

Evaluation of chickpea genotypes for tolerance to ascochyta blight

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Abstract

In Kenya dry highlands where wheat, maize, and barley are the main crop, chickpeas are considered as off-season crop (October-February) before the next cropping season. Thus these crops provide an alternative source of income to farmers. Chickpea introduction into these areas has not been adopted largely because of abiotic and biotic stresses. Ascochyta blight, a fungal disease, is one of the major hindrance to chickpea production, causing up to 100% yield loss under favorable climatic conditions in the study areas. Although the disease can be controlled by use of fungicides, host plant resistance is the cheaper approach and is ecologically sustainable. The objectives of this study were: to screen 25 chickpea genotypes for resistance to Ascochyta blight under controlled and field conditions. The field study was done in three sites: University of Eldoret Farm (LH3), Koibatek ATC (UM4) and Egerton University (LH2-LH3). The glasshouse experiment was laid in CRD design while the field experiments were laid out in RCBD design with three replications. Data on severity, initial plant stand, days to flowering, days to podding, days to maturity, plant height, spreading, hundred seed weight and grain yield were collected. Data were subjected to analysis of variance using GenStat release 14.0 and means separated using Duncan multiple range test comparisons at $\alpha = 0.05$. Test genotypes showed a significant differences ($P \leq 0.001$) in levels of resistance to Ascochyta blight attack. Genotypes Flip 94079c, Genesis 079, Genesis 090, Genesis Kalkee, Howard, Howzat, ICCV 98801, Sonali, PBA Striker, PBA Slasher, PBA Hattrick, Doolin, Thomas, Lyons, Jimbour, FlipperAmethyst, Kyabra, and Lyle showed a resistant reaction. Yorker showed moderate resistance while ICCV 00305, ICCV 00108, ICCV 92944, ICCV 95423 and ICCV 97105 were susceptible. Genotypes Jimbour, Yorker, Flip 94079c and ICCV98801 were found to be resistant, with stable grain yield and highly adaptable across the environments. Genotypes Howzat, Thomas, Sonali, Amethyst, Doolin, and Genesis 079 which were resistant to the disease but low yielding are recommended for further breeding to improve their grain yields. They are also candidates for chickpea breeding as sources of resistance to Ascochyta blight.

Keywords: Ascochyta blight, chickpeas, disease resistance, genotypes, growth parameters and genotype-interaction

Résumé

Dans les hautes terres arides du Kenya, où le blé, le maïs et l'orge sont la principale culture, les pois chiches sont considérés comme des cultures de contre-saison (octobre-février) avant la prochaine saison culturale. Ces cultures constituent donc une source alternative de revenus pour les agriculteurs. L'introduction de pois chiches dans ces zones n'a pas été largement adoptée à cause des stress abiotiques et biotiques. La brûlure ascochytiq ue, une maladie fongique, est l'un d'obstacles majeurs à la production de pois chiches, causant jusqu'à 100% de perte de rendement dans des conditions climatiques favorables dans les zones d'étude. Bien que la maladie puisse être contrôlée par l'utilisation de fongicides, la résistance des plantes hôtes est l'approche la moins coûteuse et est écologiquement durable. Les objectifs de cette étude étaient les suivants: cribler 25 génotypes de pois chiche pour la résistance à la brûlure ascochytiq ue dans des conditions contrôlées et sur le terrain. L'étude sur le terrain a été réalisée sur trois sites: Ferme de l'Université d'Eldoret (LH3), Koibatek ATC (UM4) et Université d'Egerton (LH2-LH3). L'expérience en serre a été conçue en dispositif complètement randomisé (CRD) tandis que les expériences sur le terrain ont été conçues en dispositif de blocs complets randomisés (RCBD) avec trois répétitions. Des données sur la sévérité, le peuplement initial de plantes, les jours de floraison précoce, les jours de formation des gousses précoces, les jours de maturité précoce, la hauteur de la plante, l'épandage, le poids de cent graines et le rendement en graines ont été collectées. Les données ont été soumises à une analyse de variance à l'aide de la version 14.0 de GenStat et les moyennes ont été séparées à l'aide de comparaisons de tests à plages multiples de Duncan à $\alpha = 0,05$. Les génotypes de test ont montré des différences significatives ($P \leq 0,001$) dans les niveaux de résistance à l'attaque de la brûlure ascochytiq ue. Les génotypes Flip 94079c, Genesis 079, Genesis 090, Genesis Kalkee, Howard, Howzat, ICCV 98801, Sonali, PBA Striker, PBA Slasher, PBA Hattrick, Doolin, Thomas, Lyon, Jimbour, FlipperAmethyst, Kyabra et Lyle ont montré une réaction résistante. Yorker a montré une résistance modérée alors que ICCV 00305, ICCV 00108, ICCV 92944, ICCV 95423 et ICCV 97105 étaient susceptible. Les génotypes Jimbour, Yorker, Flip 94079c et ICCV98801 se sont révélés résistants, avec un rendement en grains stable et hautement adaptable dans tous les environnements. Les génotypes Howzat, Thomas, Sonali, Amethyst, Doolin et Genesis 079 qui étaient résistants à la maladie mais à faible rendement sont recommandés pour une autre sélection afin d'améliorer leur rendement en grains. Ils sont également candidats à la sélection de pois chiches comme sources de résistance à la brûlure ascochytiq ue.

