawe Agricultural Research Center (PARC) is characterized as nitisol or loam soil (PARC, 2017).

### Genetic Divergence Analysis

Genetic dissimilarity matrix estimation and agglomerative hierarchical clustering (AHC) analyses among genotypes were performed using XLSTAT 2014 statistical package (XLSTAT, 2014). Ward's minimum variance agglomeration method was used to estimate the Euclidean distance and clustering operations produced a binary clustering tree (dendrogram), whose root was the cluster that contained all the treatments assigned to particular genotypes (Ward, 1963).The $D^2$ values obtained for pairs of clusters were considered as the calculated values of Chi-square (x2). $D^2$ values tested for significance at (5%) probability levels against the tabular Value of $x^2$ for the 'P' degree of freedom, where P is the number of parameters considered.

### Clustering of Genotypes

Based on the squared distances ($D^2$) values, the clustering of genotypes were done using Tocher's method as described by (Singh and Chaudhary, 1979).

### Estimation of Intra- and Inter-Cluster Squared Distances

Average intra and inter-cluster $D^2$ values was estimated using the formula where $\sum Di^2$ is the sum of the distance between all possible combinations (n) of the genotypes included in a cluster. The significance of the squared distances for each cluster was tested against the tabulated $\chi^2$ values at the pedigree of freedom at 5% probability level.

Where, p = number of characters used for clustering genotypes.

### Principal Component Analysis

Principal component analysis (PCA) is probably the most popular multivariate statistical technique and it is used by almost all scientific disciplines and PC has inherently more information than would any single variable alone (Iezzoni and Pritts, 1991). Principal component analysis (PCA) was used to find out the characters, which accounted more for the total variation. The principal component analysis was done to identify the characters contributing more to the total variation XLSTAT software (XLSTAT, 2014). Principal components with eigen values greater than one are only considered in the analysis (Chahal and Gosal, 2002).

### Genetic Divergence Analysis

Genetic divergence analysis based on fourteen characters of sixty-four (64) groundnut genotypes resulted in the formation of five distinct clusters comprised of eight to sixteen genotypes Table 1 and Figure 2. Cluster (I) and (III) was accounted largest amount of genotypes which constituted about thirty-two (32) genotypes each cluster with 16 genotypes with Cluster (I) (25%) and (III) (25%) respectively followed by cluster (II) with fifteen (23.44) and (IV) have nine (9) genotypes (14.06%), cluster and (V) with eight genotypes (12.5%).

**Table 1: The distribution of 64 groundnut genotypes into five distinct clusters based on $D^2$ analysis**

| No. of cluster | No. of genotypes | Name of genotypes |
|---|---|---|
| 1 | 16 | ICGV-13850,ICGV-91317,ICGV-96826,ICGV-91278,ICGV-91284,ICGV-08056,ICGV-97094,ICGV-86024,ICGV-91279,ICGV-03179,RDRGVT ICGV SM 3530,RDRGVT ICGV SM 05723,RDRGVT ICGV SM 06519,RDRGVT ICGV SM 8528, RDRGVT ICGV SM 8538,ICGV 103249. |
| 2 | 15 | ICGV-97188, ICGV-91315, ICGV-93305, ICGV-00350, RDRGVT ICGV 14788, RDRGVT ICGV SM 01514, RDRGVT ICGV SM 03519, RDRGVT ICGV SM 3520, RDRGVT ICGV SM 8533, RDRGVT ICGV 8540, RDRGVT ICGV SM 8547, ICGV 95463,ICGV-87108, ICGV-86644, ICGV -98. |
| 3 | 16 | ICGV-55437, SARTU, ICGV 06420, ICGV 05155, ICGV 07220, ICGV 0266, ICGV 13254, ICGV 13277, ICGV 13278, ICGV -95469, Manipeter, Big seed, ICGV 89328, ICGV-86928, ICGV-98404, ICGV-94100. |
| 4 | 9 | ICGV-03196, ICGV-03181, cn-34c nossittga, ICGV-89104, ICGV-96909, ICGV-14858, RDRGVT (BAKA), RDRGVT ICGV 00331, RDRGVT ICGV SM 8556. |
| 5 | 8 | ICGV-14840, ICGV-94434, ICGV 95469, ICGV 10315, ICGV 10355, ICGV 10358, ICGV 10365, ICGV 13265. |

