Journal of Plant Breeding and Crop Science

Volume 9 Number 4 April 2017
ISSN 2006-9758

Academic Journals

ABOUT JPBCS

The **Journal of Plant Breeding and Crop Science (JPBCS)** is published monthly (one volume per year) by Academic Journals.

The Journal of Plant Breeding and Crop Science (JPBCS) (ISSN: 2006-9758) is an open access journal that provides rapid publication (monthly) of articles in all areas of the subject such as Sustainable use of plant protection products, Agronomic and molecular evaluation of recombinant inbred lines (RILs) of lentil, Pollen behaviour and fertilization impairment in plants, Development of a fast and reliable ozone screening method in rice etc.

The Journal welcomes the submission of manuscripts that meet the general criteria of significance and scientific excellence. Papers will be published shortly after acceptance. All articles published in JPBCS are peer-reviewed.

Contact Us

Editorial Office: jpbcs@academicjournals.org

Help Desk: helpdesk@academicjournals.org

Website: http://www.academicjournals.org/journal/JPBCS

Submit manuscript online http://ms.academicjournals.me/

Journal of Plant Breeding and Crop Science

Table of Contents: Volume 9 Number 4 April, 2017

ARTICLE

academicJournals

Vol. 9(4), pp. 37-44, April 2017
DOI: 10.5897/JPBCS2016.0613
Article Number: CDD8AFE63644
ISSN 2006-9758

http://www.academicjournals.org/JPBCS

Journal of Plant Breeding and Crop Science

Full Length Research Paper

Inheritance of resistance to brown spot disease in upland rice in Uganda

Marco Martin Mwendo[1,2]*, Mildred Ochwo-Ssemakula[2], Saul Eric Mwale[3], Jimmy Lamo[4], Paul Gibson[2] and Richard Edema[2]

[1]Agricultural Seed Agency, Ministry of Agriculture, Livestock and Fisheries, P.O. Box 1294, Arusha, Tanzania.
[2]Department of Agricultural Production, Makerere University, P. O. Box 7062, Kampala, Uganda.
[3]Mzuzu University, Biological Sciences Department, Pvt Bag 201, Mzuzu, Malawi.
[4]National Crops Resources Research Institute (NaCRRI), National Agricultural Research Organization, P.O. Box 7084, Kampala, Uganda.

Received 16 September, 2016; Accepted 20 February, 2017

Brown spot disease caused by *Bipolaris oryzae* [Breda de Haan (Shoem.)] is one of the most important diseases affecting rice (*Oryza sativa* L.) worldwide. Host plant resistance is considered an effective, cheap and environment friendly means of managing this disease. Nine rice genotypes with varying resistance levels were crossed in a full diallel mating design including reciprocals and parents. Parents, reciprocals and F_2 progenies were evaluated in an alpha lattice design in the screen house and field trials at the National Crops Resources Research Institute in Uganda in 2013-2014. The objectives of the study were to determine the mode of inheritance for resistance to brown spot disease and characterize segregation patterns of specific F_2 progenies. Significant (P ≤0.001) variation for brown spot resistance occurred among the tested genotypes. The general combining ability (GCA) and specific combining ability (SCA) effects of brown spot disease scores were both significantly different (P≤0.001), indicating that both additive and non-additive genetic effects were present. There was, however, a predominance of non-additive genetic effects in the genetic control of brown spot resistance as shown by low estimates of baker's ratio (0.29) and narrow sense coefficient of genetic determination (0.24), implying that progeny performance could not be predicted from parents GCA effects as it was better only in specific crossing combinations. Segregation patterns also indicated that resistance to brown spot was controlled by one or two dominant genes. The reciprocal effects for the crosses were significantly different (P ≤ 0.05), suggesting that cytoplasmic genetic effects modified the expression of resistance. Care should, therefore, be taken when selecting female parents during hybridization. Family-based breeding programs would also be effective for improving resistance to brown spot in rice varieties adapted to Uganda.

Key words: Diallel analysis, gene action, non-additive effects, *Oryza sativa*, segregation patterns

INTRODUCTION

Rice is an important economic and food security crop in Uganda (MAAIF, 2008, 2009). Demand for the crop has

*Corresponding author. E-mail: mknossemakula@caes.mak.ac.ug.

Table 1. Rice parental genotypes used in full diallel crosses for brown spot resistance in Uganda

Entry code	Origin	Resistance designation
NERICA 4	Africa Rice	Highly resistant
NERICA 10	Africa Rice	Resistant
[1]E 20	NaCRRI- Namulonge	Resistant
[2]E 22	NaCRRI- Namulonge	Resistant
K5	Local - Uganda	Moderately resistant
P4R1	NaCRRI- Namulonge	Susceptible
NERICA 1	Africa Rice	Susceptible
TXD 306	Tanzania	Susceptible
PAKISTAN (UP)	Pakistan (Jica)	Susceptible

[1]E20 Pedigree:NM7-20-4- B-P-1-1, crosses (IRAT 325/WAB 365-B-1H1-HB); [2]E22 Pedigree: NM7-22-11- B-P-1-1, crosses (WAB 450-1-BL1-136-HB /WAB 450-B-136-HB).

increased in the past decade due to a rapid growth in population, urbanization and shifts in consumption patterns. This trend has been further stimulated by several economic and political initiatives, within Uganda and the East African region, which have transformed the rice value chain (MAAIF, 2009; Kilimo Trust, 2014). In the year 2002, the area under production was 80,000 hectares, with yield of 120,000 MT milled rice and average yield of 1.5 MT/ha for milled rice (FAOSTAT, 2016). By 2014, the area under production had risen to 95,000 hectares, with yield of 249,470 MT and average yield of 2.5 MT/ha for milled rice (FAOSTAT, 2016). This implies that the area under production increased by up to 15.8%, while yield increased by 51.9%. Currently, production is estimated at 260,000 MT, leaving a gap of 40,000 tonnes (Lamo, 2016). At a sufficiency level of 86.7%, Uganda is thus making great strides in meeting both local and regional demand (Kilimo Trust, 2014; Lamo, 2016). Sadly, however, these gains have been made mainly by increasing the area under production since productivity still falls far below the yield potential for developed nations at 8 t/ha (5 t/ha for upland production). This shortfall has been attributed to a number of factors, including pests and diseases, drought and water shortage and declining soil fertility (Kilimo Trust, 2014).

Brown spot is one of the major diseases limiting rice production in Uganda (Awio et al., 2015). The local varieties grown by farmers in Uganda are susceptible to the disease (Kawube et al., 2005; Odogola, 2006). In 2011, brown spot was ranked as the third most important disease after *Rice yellow mottle virus* (RYMV) disease and leaf blast (Adur et al., 2011). The disease affects both rain-fed and upland rice production, causing losses in both yield and grain quality (Singh and Singh, 2000; Savary et al., 2005). Heavily infected grains are rendered unsuitable for human consumption (Barnwal et al., 2013) and yield reductions as high as 45% occur with severe infection and 12% with moderate infection (IRRI, 1983). Disease management is possible through use of appropriate agronomic practices, pesticides, biological control and resistant varieties (Shabana et al., 2008). Sources of resistance to brown spot are available in Asia and Africa. These sources can be used for the development of resistant varieties for release to farmers (Yaqoob et al., 2011; Nneke, 2012). Differences in varietal susceptibility to brown spot (Datnoff and Lentini, 2003) and diversity within *Bipolaris oryzae* species (Kamal and Mia, 2009), however, pose a challenge to breeding for resistance. In order to overcome this problem, the use of local germplasm and pathogen isolates is required.

While varieties preferred by farmers in Uganda are NERICA 1, K5 and TXD 306 exhibit desirable attributes that include aroma and high yielding ability; these varieties are mostly susceptible to brown spot. This study was therefore done to determine the mode of gene action conditioning the inheritance of resistance to brown spot and characterize the segregation patterns of specific F_2 progenies. Knowledge of the mode of gene action from this study will help in the introgression of genes for disease resistance to local farmer preferred genotypes.

MATERIALS AND METHODS

Study area

The study location was the National Crops Resources Research Institute (NaCRRI) in Central Uganda. The Institute is located at 0° 32" N and 32° 37" E and stands at an elevation of 1150 m above sea level within the Lake Victoria crescent agro-ecological zone. It receives average annual precipitation of 1200 mm, with peaks from April to May and September to October. Two cropping seasons are experienced, namely, season A covering the period from March to July and season B covering August to December. The study reported was conducted during season 2013 A, 2013 B and 2014 A.

Development of breeding population

Nine rice genotypes with varying levels of resistance to brown spot (Table 1) were grown and crossed in a full diallel mating design with

Table 2. F2 rice populations used in studying segregation patterns for brown spot resistance in Uganda.

Crossed parents	Resistance status of parents
TXD 306 × NERICA4	S × R
NER 1 × NERICA4	S × R
E22 × PAKISTAN	R × S
E20 × NERICA1	R × S
NER 4 × TXD 306	R × S
NER 4 × NERICA1	R × S
E20 × PAKISTAN	R × S

S = Susceptible; R = Resistant.

parents and reciprocals in a screen house. The diallel mating design was used because the genotypes under study showed reaction to brown spot disease at varying levels, from highly resistant, resistant, moderately resistant to susceptible scores. Forty (40) F_1 progenies were advanced to F_2 in the screen house. The parents, reciprocals and F_2 populations were evaluated for brown spot resistance in the field.

Experimental design and management

The F_2 plants, including the reciprocals and their parents, were planted in the field at NaCRRI using an alpha-lattice design with two replications at a spacing of 5 × 10 cm (one plant per hill). About 20 to 60 F_2 plants from crosses between resistant and susceptible families were selected to be used in studying segregation patterns (Table 2). The plants were supplied with 25 kg/ha of nitrogen two weeks after transplanting. At two weeks, the plants were also inoculated mechanically with a *Bipolaris oryzae* isolate prepared in the laboratory (Motlagh et al., 2006) using a conidia suspension (1×10^5 conidia ml^{-1}) (Sato et al., 2008). To increase surface absorption, 1% Tween-20 was incorporated into the conidia suspension (Motlagh et al., 2006). Standard cultural practices like watering and hand weeding were carried out regularly.

