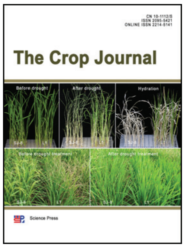
THE CROP JOURNAL XX (2017) XXX–XXX

Available online at www.sciencedirect.com

ScienceDirect



Genotype-by-environment interaction for grain yield among novel cowpea (*Vigna unguiculata* L.) selections derived by gamma irradiation☆

Lydia Horn[a,b], Hussein Shimelis[a], Fatma Sarsu[c], Learnmore Mwadzingeni[a,*], Mark D. Laing[a]

[a]African Centre for Crop Improvement, University of KwaZulu-Natal, P/Bag X01, Scottsville 3209, Pietermaritzburg, South Africa
[b]Directorate of Research and Training, Plant Production Research, Ministry of Agriculture, Water and Forestry, Private Bag 13184, Windhoek, Namibia
[c]Plant Breeding and Genetics Section, Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, Vienna, Austria

ARTICLE INFO

Article history:
Received 11 July 2017
Received in revised form 27 September 2017
Accepted 26 October 2017
Available online xxxx

Keywords:
AMMI
Cowpea
Genotype by environment interaction
GGE biplot
Mutants

ABSTRACT

This study determined the effects of genotype-by-environment (G × E) interaction and stability of yield among elite cowpea (*Vigna unguiculata* L.) selections derived by gamma irradiation. The study was conducted in Namibia at three selected sites: Bagani, Mannheim, and Omahenene, during 2014/2015 and 2015/2016. Thirty-four newly developed mutant genotypes and three local checks were evaluated using a randomized complete block design with three replications. Grain yield data were analyzed using the additive main effects and multiplicative interaction (AMMI) and the genotype main effect plus genotype-by-environment interaction (GGE) biplot methods. The AMMI and GGE biplot models explained 77.49% and 75.57% of total observed genotypic variation, respectively. Bagani and Omahenene were the environments best discriminating the test genotypes during 2014/2015 and 2015/2016, respectively. Four promising mutant genotypes: G9 (ShL3P74), G10 (ShR3P4), G12 (ShR9P5), and G4 (ShL2P4), showed wide adaptation and grain yields of 2.83, 2.06, 1.99, and 1.95 t ha^{-1}, respectively. The novel mutant lines are useful genetic resources for production or future cowpea breeding programs in Namibia or similar environments.

1. Introduction

Cowpea (*Vigna unguiculata* L.; $2n = 2\times = 22$) is an important legume crop widely grown in South America, sub-Saharan Africa, and Asia. It withstands harsh growing conditions, particularly drought stress [1,2]. The grain, young pods, and succulent leaves are used for human food, while the foliage is an important livestock feed [3]. Further, cowpea restores soil fertility through nitrogen fixation, making it an ideal component crop in rotation systems. Production and productivity of cowpea has been low in Namibia, owing to unavailability of seeds of improved cultivars, harsh climatic conditions, diseases,

---

☆ Peer review under responsibility of Crop Science Society of China and Institute of Crop Science, CAAS.

* *Corresponding author.*
E-mail address: MwadzingeniL@ukzn.ac.za (L. Mwadzingeni).

https://doi.org/10.1016/j.cj.2017.10.002
2214-5141

insect pests, and parasitic weeds [2]. The present yield of cowpea ranges from 0.10 to 0.60 t ha^{-1} in Namibia, a range far below the potentially attainable yields of 1.5 to 3.0 t ha^{-1} reported elsewhere [4]. There is thus a need to breed improved cowpea cultivars with enhanced grain yield and quality to meet local and regional production and productivity and market demands.

Design, development, and deployment of improved cultivars require adequate genetic variation, achieved through crosses involving selected parents or targeted mutagenesis [5,6]. The potential of chemical and physical mutagenic agents to induce genetic variation of cowpea for grain yield and yield-related traits has been well reported [7,8]. Induced mutagenesis has been successfully used to modify several agronomic traits of cowpea, such as plant height, maturity, seed shattering resistance, disease resistance, seed color, seed size, and yield [7–9].