**Cluster Distance of Groundnut Genotypes**

The intra and inter Euclidean cluster distances of genotypes presented in Table 2. The highest inter cluster distance were observed between cluster (II) and cluster (V) D2=1419.77, followed by cluster (IV) and cluster (V) D2=1131.22. The shortest inter cluster squared distance was found between cluster (I) and Cluster (III) D2=247.23. The largest intra cluster distance was obtained with in cluster (III) D2=409.30. The shortest intra cluster distance was obtained with in cluster (II) D2=374.60, followed by cluster (V) D2=382.54. The existence of highest inter cluster distance would indicates that there is wider diversity in the tested genotypes which creates an opportunity for groundnut improvement programs. Crossing between the shortest inter-cluster distance cluster (I) and cluster (III) results in poor genetic recombinant and is not advisable (Allard, 1960).

**Table 2: Intra (bold diagonal) and inter Euclidean distance among 64 groundnut genotypes tested at Pawe on station in 2021**

| | cluster I | II | III | IV | V |
|---|---|---|---|---|---|
| I | **407.81** | 658.53 | 247.23 | 586.93 | 769.54 |
| II | | **374.60** | 502.55 | 794.25 | 1419.77 |
| III | | | **409.30** | 434.60 | 983.79 |
| IV | | | | **288.50** | 1131.22 |
| V | | | | | **382.54** |

Chi square value ($x^2$) = at 95% level of probability (0.05) =22.36, at 99% level of probability (0.01) = 27.69.