Data collection

Disease severity was scored on five plants per plot at full panicle stage for every genotype following the standard evaluation system (SES) for rice (IRRI, 2002). The rating scale varies from 1 (highly resistant) to 9 (highly susceptible).

Statistical analysis

The data were analyzed in GENSTAT 14, using model 1, method 1 of Grifffings (1956) to determine the effects of general combining ability (GCA) and specific combining ability (SCA). Parents were considered as fixed since they were chosen considering their levels of resistance to brown spot. The Diallel analysis model 1 and method 1 were adjusted to reduce the error effect due to missing crosses following Bernado (2006). Combining ability analysis was therefore performed on 9 parental genotypes and 40 crosses (28 parental combinations and 12 reciprocals).

The statistical linear model for this analysis was:

$$Yijk = \mu + gi + gj + sij + rij + eijk$$

where μ = overall mean, gi = GCA effect of the i^{th} parent, gj = GCA effect of the j^{th} parent, sij = SCA effect of the ij^{th} genotype, rij = reciprocal effect of the ij^{th} genotype, and eijk = the environmental effect of the ijk^{th} observation.

The ratio of GCA variance to SCA variance was estimated according to Baker (1978) as:

$$X = 2\sigma^2gca / (2\sigma^2gca + \sigma^2sca)$$

where σ^2gca = GCA variance components and σ^2sca = SCA variance components.

The estimates of broad and narrow sense coefficient of genetic determination were calculated on family mean basis using the following formulas as outlined by Dabholkar (1992).

$$BSCGD = (2 \times \sigma2GCA + \sigma2SCA)/ (2 \times \sigma2GCA + \sigma2SCA + \sigma2e/r)$$

$$NSCGD = (2 \times \sigma^2_{GCA})/ (2 \times \sigma^2_{GCA} + \sigma^2_{SCA} + \sigma^2_e/r)$$

where σ^2_{GCA} and σ^2_{SCA} are variance components estimates of GCA and SCA, respectively, σ^2_e is the variance due to experimental error and r is the number of replications.

The combining ability effects of parents (GCA) and crosses (SCA) were tested for deviation from zero by using two tailed t-tests as described by Singh and Chaudhary (2004) and Dabholkar (1992). The GCA effect of each individual parent was divided by the standard error of GCA, while the SCA effect of each cross combination was divided by the standard error of SCA.

Data collected on disease severity were interpreted using frequency distribution of trait measurements (histogram) to study the segregating F_2 populations in order to understand the nature of inheritance and number of genes influencing brown spot resistance (Fehr, 1987). The distinct phenotypic classes and segregation ratios were compared with theoretical ratios using the Chi-square goodness-of-fit test. For analysis, highly resistant, resistant and moderately resistant genotypes were grouped as resistant, and all genotypes with higher scores were grouped as susceptible (Ongom et al., 2012) to best fit the reduced phenotypic classes due to epistasis effects exhibited and enable determination of the departure of observed frequencies from hypothesized frequencies. A chi-square (χ^2) probability was used, where χ^2 was significant at $P < 0.05$, the fitted model was rejected.

RESULTS

Genetic variability, combining abilities and heritability

Results of analysis of variance for resistance to brown

Table 3. Analysis of variance for combining ability for brown spot disease scores in F_2 populations and their parents.

Source	df	MS	F_{calc}	Variance component
Crosses	39	0.94***	4.94	
GCA	8	1.37***	7.21	0.14
SCA	19	1.11***	5.84	0.66
Reciprocal	12	0.39*	2.05	0.10
Error	39	0.19		
Baker's Ratio			0.29	
NS-CGD			0.24	
BS-CGD			0.83	

*, ***Statistically significant at α = 0.05, 0.001 respectively; the calculation for coefficient of genetic determination are based on entry means.

Table 4. General combining ability effects for brown spot resistance for parents.

Parents	Parental mean	GCA effects	SE_{gca}
K5	5.7	0.53***	0.066
PAKISTAN	7.0	0.35***	0.044
TXD306	7.0	0.16^{ns}	0.056
E20	3.0	-0.09^{ns}	0.036
E22	3.0	-0.23**	0.044
NER 1	5.7	0.38 ***	0.033
NER 4	4.3	-0.63***	0.030
NER 10	3.7	-0.42***	0.056
P4R1	7.0	0.31 **	0.056

**, ***Highly significant at α = 0.01, 0.001 respectively; ^{ns}Not significant at α = 0.05.

spot revealed highly significant differences (P ≤ 0.001) among parents and F_2 progenies tested (Table 3). General and specific combining ability mean squares were very significant (P ≤0.001); reciprocal mean squares were also highly significant (P ≤ 0.001). The Baker's ratio was low (0.29) while the estimate of broad sense coefficient of genetic determination was high (0.83). The transmissibility of brown spot resistance from parents to progenies, as shown by the estimate of narrow sense coefficient of genetic determination, was low (0.24).

Estimates of general combining ability effects

Parental lines K5, PAKISTAN, P4R1 and NER 1 had significant positive GCA effects (Table 4). In contrast, the lines E22, NER 4 and NER 10 had significant negative GCA effects (P ≤ 0.01, 0.001, 0.001, respectively). The line E20 had negative non-significant GCA effects, while TXD 306 had non-significant positive GCA effects.

Estimates of specific combining ability effects

The crosses K5 × NER 1, TXD 306 × NER 4, NER 4 × P4R1, PAKISTAN × E20, E 22 × E 20 and NER 1 × NER 10 had significant negative SCA effects (P ≤ 0.05, 0.01, 0.01, 0.001 respectively) (Table 5). The crosses TXD 306 × NER 1, E20 ×x K5, NER 10 × E20, NER 1 × P4R1 and E22 × NER 4 displayed significant positive SCA effects.

Reciprocal effects

Significant (P<0.05) negative reciprocal effects were realized with the NER 10 × E22 cross (Table 6). The cross NER 4 × E20 and NER 4 × NER 1 showed significant positive reciprocal effects at P<0.05.

Segregation pattern of brown spot reaction in F_2 progeny of selected crosses

F_2 progenies from the crosses showed distinct phenotypic classes for brown spot scores (Table 7). Analysis of segregation ratios revealed that crosses TXD 306 × NER4, NER 1 × NER 4, NER 4 × NER 1 and E22 × PAK conformed to the 3:1 ratio. Crosses E20 × NER 1 and NER 4 × 306 conformed to the 9:7 ratio, while cross E20

Table 5. Specific combining ability effects for brown spot resistance in F_2 rice population.

Parents	K5	PAK	TXD306	E20	E22	NER 1	NER 4	NER10	P4R1
					Female				
K5			-0.19^{ns}						
PAK					- 0.12^{ns}				0.00^{ns}
TXD306				- 0.23 ^{ns}			-1.03**		
E20	0.73*	-1.76***				0.38^{ns}	0.22 ^{ns}		
E22	-0.13^{ns}		0.23^{ns}	-1.51***		0.01^{ns}	1.35***		
NER 1	-0.74*	-0.06^{ns}	0.63^{ns}				-0.59^{ns}		
NER 4	0.27^{ns}	2.11***						0.05^{ns}	
NER10	0.06^{ns}			0.68*	0.15^{ns}	-1.13**			
P4R1				0.45^{ns}		1.14**	-1.02**		

*, **, ***Significant at α = 0.05, 0.01, 0.001 respectively; ^{ns}Not significant at α = 0.05; PAK: Pakistan upland; NER: NERICA.

Table 6. Reciprocal effects for brown spot resistance in F_2 populations.

Parents	K5	PAKS	306	E20	E22	NER1	NER 4	NER10	P4R1
K5	-	-	-	-	-	-	-	-	-
PAKS	-	-	-	-	-	-	-	-	-
306	-	-	-	-	-	-	-	-	-
E20	-	-	-	-	-	-	-	-	-
E22	-	0.17^{ns}	-	-	-	-	-	-	-
NER 1	-	- 0.50^{ns}	- 0.33^{ns}	- 0.50^{ns}	-	-	-	-	-
NER 4	-	-	0.50^{ns}	0.67*	-	0.67*	-	-	-
NER10	-	-	-	-	- 0.67*	-	0.17^{ns}	-	-
P4R1	-	- 0.17^{ns}	-	- 0.17^{ns}	-	-	- 0.17^{ns}	-	-

*Significant at α = 0.05; ^{ns}Not significant at α = 0.05; PAKS: Pakistan upland; 306: TXD 306; NER: NERICA.

Table 7. Phenotypic segregation ratios for resistance to brown spot in F_2 population.

F_2 populations			Observed		Expected		Goodness-of-fit	
Cross	No.P	Type	R	S	R	S	χ^2	Prob.
Best fit ratio 3:1								
TXD 306 × NER 4	60	S × R	50	10	45	15	2.222^{ns}	0.136
NER 1 × NER 4	60	S × R	50	10	45	15	2.222^{ns}	0.136
NER 4 × NER 1	30	R × S	27	3	28	2	3.60^{ns}	0.058
E22 × PAK	60	R × S	50	10	45	15	2.222^{ns}	0.136
E20 × NER 1	18	R × S	11	7	14	4	1.852^{ns}	0.174
NER 4 × 306	21	R × S	12	9	16	5	3.571^{ns}	0.058
E20 × PAK	18	R × S	16	3	18	6	3.555^{ns}	0.136
Best fit ratio 9:7								
E20 × NER 1	18	R × S	11	7	10	8	0.172^{ns}	0.678
NER 4 × 306	21	R × S	12	9	12	9	0.006^{ns}	0.934
Best fit ratio 15:1								
E20 × PAK	18	R × S	16	2	17	1	0.725^{ns}	0.394

No. P = No of plants: χ^2 = Chi- square test; R, S resistant and susceptible parents respectively; PAK: Pakistan; NER: NERICA; ns: non-significant at p≤ 0.05 probability level

× PAK conformed to the 15:1 ratio.