Mots clés: brûlure ascochytiq ue, pois chiches, résistance aux maladies, génotypes, paramètres de croissance et interaction-génotype

Introduction

Chickpea (*Cicer arietinum*) is an important legume crop in Eastern and Southern Africa, with Tanzania, Malawi, and Sudan being the leading producers (Kassie *et al.*, 2015). Recent findings show that East Africa has the highest yielding potential of chickpea ranging between 1.2-3.5 tons/ha, however, its production in Kenya over the years has reduced drastically with 252 tonnes in 2004 to 50 tonnes in 2013 (FAOSTAT, 2015). Regardless of being a new crop in Kenya, and currently adapted to varied agro-ecological zones throughout the country, their yields have remained much below the potential (Kimani *et al.*, 2015). This has been attributed to a series of abiotic and biotic constraints. Fungal diseases are considered the most serious biotic constraints, the most important

being Ascochyta blight (*Didymella rabiei*) complex wilt syndrome and botrytis grey mold, among others (Aslam *et al.*, 2014). Ascochyta blight is an important foliar disease of peas globally causing both grain yield and quality loss of up to 100%, resulting in considerable economic damage (Skoglund, 2011).

Development of host plant resistance as a component of integrated disease management is the cheapest, economic and the most favorable way of Ascochyta blight management. It is therefore important to select suitable genotypes based on yield components in relation to the most contributing trait to yield and resistance to diseases (Zafaranih, 2015). Thus, there is a need to evaluate elite chickpea germplasm for resistance against Ascochyta blight for adoption in the dry highlands of the country in order to be food secure. In this study, 25 chickpea genotypes were evaluated in dry highlands of North Rift Valley, Kenya with the aim of identifying genotypes that are high yielding and tolerant to Ascochyta blight. This will aid in future chickpea breeding programmes, thus stabilizing and raising productivity levels in the country.

Materials and Methods

The studies were done in the long rains (March-July) of 2015 and 2016. The glasshouse experiment was done at Egerton University while field experiments were carried out in three sites in the dry highlands of North Rift Valley, namely, Egerton University, Agricultural Training College Koibatek and the University of Eldoret Farm – Kenya.

Twenty-five chickpea varieties (with varied root traits, pod borer resistance and advanced breeding lines for yield) obtained from ICRISAT were evaluated in this study. The genotypes evaluated were; ICCV 00108, Yorker, Howard, ICCV 98801, PBA Hattrick, Jimbour, Flip 94 079c, Chania Desi 1 (ICCV 97105), Saina K1 (ICCV 95423), Genesis 079, PBA Slasher, Lyle, Doolin, Thomas, Lyons, ICCV 00305, Chania Desi 2 (ICCV 92944), Flipper, Genesis Kalkee, Sonali, Genesis 090, Amethyst, PBA Striker, Howzat and Kyabra.

The glasshouse experiment was laid out in a CRD design while field experiments were laid out in a RCBD design with three replications. Plants were spaced at 40 cm between rows and 10 cm within rows with plot sizes of 3 rows of 2 m each. Disease severity and incidence were recorded and genotypes grouped into three categories on the basis of disease response: resistant (1-3 rating), moderately resistant (4 –5 rating) and susceptible (6-9 rating).

In terms of data collection and analysis, five plants from the middle row of each plot at all the study sites were tagged randomly for evaluation and data on severity and yield components collected. The collected data were subjected to analysis of variance using Genstat release 14.0 and means separated using Duncan multiple range test comparisons at 5% level of significance.

Results and discussion

Reactions against Ascochyta blight. There was significant ($P \leq 0.001$) difference in Ascochyta blight disease severity levels among the test genotypes in the glasshouse experiment and in the three sites combined. ICCV 00108, ICCV 97105, ICCV 95423, ICCV 92944 and ICCV 00305 were rated highly susceptible to AB disease while Yorker showed some moderate resistance across the three sites. However, genotypes Amethyst, Flip 94079c, Flipper, Genesis Kalkee, HOWARD, ICCV 98801,

Jimbour, PBA Striker, Kyabra, Lyons, PBA Hattrick, Genesis 079 and Sonali were found to be resistant to *Ascochyta* blight disease (Table 1).