Genotype-by-environment (G × E) interaction analysis is an important prerequisite for recommendation of novel selections for large-scale production. It enables assessment of the relative performance and stability of genotypes for yield and yield-related traits [1,10,11]. The performance of tested genotypes is influenced by the genotype, the environment, and G × E interaction [1]. The growing environment often masks the potential genetic expression, leading to poor genetic gain from artificial selection, especially for quantitative traits such as grain yield. G × E analysis involves evaluation of novel selections across representative growing environments, which will assist breeders to recommend promising genotypes based on their narrow or broad adaptation. G × E analyses are valuable during the final stages of selection of elite breeding materials. Several statistical techniques have been widely adapted to analyze and interpret G × E data, including the additive main effect and multiplicative interaction (AMMI) and the genotype main effect plus genotype-by-environment interaction (GGE) biplot analysis [12,13].

A joint cowpea mutation breeding project was initiated between the government of Namibia and the International Atomic Energy Agency (IAEA) under a Technical Cooperation project to develop improved cultivars with better adaptation [2]. This project resulted in the selection of promising mutants with high yield potential, drought tolerance, and insect pest resistance through continuous selfing and selection from the M2 to M7 generations [14]. The selected M6 and M7 elite mutants needed to be evaluated across representative growing environments to determine their performance and yield stability for effective cultivar recommendation and to identify suitable production environments. Accordingly, the objectives of this study were to evaluate the effects of G × E interaction and yield stability among elite cowpea selections derived by gamma irradiation and to identify promising genotypes with narrow or broader adaptation for production or future breeding programs in Namibia or similar environments.

2. Material and methods

2.1. Study sites and plant material

The study was conducted at three sites: Bagani (−18°09′61.93″S, 21°56′24.14″E), Mannheim (19°12′21.4″S, 17°42′29.1″E), and Omahenene (−17°44′29.04″S, 14°78′48.21″E) during the 2014/2015 and 2015/2016 cropping seasons. This plan provided six testing environments including Bagani 2014/2015, Bagani 2015/2016, Mannheim 2014/2015, Mannheim 2015/2016, Omahenene 2014/2015, and Omahenene 2015/2016. The physicochemical properties of soils at Bagani, Mannheim and Omahenene research sites are described by Horn et al. [14]. Mean monthly and total rainfall (mm) at the three sites during 2014/2015 and 2015/2016 are presented in Table 1. The study used 37 cowpea genotypes comprising 34 newly developed mutant lines, selected for their superior agronomic performance, and three parental checks (Bira, Nakare and Shindimba). The mutants were at the M6 generation in 2014/2015 and M7 in 2015/2016. Details of the genotypes are presented in Table 2.

2.2. Experimental design and data collection

The experiments were performed using a randomized complete block design with three replications. Experimental units consisted of 8 rows of 4 m length with spacings of 20 cm within and 75 cm between rows. The crops were established under rainfed conditions with supplementary irrigation when required. Two middle rows (net plots) were harvested to estimate grain yield per plot, later converted to yield per hectare (t ha^{-1}). The outer rows were not used for yield estimation in order to control border effects and to minimize experimental error.

2.3. Data analysis

Grain yield data was subjected to a combined analysis of variance (ANOVA) using GenStat 18 statistical software [15]. The following AMMI model according to Gauch (16) was used for G × E and yield stability analyses based on the principal component analysis (PCA):

$$Y_{ge=}\ \mu + \alpha_g + \beta_e + \sum_{n=1}^{N} \lambda_n \Upsilon_{gn} \eta_{en+\theta_{ge}}$$

where Y_{ge} is the yield of genotype g in environment e, μ is the grand mean, α_g is the genotype mean deviation, β_e is the environment mean deviation, λ_n is the eigenvalue of the n^{th} principal component (PCA) axis, Υ_{gn} and η_{en} are the genotype and environmental PCA scores for the n^{th} PCA axis, and θ_{ge}, is the residual. The AMMI stability value (ASV) was calculated according to Purchase, Hatting and Van Deventer [17] as follows:

$$ASV = \sqrt{\left[\frac{IPCA1SS}{IPCA2SS}(IPCA1Score)\right]^2 + [IPCA2score]^2}$$

where SS is the sum of squares of the IPCAs and IPCA1 and IPCA2 are the first and second interaction principal component axes, respectively. Means of the genotypes were used for GGE biplot analysis.

3. Results

3.1. AMMI analysis

Mean yield for the studied traits varied widely, from 0.74 to 2.83 t ha^{-1}. Table 3 shows the mean grain yields (t ha^{-1}) of the

Please cite this article as: L. Horn, et al., Genotype-by-environment interaction for grain yield among novel cowpea (*Vigna unguiculata* L.) selections derived by gamma irradiat..., The Crop Journal (2017), https://doi.org/10.1016/j.cj.2017.10.002