DISCUSSION

Genetic variability

Results of analysis of variance for resistance to brown spot revealed significant differences among parents, reciprocals and F_2 progenies. This shows there is adequate genetic diversity among the parents and their respective crosses that could be used in population development. According to Bertan et al. (2007) superior recombinant genotypes are generated when there is significant variability in the parental genotypes.

Heritability and combining ability

The general and specific combining ability mean squares of brown spot disease scores were highly significant (P ≤0.001) indicating that both additive and non-additive genetic effects were important in the genetic control of brown spot resistance. The relative importance of additive over non-additive genetic effects as shown by Baker's ratio was low (0.29), indicating the predominance of non-additive genetic effects over additive genetic effects; hence, a low predictability of progenies performance from parents GCA effects. The progeny performance in this set of crosses was only better in specific crossing combinations and therefore could not be predicted for a wide range of crosses. The estimates of broad sense coefficient of genetic determination, which measures the proportion of phenotypic variance that is due to genetic causes, were high (0.83). This indicates that the environment did not play a key role in the expression of resistance to brown spot. The estimates of narrow sense coefficient of genetic determination, which measures the proportion of phenotypic variance that is due to transmitted genetic effects, were low (0.24) suggesting that the contribution of non-additive variance to the total genetic variance was key in controlling resistance to brown spot in this set of crosses.

Combining ability effects

Dabholkar (1992) and Singh and Chaudhary (2004) reported that parents with significant GCA effects in the desired direction for a character of interest are the best for hybridization. Parents E22, NER 4 and NER 10 had desirable significant negative GCA effects indicating they contributed to brown spot resistance in F_2 progeny. The parent K5, which was moderately resistance, had significant positive GCA effect indicating it contributed towards susceptibility to brown spot disease. The susceptible parent TXD 306 had a positive non-significant GCA effect indicating that it contributed average effects towards susceptibility that were not meaningful. The susceptible parents PAKISTAN and P4R1 had significant positive GCA effect indicating that these parents contributed susceptibility in F_2 progenies as expected. The parent NERICA 1 had non-significant positive GCA effects indicating it contributed average effects towards resistance that were not meaningful. The parent E20 had non-significant negative GCA effects indicating it did not contribute to resistance. Therefore, NER 4, E22, and NERICA 10 were the best combiners for resistance to brown spot. These parents can be used in the breeding programme to introduce resistance genes to locally adapted rice germplasm.

Crosses TXD 306 × NER 4, NER 1 × K5, E20 × PAKISTAN, NER 10 × NER 1, E 22 × E 20 and NER 4 × P4R1 had significant negative SCA effects indicating they contributed to resistance. The crosses between TXD 306 × NER 1, E20 × K5, NER 10 × E20, NER 1 × P4R1, and E22 × NER 4 displayed significantly positive SCA effects indicating they have little value as they will contribute to susceptible progenies. These crosses are undesirable in a hybridization program since they would produce high frequencies of susceptible progeny (Dabholkar, 1992). Significant SCA effects suggest that resistance levels in progeny of certain parental combinations were significantly higher or lower than the predictions based on the parents' GCA effects. Improvement of resistance to brown spot could, thus, be accomplished by selection of crosses having high significant negative SCA effects and advancing progenies to later generations. Also, highly significant reciprocal effects found in the populations generated suggest presence of cytoplasmic or maternal effects. Further studies involving the parents with suspected cytoplasmic or maternal effects is required in order to guide breeding for improved resistance to brown spot. Parents of these crosses can be used for bi-parental mating or reciprocal recurrent selection for developing varieties with resistance to brown spot disease. The differences between reciprocal crosses indicated maternal contribution towards moderating resistance (Crusio, 1987). The study revealed significant reciprocal effects for NER 10 (P ≤0.05) and NER 4, suggesting the presence of cytoplasmic or maternal effects contributing to brown spot resistance. Thus, care should be taken to use the more resistant parent as female when making crosses for resistance to brown spot as it has been observed that the maternal effects plays a role in conditioning resistance.

Segregation patterns of selected F_2 progenies

The F_2 progenies from the crosses showed distinct phenotypic classes for brown spot scores. Analysis of segregation ratios revealed that crosses TXD 306 × NER4, NER 1 × NER 4, NER 4 × NER 1 and E22 × PAK conformed to the 3:1 ratio, suggesting the presence of at least one gene showing dominance (Allard, 1999).

Crosses E20 × NER 1 and NER 4 × 306 agreed with the 9:7 ratio, indicating presence of complementary dominant alleles (duplicate recessive epistasis). The cross E20 × PAK conformed to the 15:1 ratio, highlighting the presence of dominant alleles at either of the two loci that masked the expression of recessive alleles (duplicate dominant epistasis) (Fehr, 1987).

The separation of allelic pairs and their distribution to different cells during meiosis influences phenotypic expression of an individual (Fehr, 1987). In this study, F_2 progenies for selected crosses between resistant and susceptible rice genotypes displayed phenotypically-distinct classes based on brown spot scores, indicating that qualitative inheritance is primarily controlled by one or few genes. This suggests that individual alleles of a major gene can be predicted and readily identified on the basis of the genotype (Fehr, 1987). Goel et al. (2006) reported inheritance of brown spot resistance to involve additive and dominant effects as well as interaction between loci for the inheritance of resistance from crosses involving *Oryza nivara* germplasm. Harap (1979) and Balal et al. (1979) suggested two dominant genes were associated with resistance, while one gene was associated with susceptibility. Nagai and Hara (1930) suggested that resistance to brown spot disease is dominant while Adair (1941) suggested the involvement of several recessive genes.

Conclusions

This study revealed the influence of both additive and non-additive genes effects in the genetic control of brown spot disease resistance. The genes for resistance can, therefore, be transferred from one genotype to another through family-based breeding programs such as pedigree selection, single seed descent and back-crossing. The role of cytoplasmic gene effects in modifying resistance was also elucidated, suggesting careful selection of desirable female parents during hybridization. Segregating patterns for crosses between resistant and susceptible parents showed dominance of resistance, indicating resistance is controlled by one or a few genes.

CONFLICT OF INTEREST

The authors have not declared any conflict of interest.

ACKNOWLEDGEMENTS

This study was funded by the Innovative Agricultural Research Initiative (*i*AGRI) through the Regional Universities Forum for Capacity Building in Agriculture (RUFORUM).

REFERENCES

Adair CR (1941). Inheritance in rice of reaction to *Helminthosporium oryzae* and *Cercospora oryzae*. Technical bulletin. United States: Department of Agriculture. 772:18.

Adur OSE, Otim M, Alibu S, Ekobu M, Lamo J (2011). Farmers' knowledge and management of rice diseases under lowland ecology in Uganda. Paper presented at the Second Biennial Scientific Conference of the National Agricultural Research Organization, November 3-7, 2014, Munyonyo, Uganda. P. 89

Awio T, Bua B, Karungi J (2015). Assessing the Effects of Water Management Regimes and Rice Residue on Growth and Yield of Rice in Uganda. Am. J. Exp. Agric. 7(2):141-149.

Baker RJ (1978). Issues in diallel analysis. Crop Sci. 18:533-536.

Balal MS, Omar RA, El-Khadem MM, Aidy IR (1979). Inheritance of resistance to the brown spot disease of rice, *Cochliobolus miyabeanus*. Agric. Res. Rev. 57:119-33.

Barnwal MK, Kotasthane A, Magculia N, Mukherjee PK, Savary S, Sharma AK, Singh HB, Singh US, Sparks AH, Variar M, Zaidi N (2013). A review on crop losses, epidemiology and disease management of rice brown spot to identify research priorities and knowledge gaps. Eur. J. Plant Pathol. 136:443-457.

Bernado R (2006). Best linear unbiased prediction of maize single cross performance. Crop Sci. 35:50-56.

Bertan I, Fernando IF, Antonio C (2007). Parental Selection Strategies in Plant Breeding Programs. J. Crop Sci. Biotechnol. 10(4):211-222.

Crusio WE (1987). A note on the analysis of reciprocal effects in diallel crosses. J. Genet. 66(3):177-185.

Dabholkar AR (1992). Elements of Biometrical Genetics, 1 st ed. New Delhi: Ashok and Kumat Mittal.

Datnoff EL, Lentini S (2003). Brown Spot in Florida Rice. Technical bulletin. University of Florida, IFAS No. PP 128. Available at: http://ipm.ifas.ufl.edu/pdfs/RH00700.pdf.

FAOSTAT (2016). Food and Agricultural Organization of United Nations Database 2016. Available at: http://www.fao.org/faostat/en/#data/QC. Accessed on Dec 12, 2016.

Fehr WR (1987). Principle of cultivar development. Volume 1. In I. 0-02-94-9920-8(v.1), ed. Theory and technique.Iowa State university. London: Macmillan publishing company. pp. 95-103.

Goel RK, Bala R, Singh K (2006). Genetic characterization of resistance to brown leaf spot caused by Drechslera oryzae in some wild rice (*Oryza sativa*) lines. Ind. J. Agric. Sci. 76:705-707.

Griffings B (1956). Concept of general and specific combining ability in relation to diallel crossing systems. Aust. J. Biol. Sci. 9:463-493.

IRRI (1983). Field problems of tropical rice. International Rice Research Institute. Manila (Philippines). 172.

IRRI (2002). Standard evaluation system for rice. Manila, Philippine: IIRI.

Kamal MM, Mia MAT (2009). Diversity and pathogenicity of the rice brown spot pathogen, Bipolaris oryzae (Breda de Haan) Shoem. Bang. J. Bot. 38(2):119-25.

Kawube G, Kanobe C, Edema R, Tusiime G, Mudingotto PJ, Adipala E (2005). Efficacy of manual seed sorting methods in reduction of transmission of rice. Afr. Crop Sci. Conf. Proc. 7:1363-1367.

Kilimo Trust (2014). Expanding Rice Markets in the East African Community (EAC) Region. Available at: http://cari-project.org/wp-content/uploads/2015/03/RICE-REPORT-EAC-for-web.pdf . Accessed on September 16, 2016.

Lamo J (2016). Public-private partnership scales up use of new climate-resilient rice varieties in Uganda. Available at: http://africarice.blogspot.ug/2016/08/public-private- partnership-scales-up.html. Accessed on September 3, 2016.