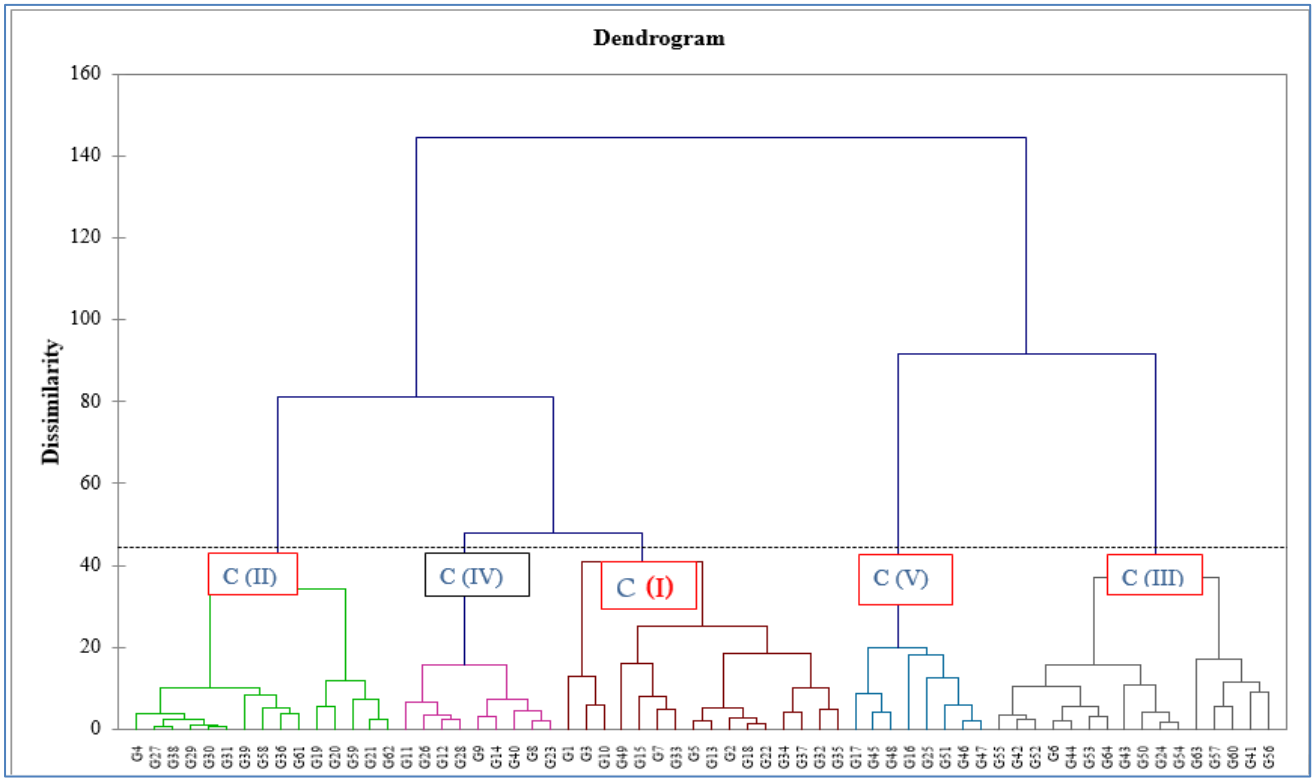


**Figure 1: Dendrogram of 64 genotypes of groundnut based on evaluation of 14 traits**

**Cluster Mean Analysis**

The cluster means for fourteen groundnut traits are presented in Table 3. Genotypes in cluster (I) were characterized by the highest mean value of protein content and characterized by lowest mean value of days to flowering and days to maturity. Genotypes in cluster (II) were characterized by their highest mean values of plant height while number of seed per pod, number of pod per pod and number of branch per plant, hundred seed weight, kernel yield and protein content characterize cluster two by their lowest mean value. Genotypes in cluster (III) were characterized by the highest mean of days to flowering, days to maturity and oil content. With lowest mean value of shelling percentage and plant height. Genotypes in cluster (IV) were characterized by the highest mean value of biomass yield, shelling percentage and oil content. Cluster (IV) also characterized by the second largest mean value of Protein content, plant height and characterize by lowest mean value of harvest index.

Genotypes in cluster (V) were characterized by the highest mean value of number of branch per plant, number of pod per plant, number of seed per pod, harvest index, hundred seed weight and kernel yield. Therefore genotypes in this cluster could be desirable for human consumption due to their highest kernel yield. On the contrary, by the second lowest mean value of plant height, oil content. Genotypes in (V) will be used as best alternative for the simultaneous improvement of kernel yield. The genotypes grouped together indicate the similarity among individuals in the same group so, crossing between the genotype of the same group may not bring good sergeants. Whereas, genotypes maintained under different groups had specific traits and it may give desirable genetic recombinants in developing high yielding varieties if they are used in hybridization program. The present study revealed that sufficient variability existed in groundnut genotypes tested under the environment and these give opportunities for genetic advancement through direct selection for future genetic improvement and hybridization program.

**Table 3: Cluster means analysis of fourteen traits of 64 groundnut genotypes tested at Pawe on station in 2021.**

| Class | DF | DM | PHT | NBPP | NPP | NSPP | BMY | PY | HI | HSW | Sh% | KY | oil | PC |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 44.97 | 92.66 | 38.33 | 4.63 | 13.86 | 23.96 | 1360.60 | 1483.76 | 42.67 | 35.48 | 75.28 | 1165.24 | 43.24 | 22.40 |
| II | 46.17 | 99.70 | 42.45 | 4.27 | 9.85 | 17.50 | 1168.58 | 1005.07 | 37.18 | 31.70 | 72.14 | 756.01 | 45.67 | 20.76 |
| III | 47.72 | 105.00 | 32.77 | 6.85 | 11.13 | 19.53 | 1453.87 | 1354.14 | 38.22 | 42.89 | 68.77 | 977.45 | 47.38 | 21.43 |
| IV | 46.39 | 99.33 | 38.10 | 4.44 | 11.47 | 18.91 | 1878.87 | 1266.42 | 30.88 | 38.23 | 75.52 | 996.64 | 46.04 | 22.34 |
| V | 47.63 | 103.81 | 32.76 | 7.24 | 16.29 | 27.96 | 1435.80 | 2105.55 | 49.55 | 44.66 | 73.37 | 1611.99 | 43.42 | 21.53 |

DF=days to 50% flowering, DM = days to 95% maturity, PHT=plant height, NBPP= number of branches per plant, NPP = number of pods per plant, NSPP = number of seeds per pod, BMY = Biomass yield, PY= Pod yield, HI = harvest index, HSW =hundred seed weight, SP= shelling percentage, KY= kernel yield, pc=protein content%, oil content %.