Table 1. Varying reactions of chickpea genotypes against *Ascochyta* blight under three field conditions in Kenya

Material Source	Disease reactions		
	Resistant (R)	Moderate resistance (MR)	Susceptible (S)
Egerton University	Doolin, Genesis 090, Howzat, PBA Slasher, Thomas, Amethyst, Flip 94079c, Lyle, Flipper, Genesis Kalkee, Howard, ICCV 98801, Jimbour, Kyabra, Lyons, PBA Hattrick, Sonali, PBA Striker, Thomas	Yorker	ICCV 97105, ICCV 95423, ICCV 92944, ICCV 00305, ICCV 00108

* Data based on results from three sites

Agronomic and morphological traits. There were significant genotype by site interaction ($P \leq 0.01$) for 100 seed weight, plant height and grain yield. Genotypes had low variation in initial plant stand, days to first podding and spreading ($P \leq 0.05$). Sites also differed significantly ($P \leq 0.001$) for most of the morphological traits measured with exception of days to first podding and spreading. Across the sites, each genotype responded differently under the disease pressure. PBA Hattrick and Thomas had high initial plant stand count per plot. ICCV 00108 recorded the highest severity levels while Doolin, Genesis 090, Howzat, PBA Slasher, and Thomas recorded the lowest severity levels.

Association among disease severity levels, growth parameters, and grain yields. Disease severity levels of the genotypes had a negative correlation with several growth parameters such as initial plant stand, days to 50% flowering, days to first podding, days to 50% podding, plant height and hundred seed weight. There was also a negative correlation between disease severity and grain yield among the test genotypes (Table 2).

Twenty chickpea genotypes were found to be resistant and moderately resistant to *Ascochyta* blight across the three study sites, unlike in the glasshouse experiment. Atik *et al.* (2011) also found out that a number of genotypes were resistant at all the growth stages against *Ascochyta* blight under field conditions. Plant age had a profound effect on the susceptibility/resistance of the genotypes in the glasshouse and field experiment. Blight incidence and severity were low in seedling stage and high at podding and maturity stages indicating that disease resistance decreases with plant age. There was a significant ($P \leq 0.001$) difference in severity levels across the sites across plant growth stages and sites. This is attributed to conducive environmental conditions favoring disease development. Amin and Melkamu (2014) noted that disease severity increases with increase in relative humidity, cloudiness and prolonged wet weather favours development of *Ascochyta* blight epidemics.

Table 2. Correlation analysis for Ascochyta blight disease severity levels, growth parameters, and grain yields

	SEVERITY	IPS	D50F	D1STP	D50P	SPREADING	PH	NSPP	100SW
IPS	-0.79****								
D50F	-0.31ns	0.54****							
D1STP	-0.44***	0.72****	0.78****						
D50P	-0.64***	0.72****	0.50***	0.70****					
SPREADING	0.80****	-0.92****	0.05ns	-0.51***	-0.61****				
PH	-0.83****	0.72****	0.27ns	0.36*	0.58****	-0.69****			
NSPP	0.35*	-0.69***	-0.50***	-0.64****	-0.49***	0.60****	-0.23ns		
100SW	-0.84****	0.93****	0.39*	0.54****	0.70****	-0.93****	0.73****	-0.55****	
GY	-0.68****	0.74****	0.22ns	0.40*	0.52****	-0.73****	0.69****	-0.27ns	0.73****

Key: IPS - Initial plant stand, D50F - Days to 50% flowering, D1stP - Days to first podding, D50P - Days to 50% podding, PH - Plant height, NSPP - Number of seed per pod, 100sw - Hundred seed weight, GY - Grain yield, * significant at 0.05, ** significant at 0.01, *** significant at 0.001, **** significant at 0.0001, ns – not significant

Most plant agronomic traits, i.e., plant height, spreading, hundred seed weight and grain yield had significant in genotype-environment interaction at ($P \leq 0.01$). Susceptible genotypes had lower or no yields as the disease caused chlorosis and premature abscission with increased incidence and severity levels. This agrees with the report by Atik *et al.* (2013) who reported that low yield as Ascochyta blight disease caused drooping of apical stems, defoliation, breaking and drying of branches, which in turn, reduced crop yield. The warm and drier conditions in Koibatek ATC located in upper midlands (UM4) favored higher grain yield than University of Eldoret Farm and Egerton University which are cold and wet. Some of these genotypes, i.e., Jimbour, Doolin, Thomas, Genesis 090 and Yorker had high seed weight, grain yield and low disease severity levels. These are possible candidates for adoption by farmers. Yield parameters such as initial plant stand, plant height, hundred seed weight and days to podding had a positive correlation with grain yield performance. Breeders aiming at increasing yields in chickpea should target these yield-related components. Disease severity, however, had a negative correlation with grain yield indicating the need to breed for resistance to the disease.

Conclusions

Resistant genotypes had better grain yields and should be promoted for adoption in the dry highlands of North Rift Valley of Kenya. Genotypes Howzat, Thomas, Sonali, Amethyst, Doolin, and Genesis 079 were resistant but low yielding. Genotypes Jimbour, Yorker, Flip 94079c and ICCV 98801 had stable grain yield and were resistant across the environments (University of Eldoret, Koibatek ATC and Egerton University) and should be advanced to on-farm and multi-location trails for possible release.

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