MAAIF (2008). Ministry of Agriculture, Animal Industry and Fisheries development Strategy and Investment plan (2009/10 – 2013/14).

MAAIF (2009). Ministry of Agriculture, Animal Industry and Fisheries final draft development strategy and investment plan (2010/11 – 2014/15).

Motlagh SMR, Zamanizadeh HR, Hedjaraude GHA, Okhovvat M (2006). Identification of the causal agent fungi of rice brown spot disease. J. Agric. Sci. Nat. Res. 12:136-145.

Nagai I, Hara S (1930). On the inheritance of variegation disease in a strain of rice-plant. Jap. J. Bot. 5:41.

Nneke NE (2012). Screening lowland rice varieties for resistance to brown spot disease in Enyong creek rice field in Akwa Ibom state of Nigeria. Glob. J. Pure Appl. Sci. 18(1):5-10.

Odogola WR (2006). Final Survey Report on the Status of Rice Production, Processing and Marketing in Uganda. Kampala, Uganda. P 77.

Ongom PO, Nkalubo ST, Gibson PT, Mukankusi CM, Rubaihayo PR (2012). Evaluating Genetic Association between Fusarium and Pythium Root Rots Resistances in the Bean Genotype RWR 719. Afr. Crop Sci. J. 20(1):31-39.

Sato H, Ando I, Hirabayashi H, Takeuchi Y, Arase S, Kihara J (2008). QTL analysis of brown spot resistance in rice (*Oryza sativa* L.). Breed. Sci. 58: 93-96.

Savary S, Castilla N, Elazegui FA, Teng PS (2005). Multiple effects of two drivers of agricultural change, labour. Field Crops Res. 91:263-271.

Shabana YM, Abdel-Fattah GM, Ismail AE (2008). Control of brown spot pathogen of rice (*Bipolaris Oryzae*) Using Some phenolic antioxidants. Braz. J. Microbiol. 39:438-444.

Singh RK, Chaudhary BD (2005). Biometrical Methods in Quantitative Genetic Analysis. 3rd ed. New Delhi: Kalyani Publishers.

Singh VP, Singh RK (2000). Rainfed rice: A source book of best practices and strategies in eastern India. International Rice Research Institute. P 292.

Yaqoob M, Mann RA, Iqbal SM, Anwar M (2011). Reaction of rice genotypes to brown spot disease pathogen *Cochliobolus miyabeanus* under drought conditions. Mycopathology 9(1):9-11.

academicJournals

Vol. 9(4), pp. 45-53, April 2017
DOI: 10.5897/JPBCS2017.0647
Article Number: 0312D1663646
ISSN 2006-9758

http://www.academicjournals.org/JPBCS

Journal of Plant Breeding and Crop Science

Full Length Research Paper

Genotype × environment interactions and oil content stability analysis of peanut (*Arachis hypogaea* L.) in Northern Cameroon

Souina Dolinassou[1], Jean Baptiste Tchiagam Noubissié[1*], Malhala Mamoudou[1], Richard Marcel Nguimbou[2] and Nicolas Yanou Njintang[1,2]

[1]Department of Biological Sciences, Faculty of Science, University of Ngaoundéré, P.O. Box 454, Ngaoundéré, Cameroon.
[2]Department of Food Science and Nutrition, National School of Agro-Industrial Science (ENSAI), University of Ngaoundéré, P.O. Box 455, Ngaoundéré, Cameroon.

Received 7 December, 2016; Accepted 20 March, 2017

High oil content of peanut is a crucial trait for the processing industry, especially in developing countries where most peanuts are for a major source of cooking oil. Twelve peanut (*Arachis hypogaea* L.) varieties were evaluated at three northern Cameroon locations for two consecutive seasons in order to estimate variability and stability of performance for seed oil content. A randomized complete block design replicated thrice was applied in each location and year. Oil content was studied for genotype by environment interaction (GEI) using four stability parameters and, additive main effects and multiplicative interaction analysis (AMMI). Analysis of variance showed significant differences ($p<0.05$) between genotypes, locations and GEI, accounted respectively for 60.00, 19.20 and 20.80% of the total variation. Highest oil contents were recorded from genotypes Blanc, Ad-Mapienta and Gobo-55-437, while lines NW-Red Esimbi and Ouest-A2 gave the lowest oil percentages. IPCA1 of AMMI was significant and captured the largest portion of variation (67.2%) of the total GEI. Stability analysis identified the high oil content genotypes Blanc and Campana as the best lines for multilocation trials. These varieties could be released .for cultivation and used in breeding programs and development of mapping population to identify quantitative trait loci governing oil content.

Key words: *Arachis hypogaea*, oil content, genotype x environment interaction, stability analysis, Northern Cameroon.

INTRODUCTION

Peanut (*Arachis hypogaea* L.) whose global annual kernels production stands at approximately 38.5 million tonnes is an important annual oilseed and protein crop cultivated on about 24.5 million hectares worldwide (Food and Agriculture Organization, 2014). The nuts are crushed to remove the kernels that are a source of protein, vegetable oil, cakes and many industrial products.

About 60% of the total peanut production is crushed for

*Corresponding author. E-mail: jbnoubissitch@yahoo.fr.

edible oil and industrial uses, while 30% is consumed in food uses (Janila et al., 2016). Groundnut oil production ranks sixth in the world, and second in Africa among various other vegetable oils contributing respectivrely 3.28 and 19.74% to the total vegetable oil basket (Janila et al., 2016). In Cameroon, groundnut is grown on nearly 380 000 ha with an annual production of about 540 000 t of kernels with Northern Cameroon accounting for more than 56% of the national production (Hamasselbe, 2008). Within the framework of Peanut Germplasm Project (GGP), varieties mostly from International Crops Research Institute for Semi Arid Tropics (ICRISAT) have been recommended in the three growing areas in the region, considering especially their earliness, the resistance to major pathogens and the yield (Mekontchou et al., 2006; Dolinassou et al., 2016). Peanut is one of the premium oilseed in northern cameroon while its oil is largely consumed and the cake obtained after oil extraction is used in making enriched foods. Peanut kernels contain 36 to 60% of high quality edible oil with higher proportion of unsatured fatty acid (Hassan et al., 2005). It contains resvaratrol, a polyphenol antioxidant, which has been found to provide protective function against cancers, heart disease, degenerative nerve disease and viral infections (Asibuo et al., 2008). As high kernel yield and oil content are the main goals of the most plant breeding programs in Africa (Janila et al., 2013), it is important to upgrade the peanut program in northern cameroon by selecting in each of the three growing areas, superior cultivars with wide or specific adapation.

The performance of a genotype is determined by three factors: Genotypic effect, environmental effect and their interactions. The adaptability and stability of a variety over diverse environments is usually tested by its degree of interaction with different growing environments (Okuno et al., 1971). failure of genotypes to respond consistently to variable environmental conditions is attributed to genotype by environment interaction (GEI). A genotype is considered to be more adaptive or stable if it has a high mean yield but low degree of fluctuation in yielding ability when grown over diverse environments (Finlay and Wilkinson, 1963). Knowledge of GEI is advantageous to increase efficiency of breeding program and selection of best genotypes. In meeting the demands for varieties better adapted to changing conditions, the plant breeder is faced with the options of breeding for either closely defined or a wider range of ecologic environment. Numerous studies highlighted variability and significant interactions between environments and genotypes for oil content in groundnut (Bansal et al., 1993; Dwivedi et al., 1993; Barrientos-Priego et al., 2002; Isleib et al., 2008; Singkhan et al., 2010; Baring et al., 2013; Janila et al., 2016) and other crops including rapeseed (Shafti et al., 1992; Marjanovic-Jeromela et al., 2008), soybean (Fekadu et al., 2009; Bueno et al., 2013), sesame (Zenebe and Hussein, 2010; Abate et al., 2015) and linseed (Berti et al., 2010; Alem and Tadesse, 2014). Varietal improvement for stability in seed oil content or adaptation to specific environment should be given due consideration. In the sudano sahelian zone of Cameroon; GEI analysis in groundnut has not received adequate attention comparable to the crops importance (Dolinassou et al., 2016). Plant breeders generally agree on the importance of high performance stability, but there are fewer consensuses on the most appropriate definition of stability and on methods to measure and improve performance stability (Gauch, 1992; Ferreira et al., 2006). The static concept of stability is characterised by constant genotype performance over different environmental conditions while the dynamic stability is characterised by the performance of a given genotype compared to environmental mean (Becker and Leon, 1988). In the presence of significant GEI, there are a number of simple or multiple linear regression methods, nonlinear procedures and multivariate stability parameters used to identify stable and high yielding genotypes (Becker and Leon, 1988; Purchasse, 1997). Linear regression proposed by Finlay and Wilkinson (1963) is the model most often used in the study of adaptability and dynamic stability, while the ecovalence (Wricke, 1962), the stability variance (Shukla, 1972) and the AMMI Stability Value (Purchasse, 1997) are procedures used for static variance. Among multivariate methods, AMMI (Main Additive effects and Multiplicative Interaction) analysis integrates variance analysis of the main effects (environments and genotypes) with principal component analysis for the multiple effects of GEI (Zobel et al., 1988).

The major objective of this study was to understand the adaptation of twelve groundnut varieties in northern Cameroon by assessing the effects of genotype, environment and their interaction in terms of seed oil content. Responsiveness and stability of genotypes to the three varying environments (Wakwa, Pitoa and Gobo) were investigated using combination of four stability parameters: ecovalence (*Wi*), regression coefficient (*bi*), stability variance (σ_i^2) and AMMI's Stability Value (*ASV*) and AMMI model analysis.

MATERIALS AND METHODS

Testing environments

After a preliminary trial in 2012 at the Ngaoundéré University campus, field experiments were conducted during 2013 and 2014 rainy-season, at three locations of Northern Cameroon: Wakwa (7°13'N, 13°34'E) in the Adamawa region, Pitoa (9°22'N, 13°31'E) in the North region and Gobo (10°1'N, 15°24'E) in the Far North region. These locations were situated within the altitudinal ranges of 300 to 1400 m at sea level, and represent the varying agro-ecologies of the major groundnut growing areas (Dolinassou et al., 2016). The test locations, selected to sample climatic and edaphic conditions, vary in latitude, rainfall, soil types, temperature and other agro-climatic factors. Information on planting dates, site

Table 1. Environmental characteristics of experimental sites.