**Principal Component Analysis**

Principal component analysis (PCA) is one of the multivariate statistical techniques which is a powerful tool for investigating and summarizing underlying trends in complex data structures (Legendre and Legendre, 1998). The results of principal component analysis for fourteen traits of 64 groundnut genotypes are presented in Table 4. The variation among 64 genotypes was assessed through principal component analysis based on the morphological traits. Principal components (PCs) with eigen values greater than unity, and component lodgings greater than ± 0.3 were considered to be meaningful and valuable (Hair *et al.,* 1998). The first four principal components for (PCs) accounted 70.03% of the total variation. The first principal component has an eigen value of 4.37 and explained (31.24% of the total variation. The variation in principal component (1) was mainly due to the positive loading effect of kernel yield (0.45), pod yield (0.44), number of pod per plant (0.38), number of seed per pod (0.38) and harvest index (0.34) generally traits which have ± 0.3 are important contributors for the total variation. Similar results, were reported by (Anthony, 2014; Patil *et al.,* 2020).

The second principal component has an eigen value of 2.61 and accounted for18.61% of the variation and the major contributing traits were days to maturity (0.45), number of branches per plant (0.44), hundred seed weight (0.33), days to flowering (0.26) oil content (0.26) with high positive loading effect similarly findings were reported by (Mubai, 2019). Whereas, shelling percentage (-0.38), plant height (-0.34), protein content (-0.23), had negative loading effect in PCA two. The third principal component, has an eigen value of 1.53 and accounted10.95% of the variation, and traits with high positive loading effects were observed for biomass yield (0.75), shelling percentage (0.19), protein content (0.18) while harvest index (-0.53) and plant height (-0.27) has negative loading effect. In the fourth principal component, has an eigen value of 1.29 and accounted (9.24%) of the variation, traits with high and positive loading effect were harvest index (0.47), oil content (0.31), kernel yield (0.23), shelling percentage (0.21), pod yield (0.20) whereas negative high loading effect were observed for days to flowering (-0.49), number of pod per plant (-0.34), number of seed per pod (-0.33), number of branch per plant (-0.22) similar, results were reported by (Anthony, 2014; Valombola, 2020).

**Table 4: Factor loadings, variance explained and Eigen values of fourteen traits and sixty four (64) groundnut genotypes evaluated at Pawe on station in 2021**

| Trait | PC1 | PC2 | PC3 | PC4 |
|---|---|---|---|---|
| DF | 0.11 | 0.26 | -0.02 | -0.49 |
| DM | 0.03 | 0.45 | -0.07 | -0.04 |
| PHT | -0.20 | -0.34 | -0.27 | -0.03 |
| NBPP | 0.18 | 0.44 | 0.02 | -0.22 |
| NPP | 0.38 | -0.15 | 0.03 | -0.34 |
| NSPP | 0.38 | -0.13 | 0.00 | -0.33 |
| BMY | 0.03 | 0.08 | 0.75 | 0.06 |
| PY | 0.44 | 0.03 | 0.01 | 0.20 |
| HI | 0.34 | -0.06 | -0.53 | 0.14 |
| HSW | 0.21 | 0.33 | -0.03 | 0.47 |
| sh% | 0.15 | -0.38 | 0.19 | 0.21 |
| KY | 0.45 | -0.04 | 0.05 | 0.23 |
| Oil% | -0.13 | 0.26 | -0.10 | 0.31 |
| Protein% | 0.16 | -0.23 | 0.18 | 0.06 |
| Eigen value | 4.37 | 2.61 | 1.53 | 1.29 |
| Variability (%) | 31.24 | 18.61 | 10.95 | 9.24 |
| Cumulative % | 31.24 | 49.85 | 60.80 | 70.03 |

DF=days to 50% flowering, DM = days to 95% maturity, PHT=plant height, NBPP= number of branches per plant, NPP = number of pods per plant,

NSPP = number of seeds per pod, BMY = Biomass yield, PY= Pod yield, HI = harvest index, HSW =hundred seed weight, SP= shelling percentage, KY= kernel yield, pc=protein content%, oil content %.