Location	Region	Growing period	Environmental variables				
			Altitude (m)	Rainfall (mm)	TP (°C)	RH (%)	Soil type
Gobo	Far North	July-November	339	860	27	69	Sandy clay
Pitoa	North	June-October	476	945	28	66	Clay loam
Wakwa	Adamawa	April-July	1279	1539	22	80	Silt clay

TP, Temperature; RH, relative humidity.

Table 2. Peanut varieties used in the study.

Genotypes	Code	Botanical type	Released date	Growing region	Cycle (days)	Kernel yield ($kg.ha^{-1}$)	100-seed weight (g)
Ad-Mapienta	1	Virginia	1950	AD	105-120	1485-2068	74.78
Blanc	2	Valencia	2005	C, E, N	100-110	1587-2286	41.47
Campana	3	Virginia	1990	AD, N, FN	115-120	1559-1730	53.78
Dourou	4	Spanish	1960	AD, N, FN	110-115	2053-2203	53.11
Gobo-55-437	5	Spanish	1960	FN	90-95	1187-2322	39.89
G-M-28-206	6	Virginia	1950	N, E	115-125	1142-1859	51.11
ICGV 86003	7	Spanish	2003	N, FN	90-95	1375-1622	54.13
JL 28	8	Spanish	1980	N, FN	90-95	1764-1891	51.79
K1332-78	9	Virginia	1980	N, E	115-120	913-2171	43.44
NW-Red Esimbi	10	Spanish	1950	NW	100-105	401-526	44.89
Ouest-A2	11	Spanish	1950	W	100-105	1127-1470	42.33
RMP 91	12	Virgina	1990	N	135-145	1136-1697	51.00

Sources: Hamasselbe (2008), Dolinassou et al. (2016); AD, Adamawa; CE, Center; E, East; FN, Far North; N, North, NW: North West, W: West

designation and environmental variables is contained in Table 1.

Genotypes

Twelve peanut advanced lines obtained from the Institute of Agricultural Research for Development (IRAD of Maroua, Cameroon) and from Cotton Development Company (SODECOTON) were included in the study (Table 2). Experimental materials comprised of nine popular cultivars viz., Ad-Mapienta, Campana, Dourou, Gobo-55-437, G-M-28-206, CGV86003, JL 28, K1332-78 and RMP 91, recommended for cultivation in northern Cameroon; two lines frequently cultivated in the western highlands of Cameroon (NW-Red Esimbi and Ouest-A2) and, an exotic check developed at ICRISAT and released as new variety in Cameroon (Blanc). Some of the key traits of the selected lines (Table 2) include confectionary type, tolerance to *Aspergillus flavus*, and resistance to foliar fungal diseases, kernel yield and duration-type maturing (Mekontchou et al., 2006; Hamasselbe, 2008; Dolinassou et al., 2016).

Field experimental trials and oil content estimation

In each location and each year, the field experimental design was laid out using randomized complete block design with three replications. Each plot unit consisted of one row of 2.0 m broad × 3 m length spaced 1.0 m apart. Two seeds of each variety were sown at an intra-row spacing of 30 cm and thinned to one plant per hill, 20 days after sowing (DAS). Normal cultural practices were followed. There was no application of inorganic fertilizers and chemicals throughout the plantings. At maturity, harvesting was done on ten randomly selected plants, when the pods were ready for picking. Kernels were later dried in an oven at 60°C for about 12 h.

The crude oil was evaluated by continuous extraction in a soxhlet apparatus using hexane as solvent, as described by Kohel (1980). Dried groundnut whole seeds were ground in Moulinex Model SeB PREP'LINE 850. For solvent extraction, 1 g of ground seeds for each sample was placed into a cellulose paper cone in a l-L Soxhlet extractor for 8 h. The oil was then recovered by evaporating of the solvent using rotary evaporator and residual solvent was removed by drying in an oven at 60°C for 1 h and flushing with 99.9% nitrogen. Oil content (%) was estimated per replication for all six environments. Oil percentage of the samples was analyzed at the SODECOTON Oil Analytical Laboratory at Maroua.

Statistical analysis

Data of the 12 pure lines across the six environments were subjected to analysis of variance (ANOVA) using computer program Statgraphics Plus, version 3. The genotypic and environmental means were compared using least significant difference (LSD) at 5% level of probability. The coefficient of variation (CV) for each environment was estimated from the standard deviation divided by the environmental mean (×100%).

Heritability in broad-sense (h^2) was estimated as the ratio of the

Table 3. Variability and heritability of oil content of the 12 groundnut cultivars evaluated across three locations in northern Cameroon during cropping seasons 2013 and 2014.

Genotype	Oil content (%)						
	Wakwa		Pitoa		Gobo		Genotype mean
	2013	2014	2013	2014	2013	2014	
Ad-Mapienta	58.08^{b}	56.67^{b}	58.82^{ab}	58.48^{c}	59.27^{c}	57.09d	58.06±1.01^{b}
Blanc	61.19^{a}	61.33^{a}	59.95^{a}	62.40^{a}	62.92^{a}	62.20^{a}	61.66±1.06^{a}
Campana	55.96^{c}	55.58^{c}	57.98^{b}	56.62^{d}	59.36^{c}	58.15^{c}	56.86±1.54^{cd}
Dourou	53.46^{e}	54.42^{d}	56.81^{c}	58.26^{c}	58.03^{d}	57.42^{d}	56.32±1.99^{cd}
Gobo-55-437	53.74^{e}	56.34^{bc}	55.70^{d}	59.95^{b}	60.54^{b}	60.08^{b}	57.73±2.83^{bc}
G-M-28-206	54.76^{d}	56.08^{bc}	55.71^{d}	56.13^{de}	60.01^{bc}	53.78^{f}	55.29±2.12^{cd}
ICGV 86003	52.92^{e}	51.19^{f}	54.76^{e}	55.35^{ef}	56.77^{e}	55.65^{e}	54.44±2.03^{de}
JL 28	53.23^{e}	48.71^{g}	52.66^{f}	54.92^{f}	57.77^{de}	58.77^{c}	54.34±3.67^{de}
K1332-78	49.78^{f}	51.12^{f}	48.84^{g}	50.49^{h}	54.07^{f}	54.65^{ef}	51.49±2.35^{f}
NW-Red Esimbi	49.82^{f}	51.58^{f}	47.67^{h}	48.22^{i}	52.72^{g}	49.46^{g}	49.91±1.93^{g}
Ouest-A2	45.25^{g}	46.55^{h}	48.32^{gh}	48.37^{i}	48.23^{h}	48.25^{h}	47.49±1.30^{g}
RMP 91	49.29^{f}	52.62^{e}	48.98^{g}	53.20^{g}	57.04^{e}	58.48^{c}	53.27±3.90^{e}
Environment's mean	53.12^{b}	53.51^{b}	53.85^{b}	55.19^{ab}	57.22^{a}	56.16^{a}	54.73
CV (%)	8.02	7.51	8.19	8.08	6.90	7.32	7.04
h^2	0.72	0.67	0.82	0.71	0.67	0.74	0.72
Repeatability	0.86**		0.92**		0.86**		

CV, Coefficient of variation; h^2, broad-sense heritability; means followed by the same letter are not significantly different at 5% level of probability; **, Significant at the 0.01 probability level.

genetic variance (σ^2_g) on the phenotypic variance (σ^2_p) as outlined by Johnson et al. (1955) and Noubissié et al. (2012):

$$h^2 = \sigma^2_g / \sigma^2_p = (\sigma^2_p - \sigma^2_e) / \sigma^2_p = (\sigma^2_l - \sigma^2_i) / \sigma^2_l$$

Where σ^2_p the total phenotypic variance was obtained from the inter-varietal variance (σ^2_l) among the twelve genotypes, and σ^2_e the environmental variance estimated from the average of the intra-varietal variance (σ^2_i) among plants of each pure lines. In each location, the repeatability is the Karl Pearson's coefficient of correlation between the two crop seasons.

The combined analysis of variance across locations was done using by Hardwick and Wood (1972) model with genotypes being considered as fixed effects and replications within environments being random mode in order to evaluate the effect of difference between genotypes, across locations and also to determine whether their interaction was significant. Genotype × environment interaction (GEI) was quantified using pooled analysis of variance, which partitions the total variance into its component parts (genotype, environment, GEI, pooled error).

Different stability models were performed: the Finlay and Wilkinson's joint regression analysis (*bi*) (1963), Wricke's ecovalence (*Wi*) (1962), Shukla's procedure of stability (σi^2) (1972), and the AMMI's stability value (*ASV*) as described by Purchasse (1997) as:

$$ASV = [((\text{IPCA1 sum of square} / \text{IPCA2 sum of square}) \times \text{IPCA1 score})^2 + (\text{IPCA2 score})^2]^{½}$$

Where, IPCA1 and IPCA2 are interaction of principal component axis one and two.

To graphically explain the GEI and adaptation of genotypes to environments, the AMMI1 biplot between the IPCA1 scores and genotypes and environments means was used. The more IPCA scores approximate to zero, the more stable the genotype over all environments sampled. Genotypes that are close to each other tend to have similar performance and those that are close to environment indicates their specific adaptation (Gauch, 1992). The greater the IPCA scores, either positive or negative, as it is a relative value, the more specifically adapted a genotype is to certain environments (Crossa et al., 1991). All analyses on GEI and stability analysis were performed using the GEST 98 micro-computer program (Ukai, 2000).

RESULTS AND DISCUSSION

Range of variability and heritability across environments

The mean, coefficient of variation, heritability and repeatability of oil content for each environment and across environments are presented in Table 3. The mean oil content of varieties across environments ranged from 47.49% for Ouest-A2 to 61.66% for Blanc with the grand mean yield of 54.73%. The five top ranked lines for seed oil percentage were Blanc, Ad-Mapienta, Gobo -55-437, Campana and Dourou, and those showing the lowest oil content were Ouest-A2 and NW-Red. The mean oil content over six environments of peanut genotypes varied between 53.12 and 57.22% Among locations, the highest mean oil content values were recorded at Gobo (57.22 and 56.16%) whereas the lowest values were noted at Wakwa (53.12 and 53.51%). Variability for oil

Table 4. Combined analysis of variance for oil content in the study of 12 groundnut cultivars in six environments.

Source of variation	df	SS	MS	% SS	F-value	P
Genotype (G)	11	806.08	73.27	60.00	17.87	<0.001
Environment (E)	5	258.05	51.61	19.20	12.58	<0.001
GEI	55	279.41	5.08	20.80	1.24	<0.05
Residual	44	196.55	4.47		1.09	
Total	71	1343.54				

df, degree of freedom; GEI, genotype by environment interaction; SS, sum of square; MS, Mean square; % SS, percentage of the sum of square; P, level of probability.

content in kernel was reported in groundnut by many authors (Dwivedi et al., 1990; Bansal et al., 1993; Badigannavar et al., 2002; Asibuo et al., 2008; Atasie et al., 2009; Noubissié et al., 2012). It appeared that, in the studied materials, most of the analyzed varieties fell into the category of high oil percentage. Low oil content peanuts are preferred for table purposes and food preparations with low calorific values. For this trait, the estimates of the coefficients of variation (CV) were low across the six environments ranging from 6.90 to 8.19%. Bueno et al. (2013) found CV ranging from 1.92 to 4.33 for oil content in soybean cultivated in four locations at Brazil.

The coefficient of correlation between the two growing seasons (repeatability) was highly significant ($p<0.01$) and varied from 0.86 to 0.92 depending on locations, suggesting that the climatic differences among years did not affect the oil content significantly. Earlier studies have shown the non-significance of genotype x year interaction for oil content in peanut (Dwivedi et al., 1993) and in flaxseed (Berti et al., 2010). Janila et al. (2016) also recorded a small variation between rainy seasons for mean oil content, but noted that the oil yield was higher in post-rainy seasons by 72% than rainy seasons.

High broad-sense heritability values varying between 0.67 and 0.72 were recorded in the six tested environments, suggesting the possible genetic gains through selection for oil content. Bansal et al. (1993), Noubissié et al. (2012), Baring et al. (2013), Baring et al. (2013), and Janila et al. (2016) also observed high heritability for this trait in peanut. In soybean, Bueno et al. (2013) found a heritability value of 0.79 for this trait. According to Wilson et al. (2013), progress can be made toward developing seed with improved oil concentration since the vast majority of variation for this trait is genetic with preponderance of additive effects. In contrast to observed high heritability for oil content in the present study, Atasie et al. (2009), reported low heritability for seed oil percentage in peanut. Estimates of heritability in the broad sense are important in plants because they are connected to the selection, and the larger the estimated value of this parameter is, the greater will be the chance of success with selection. However, the pronounced difference in seed oil content over locations is an indication that these characters are under both genetic and environmental effects. The higher genotypic variation relative to environmental counterparts is consistent with the autogamous nature of groundnut with homozygosity at various loci (Janila et al., 2013). Oil yield in peanut is influenced by many different components, including oil concentration, seed mass and mean oil produced per seed (Wilson et al., 2013). As highlighted by Singh and Ahuja (1985), Hassan et al. (2005), Zheljazkov et al. (2009) and Berti et al. (2010), oil accumulation in different oilseeeds is affected by number of factors such as temperature, moisture availability, plant density, soil type, fertilization, total sunshine hours particularly from flowering to maturity and their interaction. Bueno et al. (2013) noted that oil content is higher when the soybean is cultivated in warmer environments and lower when the seeds are ripen in cold temperatures. Significant positive correlations between oil content and seed mass, and kernel yield were previously reported (Dwivedi et al., 1990; Noubissié et al., 2012). In contrast, Wilson et al. (2013) noted an inverse relationship between seed weight and oil content in a selected population.

Combined analysis of variance

The combined analysis of variance (Table 4) showed that there are significant differences ($p<0.05$) for peanut genotypes, environments and their interaction. Seed oil content was significantly affected by genotypes which explained 60.0% of the total variation, while environment and GEI captured respectively 19.2% and 20.8% of the total sum of square. In this study, significance of all sources of variation indicated differential behaviour of tested genotypes, which was not consistent with different environments. A large sum of square for genotypes indicated diversity of tested lines, with large difference among genotypic means causing variation in the seed oil accumulation. Similar results were recorded on sesame oil content by Zenebe and Hussein (2010). In Ethiopia, Abate et al. (2015) noted that the proportion of variance captured by effect of genotype, environment and GEI was respectively 91.5, 1.43 and 7.1% of the total variation, also suggesting less effect of environment on

Table 5. Genotypic stability parameters for 12 groundnut genotypes across three environments.

Genotype	Code	*bi*	W_i	σ_i^2	IPCA1	IPCA2	*ASV*
Ad-Mapienta	1	0.63 (4)	12.85 (5)	0.63 (5)	1.47	-0.89	1.56 (7)
Blanc	2	1.10 (9)	7.30 (2)	0.30 (2)	0.35	0.78	0.68 (2)
Campana	3	0.99 (6)	2.51 (1)	0.02 (1)	-0.28	-0.57	0.64 (1)
Dourou	4	0.74 (5)	14.14 (6)	0.71 (6)	0.39	0.19	1.45 (5)
Gobo -55-437	5	1.28 (10)	24.94 (9)	1.34 (9)	1.46	-1.40	2.25 (10)
G-M-28-206	6	0.43 (3)	8.45 (3)	0.31 (3)	0.57	-0.22	0.88 (3)
ICGV86003	7	1.02 (7)	8.80 (4)	0.39 (4)	-0.65	0.51	0.91 (4)
JL 28	8	2.22 (12)	62.80 (12)	3.56 (12)	-1.87	-0.88	3.80 (11)
K1332-78	9	1.06 (8)	14.48 (7)	0.73 (7)	-1.08	1.15	1.48 (6)
NW-Red Esimbi	10	0.25 (1)	25.55 (10)	1.38 (10)	0.96	-0.96	2.07 (9)
Ouest-A2	11	0.37 (2)	20.43 (8)	1.07 (8)	-1.31	1.17	1.94 (8)
RMP 91	12	1.89 (11)	61.24 (11)	3.47 (11)	-1.68	1.29	3.97 (12)

bi, Finlay and Wilkinson's regression coefficient; *Wi*, Wricke's ecovalence; σ_i^2, Shukla's stability variance; *ASV*, AMMI's stability value; IPCA, Interaction principal component axis; Number between parenthesis denote ranking of varieties for each stability parameter.

oil content as compared to the effect of genotypes. In contrast, Marjanovic-Jeromela et al. (2008) noted that environmental effects as well as GEI had the strongest effect on oil yield expression in rapeseed. Significant interactions in groundnut for seed oil content have been early reported by several studies (Dwivedi et al., 1993; Singkham et al., 2010; Baring et al., 2013; Janila et al., 2016). When GEI is highly significant for a particular trait as yield, no valid comparison could be made regarding the relative performance of genotypes over all environments. The GEI has three adverse effects in plant breeding: (i) It reduces the correlation between genotypic and phenotypic values, decreasing the progress from the selection and making the selection of superior and stable genotypes in a wide range of environments difficult; (ii) As a component of a trait phenotypic variance, it decreases heritability and hinders breeding for complex traits; and (iii) It also masks the potential benefits of exotic materials introgression (Fan et al., 2007). However for specific selection being achieved GEI will help select genotypes for each environment. A wide range of soils and climatic conditions are encountered in Northern Cameroon.

AMMI model analysis

The AMMI model, which combines the standard analysis of variance with principal component analysis, is fully informative for both the main effect as well as the multiplicative effects, for clearly understanding the GEI (Zobel et al., 1988). The ANOVA from AMMI model also demonstrated the significance of GEI ($p<0.05$) showing that certain varieties performed better and their oil accumulation differed from location to location. The significant GEI were decomposed into the first and two Interaction Principal Components Axes (IPCA1 and IPCA2) that globally captured 84.7% of the interaction sum of squares. The first IPCA was significant and accounted for 67.2% while IPCA2 explained 17.5% of the GEI respectively. The combined mean squares (MS) for the two IPCA axes were 18.9 times that of the residual MS, suggesting that the two IPCAs were sufficient predictive model to explain GEI in oil content. Similar results were also reported for this trait by Abate et al. (2015) in sesame.

Stability and adaptability of genotypes

The values of different stability parameters for the oil content of each groundnut genotype and ranking are presented in Table 5. The values of *bi* adaptability parameter of Finlay and Wilkinson (1963) ranged from 0.25 (NW-Red Esimbi) to 2.21 (JL 28). According to Finlay and Wilkinson (1963) model of analysis of stability, a stable variety is one which has above mean yield and a regression coefficient of unity ($bi=1$). The varieties Blanc, ICGV86003, and Campana with *bi* values close to unity and above-average oil content showed general adaptability. In contrast, K1332-78 which has a regression coefficient approximating 1.0 but consistently produced below-average oil content is poorly adapted to all tested environments. ICGV86003 has average stability over environments since it produced average oil content and has a linear regression coefficient of the order of 1.0. High value of regression coefficient ($bi>1.0$) indicates that the variety is sensitive to environmental changes and more responsive for input rich environment, while low value ($bi<1.0$) is an indication that the variety has greater resistance to environmental changes and may be adopted in poor environment. Genotypes JL 28, RMP 91 and Gobo-55-437 showed *bi* larger than 1.0 so they are indicated in superior or higher yielding environments,

while cultivars NW-Red Esimbi, Ouest-A2, GM-28-206, Ad-Mapienta and Dourou were considered to be adapted to lower yielding or unfavorable environments since their *bi* values were smaller than 1.0. According to Ferreira et al. (2006), among breeders, the main criticisms of linear regression models are: The dependence of the environmental index on the mean performance of genotypes and the use of biased estimators of regression coefficients since the independent variable is measured with error.