## CONCLUSION AND RECOMMENDATIONS

The studied genotypes were clustered in to five groups and the largest distance was recorded between cluster II and V. Since, the larger the distance the higher the heterogeneity and the best parent for recombination crossing of II with cluster V could result best recombinant. The first four principal components with eigen values greater than one was significant and accounted 70.30 % of the total variation. Kernel yield was the highest contributor for the variation in the 1st component while, days to maturity, biomass yield, hundred seed weight were in the 2nd 3rd and 4th components, respectively. So, genotypes which are highly contributors are conserved for genetic resource conservation and important for future groundnut breeding program. Generally this study was performed on single location for only one season since phenotypic expression is affected by environmental conditions, the data generated in this study may not be similar over location. Therefore materials on this study will be checked in different environment for more seasons to get more promising Genotypes. However, molecular genetic variability would provide more appropriate and satisfactory result therefore, there is a need to perform molecular characterization on those genotypes in order to identify the genetic variability and heritability of yield and yield related traits at molecular level.

## REFERENCES


- Allard, R. (1960). Principles of plant breeding. John Willey and Sons. *Inc. New York* 485.
- Anthony, A. (2014).Analysis of genetic diversity of some groundnut (ArachishypogaeaL.) genotypes using principal component analysis. M. Sc. thesis. Faculty of agriculture, Ahmadu Bello University, Zaria, Nigeria.
- Chahal, G., & Gosal, S. (2002). *Principles and procedures of plant breeding: Biotechnological and conventional approaches.* Alpha Science Int'l Ltd.
- Central statistical agency agricultural sample survey 2020/21 (2013 E.c.) volume I report on area and production of major crops
- Francisco, M. L. D., & Resurreccion, A. (2008). Functional components in peanuts. *Critical reviews in food science and nutrition*, *48*(8), 715-746.
- Hamidou, F., Harou, A., Achirou, B., Halilou, O., & Bakasso, Y. (2018). Nitrogen fixation by groundnut and cowpea for productivity improvement in drought conditions in the sahel. *Tropicultura (TSI)*, *36*(1), 63-79.
- Iezzoni, A. F., & Pritts, M. P. (1991). Applications of principal component analysis to horticultural research. *Hort Science*, *26*(4), 334-338.
- Jibrin, M., Habu, S., Echekwu, C., Abdullahi, U., & Usman, I. (2016). Phenotypic and genotypic variance and heritability estimates for oil content and other agronomic traits in groundnut (Arachis hypogaea L.). *Int. J. Sci. Res. Eng. Stud*, *3*, 29-32.
- Mubai, N. H. (2019).Genetic variability, path coefficient and marker-trait association analysis for resistance to rosette disease in groundnut.
- Pasupuleti, J., Nigam, S., Pandey, M. K., Nagesh, P., & Varshney, R. K. (2013). Groundnut improvement: use of genetic and genomic tools. *Frontiers in plant science*, *4*, 23.
- Patil, R., Viswanatha, K., Upadhyaya, H., Lokesha, R., Khan, H., & Gururaj, S. (2020). Genetic diversity, association and principle component analyses for agronomical and quality traits in genomic selection training population of groundnut (Arachis hypogaea L.). *Indian J. Genet. Plant Breed*, *80*, 282-290.
- Singh, R., & Chaudhary, B. (1979).Biometrical methods in quantitative genetic analysis.
- Stalker, T. & Wilson, R. (2015). *Peanuts: genetics, processing, and utilization.* Elsevier.
- Valombola, J. S. (2020).Assessment of farmer preferences, constraints and angro-morphological variation among Bambara groundnut (Vigna subterranea (L.) Verdc.) accessions as a basis for seed yield selection index. University of Namibia.
- Vinithashri, G., Manivannan, N., Viswanathan, P., & Selvakumar, T. (2019). Genetic variability, heritability and genetic advance of yield and related traits in F3 generation of groundnut (Arachis hypogaea L.). *Electronic Journal of Plant Breeding*, *10*(3), 1292-1297.
- Hagos, A., & Bekele, A. (2018). Cost and returns of soybean production in Assosa Zone of Benishangul Gumuz Region of Ethiopia. *Journal of Development and Agricultural Economics*, *10*(11), 377-383.


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