Shukla's stability variance parameter (σ_i^2) (Shukla, 1972) and ecovalence (*Wi*) which is the contribution of a genotype to GEI sum square (Wricke, 1962) ranged from 2.51 to 62.8 and 0.002 to 3.56, respectively. The stability variance is a linear combination of the ecovalence, and both *Wi* and σ_i^2 are equivalent for ranking purpose (Becker and Leon, 1988). The difference in magnitude indicated the variation in degree of stability. Low values were recorded for genotypes Campana; Blanc, GM-28-206 and ICGV86003, while largest values were noted for genotypes were JL 28, RMP 91 and NW-Red Esimbi. The AMMI stability value (*ASV*) ranged from 0.64 for genotype Campana to 3.97 for line RMP 91. Genotypes Campana, Blanc, GM-28-206 and Dourou had lowest *ASV* values while RMP 91, JL 28 and Gobo-55-437 presented the highest values of *ASV*. In fact, *ASV* is the distance from zero in a two scatter gram of IPCA1 scores against IPCA2 score. According to Ferreira et al. (2006), the *ASV* was considered to be the most appropriate single method of describing the stability of genotypes. A variety with high mean and least *ASV* is the most stable. The larger the *ASV* value, the more specifically adapted a genotype is to certain environments and *vice versa* (Purchasse, 1997). Accordingly, the varieties Campana and Blanc were considered stable across all environments, which was in accordance with the results of other stability parameters. Ad-Mapienta and Gobo-55-437 are suited to specific environments.

The ideal genotype should have the highest mean performance and be absolutely stable with zero GEI (Okuno et al., 1971). In general, the data obtained on stability showed that none of the tested genotypes could be considered as completely stable. Similar observation has been previousely reported in groundnut for oil content (Bansal et al., 1993; Barrientis-Priego et al., 2002; Baring et al., 2013; Janila et al., 2016). In analysis of cultivar stability, Abate et al. (2016) found significant correlation between the stability measures *ASV*, *Wi*, and σ_i^2 but noted that *bi* had limited association with other methods.

AMMI1 biplot analysis

The AMMI biplot analysis provides a graphical representation to summarize information on main effect and interaction effect of both genotypes and environments (Figure 1). The IPCA1 was represented in the y-axis where the genotype and environment mean represented on the x-axis in the so-called AMMI1 biplot. By plotting both the genotypes and environments on the same graph, the associations between genotypes and locations can be seen clearly. The displacement along the abscissa reflected differences in main effects, whereas displacement along the ordinate exhibited variation in interaction effects. Genotypes and environments with IPCA1 score greater than zero are classified as high yielding genotypes and favorable environments, whereas those with negative IPCA1 value are classified as low yielding genotypes and poor environments. It is clear from the graph that the points for varieties were more scattered than the points for environments confirming that the variability due to the genotypes was higher than that due to environments. Genotypes or environments located on the right side of perpendicular line have higher oil content than those on the left side. Accordingly for oil percentage, genotypes such as Blanc, Ad-Mapienta, Gobo-55-437, Dourou, Campana and GM-28-206 were high yielder genotypes as they laid-down on the right side of the vertical line. Conversely, genotypes Ouest-A2, NW-Red Esimbi, K1332-78, JL 28 and ICGV86003 had below grand mean. The environments also showed variability in both main effects and interactions. Regarding the environments, G2 (Gobo, 2014), G1 (Gobo, 2013) and P2 (Pitoa, 2014) located on the right hand side of the midpoint of the main effect with positive IPCA1 scores were considered as favorable and high potential environments for seed oil content. P1 (Pitoa, 2013) seemed to be moderately favorable while W1 (Wakwa, 2013) and W2 (Wakwa, 2014) were considered unfavorable and lower potential testing environments for seed oil content among the genotypes evaluated. G2 was highly interactive having high interactions effects. Whatever the direction is, the greater the IPCA scores, the more specifically adapted these genotypes were to certain environments (Zobel et al., 1988; Crossa et al., 1991). With regard to IPCA1 scores, genotypes Campana and Blanc with the lowest scores near zero (either positive or negative) have little interaction effects and were considered as stable across environments. In contrast, RMP 91, JL 28, Gobo-55-437 and Ad-Mapienta, with the highest IPCA1 scores, were the most divergent. Varieties Gobo-55-437 and Ad-Mapienta, with high oil percentage and large IPCA1 scores were considered as having specific adaptability to favorable environments. Low producing oil content and small-seeded genotypes Ouest-A2, NW-Red Esimbi, and K1332-78 are unstable or not adaptable to any of the environments for oil content. Deshmukh et al. (1986) highlighted that large-seeded peanut genotypes with low oil content may be preferred for confectionary purposes. Genotype and environment with IPCA1 score of the same sign produce positive interaction effects; whereas combination of opposite sign shows negative interaction Gauch, 1992).

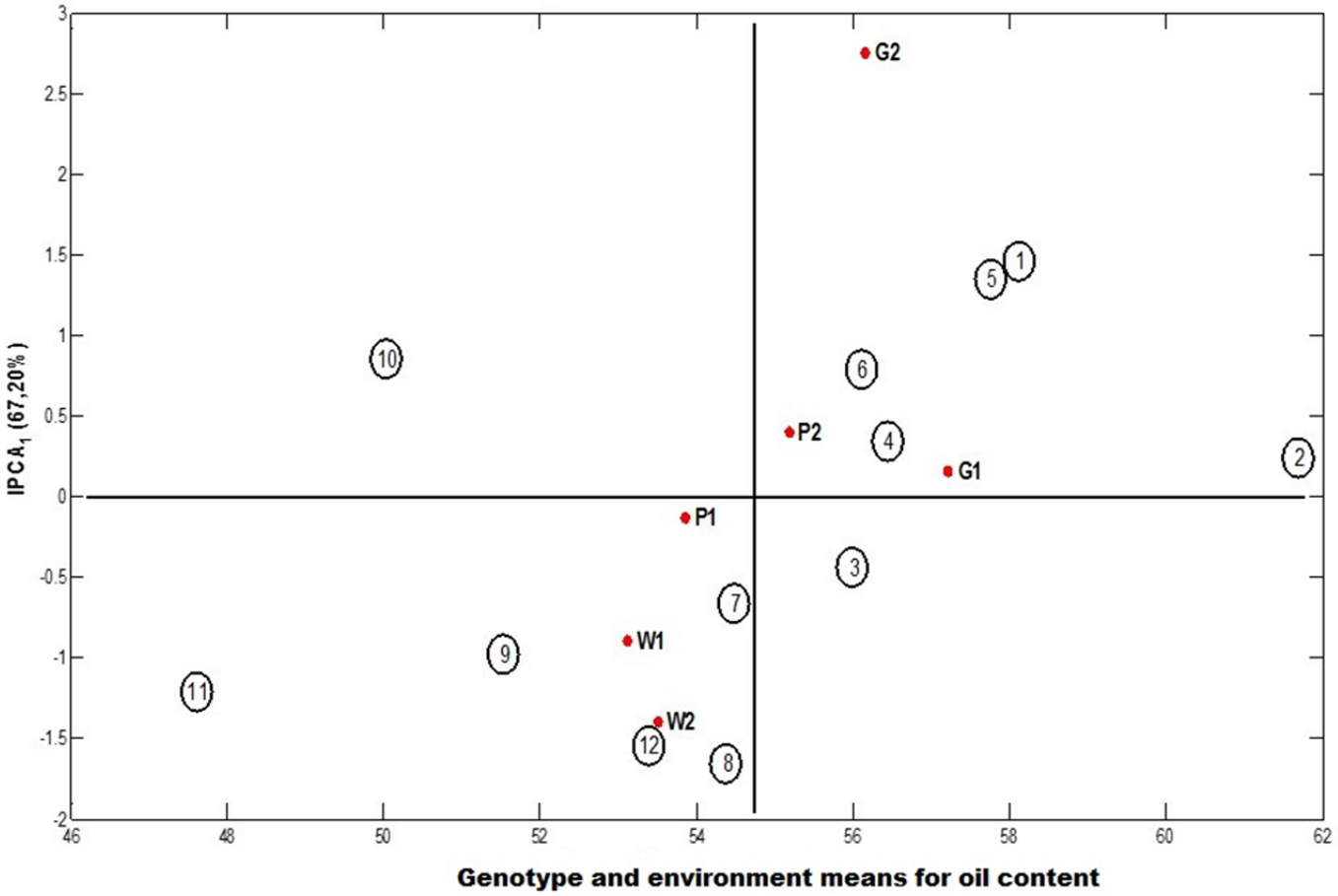

Figure 1. AMMI biplot of interaction principal component axis-1 (IPCA1) against mean oil content of twelve genotype and three environments. Genotypes plotted as 1, Ad-Mapienta; 2, Blanc; 3, Campana; 4, Dourou; 5, Gobo-55-437; 6, G-M-28-206; 7, ICGV86003; 8, JL 28; 9, K1332-78; 10, NW-Red Esimbi; 11, Ouest-A2; 12, RMP 91 and environments plotted as G1 (Gobo 2013); G2 (Gobo 2014); P1 (Pitoa 2013); P2 (Pitoa 2014); W1 (Wakwa; 2013) and W2 (Wakwa; 2014)

(AMMI analysis was also conducted and stability of peanut genotypes for oil content was predicted on the basis of mean performance and the magnitude of IPCA1 score elsewhere (Barrientos-Priego et al., 2002; Isleib et al., 2008)

Conclusion

In the development and release of groundnut genotypes for cultivation, analysis of GEI is necessary to determine the stability of performance of the variety across environment. From the study, among the top five genotypes for oil content, only Blanc, a kernel high-yielding variety, and Campana were suitable for all environments and these varieties could be recommended for wide cultivation across the areas of Northern Cameroon. Of the twelve genotypes tested, Ad-Mapienta and Gobo-55-437 are promising materials specifically adapted to the favorable environment around Gobo. The results of this study could be used by breeding programs, as well as national institutions committed to testing or recommending crop varieties for more effective selection and development of mapping population to identify quantitative trait loci governing oil content. In peanut, Sarvamangala et al. (2011) identified quantitative trait loci for oil content and oil quality.

CONFLICTS OF INTERESTS

The authors have not declared any conflict of interests.

ACKNOWLEDGEMENTS

The lead author is cordially grateful to the funding of the International Foundation for Science (IFS grant C5599-1). The authors acknowledge with thanks the staff of the SODECOTON for kindly providing their laboratory for analysis. They also obliged to Pr Ukai Yasuo of the University of Tokyo for providing the microcomputer

program GEST 98.

REFERENCES

Abate M, Mekbib F, Ayana A, Nigussie M (2015). Genotype x environment and stability analysis of oil content in sesame (*Sesamun indicum* L.) evaluated across diverse agro-ecologies of Awash Valleys in Ethiopia. Am. J. Exp. Agric. 9(2):1-12.

Alem C, Tadesse D (2014). Study on genotype x environment interaction of seed yield, oil content, fatty acid profile and stability analysis of yield related trait in linseed (*Linum usitatissimun* L.) in North Western Ethiopia. Int. J. Plant Breed. Genet. 8(2):66-73.

Asibuo JY, Akromah R, Safo-Katanka O, Adu-Dapaah HK, Ohemeng-Dapaah S, Agyeman A (2008). Chemical composition of groundnut, *Arachis hypogaea* (L.) landraces. Afr. J. Biotechnol. 7(13):2203-2208.

Atasie VN, Akinhami TF, Ojiodu CC (2009). Proximate analysis and physicochemical properties of groundnut (*Arachis hypogaea* L.). Pak. J. Nutr. 8(2):194-197.

Badigannavar AM, Kale DM, Murty GSS (2002). Genetic base and diversity in peanut genotypes. Plant Breed. 121:348-353.

Bansal UK, Satija DR, Ahuja KL (1993). Oil composition of diverse groundnut (*Arachis hypogaea* L.) genotypes in relation to different environments. J. Sci. Food Agric. 63:17-19.

Baring MR, Wilson JN, Burow MD, Simpson CE, Ayers JL, Cason JM (2013). Variability of total oil content in peanut across the state of Texas. J. Crop Improvement 28(28):125-136.

Barrientos-Priego L, Isleib TG, Pattee HE (2002). Variation in oil content among Mexican and Peruvian *hirsuta* peanut landraces and Virginia type *hypogaea* lines. Peanut Sci. 29:72-77.

Becker HC, Leon J (1988). Stability analysis in plant breeding. Plant Breed. 101:1-23.

Berti M, Fisher S, Wilckens R, Heira F, Johnson B (2010). Adaptation and genotype x environment interaction of flaxseed (*Linum usitatissimun* L.) genotypes in south central Chile. Chilean J. Agric. Res. 70(3):345-356.

Bueno RD, Borges LL, Aruda KMA, Bhering LL, De Barros EG, Moreira MA (2013). Genetic parameters and genotype x environment interactions for productivity, oil and protein content in soybean. Afr. J. Agri. Res. 8(38):4853-4859.

Crossa J, Fox PN, Preiffer WH, Rajaram S, Gauch HG (1991). AMMI adjustment for statistical analysis of an international wheat yield trial. Theor. Appl. Genet. 81:27-37.

Deshmukh SN, Basu MS, Reddy PS (1986). Genetic variability, character association and path coefficients of quantitative traits in Virginia bunch varieties of groundnut. Ind. J. Agric. Sci. 56:816-821.

Dolinassou S, Noubissié TJB, Djirantal AK, Njintang YN (2016). Genotype x environment interaction and kernel yield-stability of groundnut (*Arachis hypogaea* L.) in northern Cameroon. J. Appl. Biol. Biotechnol. 4(01):001-007.

Dwivedi SL, Jambunathan R, Nigam SN, Raghunath K, Ravi Shankar K, Nagabhushanam GVS (1990). Relationship of seed mass to oil and protein contents in peanut (*Arachis hypogaea* L.). Peanut Sci. 17(2):48-52.

Dwivedi SL, Nigam SN, Jambunathan R, Sahrawat KL, Nagabhushanam GVS, Raghunath K (1993). Effect of genotype and environment on oil content quality parameters and their correlation in peanut (*Arachis hypogaea* L.). Peanut Sci. 20(2):84-89.

Fan XM, Kang MS, Chen H, Zhang Y, Tan Y, Xu C (2007). Yield stability of maize hybrids evaluated in multi-environment trials in Yunnan, China. Agron. J. 99:220-228.

Fekadu G, Mohammed H, Alemaw G. (2009). Genotype x environment interactions and stability of soybean for grain yield and nutrition quality. Afr. Crop Sci. J. 17(2):87-89.

Ferreira DE, Demetrio CGB, Manly BFJ, Machado AA, Venkovsky R (2006). Statistical models in agriculture: biometrical methods for evaluating phenotypic stability in plant breeding. Cerne 12:373-388.

Finlay KW, Wilkinson GN (1963). The analysis of adaptation in a plant breeding program. Austr. J. Agric. Res. 14:742-754.

Food and Agriculture Organization of the United Nations (2014). FAO-STAT database. http://faostat.fao.org.

Gauch HG (1992). Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Crop Sci. 46:1488-14500.

Hamasselbe A (2008). La revalorisation de la filière arachide dans la zone soudano sahélienne du Nord Cameroun. Tropicultura 26(4):200-205.

Hardwick RC, Wood JT (1972). Regression methods for studying genotype-environment interactions. Heredity 28:209-222.

Hassan FU, Abdul M, Ejaz M (2005). Determinants of oil and fatty acid accumulation in peanut. Int. J. Agric. Biol. 7(6):895-899.

Isleib TG, Tillman BL, Pattee HE, Sanders TH, Hendrix KW, Dean LO (2008). Genotype-by-environment interactions for seed composition traits of breeding lines in the uniform peanut performance test. Peanut Sci. 35:130-138.

Janila P, Nigam SN, Pandey MK, Nagesh P, Varshney RK (2013). Groundnut improvement: use of genetic and genomic tools. Frontiers in Plant Science 4a23. doi:10.3389/fpls.2013.00023

Janila P, Manohar SS, Patne N, Variath MT, Nigam SN (2016). Genotype × environment interactions for oil content in peanut and stable high-oil-yielding sources. Crop Sci., 56:01-10.

Johnson HW, Robinson HF, Comstock RE (1955). Estimates of genetic and environmental variability in soybeans. Agron. J. 47:314-318.

Kohel RJ (1980). Genetic studies of seed oil content in cotton. Crop Sci. 20(6):784-787.

Marjanovic-Jeromela A, Marinkovic R, Mijic A, Jankulovska M, Zdunic Z, Nagl N (2008). Oil yield stability of winter rapeseed (*Brassica napus* L.) genotypes. Agric. Conspec. Sci. 73(4):217-220.

Mekontchou T, Ngueguim M, Fobasso M (2006). Stability analysis for yield and yield components of selected peanut breeding lines (*Arachis hypogaea* L.) in the North province of Cameroon. Tropicultura 24(2):90-94.

Noubissié TJB, Njintang YN, Dolinassou S (2012). Heritability studies of protein and oil contents in groundnut (*Arachis hypogaea* L.) genotypes. International Journal of Innovations in Biosciences, 2(3):162-171.

Okuno C, Kikuchi F, Kumagai K, Shiyomi M, Tabuchi H (1971). Evaluation of varietal performance in several environments. Bull. Nat. Inst. Agric. 18:93-147.

Purchasse JL (1997). Parametric analysis to describe G× E interaction and yield stability in winter wheat. Ph.D thesis, Faculty of agriculture, University of the Free State, Bloemfontein, South Africa.

Sarvamangala C, Godwa MVC, Varshney RK (2011). Identification of quantitative trait loci for protein content, oil content and oil quality for groundnut (*Arachis hypogaea* L). Field Crops Res. 122(1):49-59.

Shafti B, Malher KA, Price WJ, Auld DL (1992). Genotype x environment interaction effects on winter rapeseed yield and oil content. Crop Sci. 32:922-927.

Singh KP, Ahuja KN (1985). Dry matter accumulation, oil content and nutrient uptake in groundnut (*Arachis hypogaea* L. cv. T64) as affected by fertilizers and plant density. Ind. J. Agron. 30:40-45.

Singkham NS, Jogloy S, Kesmala T, Swatsitang P, Jaisil P, Puppala N (2010). Genotypic variability and genotype by environment interactions in oil and fatty acid in high, intermediate and low oleic acid peanut genotypes. J. Agric. Food Chem. 58: 6257-6263.

Shukla GK (1972). Some statistical aspects of partitioning genotype-environmental components of variability. Heredity 29:237-245.

Ukai Y (2000). GEST. Programs for the analysis of genotype x environment interaction. Migimomi, Tsuchiura, Ibaraki 300-0837, Japan.

Wilson JN, Baring MR, Burow MD, Rooney WL, Simpson CE (2013). Diallel analysis of oil production components in peanut (*Arachis hypogaea* L.). Int. J. Agron. htpp://dx.doi.org/10.1155/2013/975701.

Wricke G (1962). Ueber eine method zur erfassung der oekologischen streubreite in feldversuchen. Z. Pfanzenzucht 47:92-96.

Zenebe M, Hussein M (2010). Study of genotype x environment interaction of oil content in sesame (*Sesamum indicum* L.). World J. Fungal, Plant Biol. 1(1):15-20.

Zheljazkov VD, Vick BA, Baldwin BS, Buehring N, Astatkie T, Johnson B (2009). Oil content and saturated fatty acids in sunflower as a function of planting date, nitrogen rate, hybrid. Agron. J. 101:1003-1011.

Zobel RW, Wright MJ, Gauch HG (1988). Statistical analysis of a yield trial. Agron. J. 80:388-393.

Journal of Plant Breeding and Crop Science

Related Journals Published by Academic Journals

- *African Journal of Agricultural Research*
- *Journal of Horticulture and Forestry*
- *Journal of Cereals and Oilseeds*
- *International Journal of Livestock Production*
- *International Journal of Fisheries and Aquaculture*
- *Journal of Development and Agricultural Economics*

academicJournals