

**MAKERERE UNIVERSITY**

**ENHANCING GENETIC RESISTANCE TO SOYBEAN RUST DISEASE**

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## ABSTRACT

Soybean (*Glycine max* L.) is increasingly playing an important nutritive role in the food and feed industry in most countries. However, the crop is currently threatened by soybean rust disease (*Phakopsora pachyrhizi*). The rapid spread of soybean rust, coupled with its potential for causing severe yield losses, makes it an important disease in soybean growing countries. A major impediment to breeding for resistance to soybean rust is the lack of stable sources of resistance to the highly variable pathogen in different soybean producing areas.

Therefore the study sought to assess comparative virulence of five diverse field isolates from major soybean producing areas in Uganda, and identify soybean lines with resistance to isolates of soybean rust in seedling and adult plants under screen house and field conditions, respectively. When inoculated with the five field isolates, all twelve lines evaluated showed diverse and mixed reactions, suggesting each location differed in soybean rust races and/or virulence. Experimental sites where many diverse soybean lines are grown every year had the greatest diversity of soybean rust. The effectiveness of specific resistance genes was restricted to certain locations and gene *Rpp2* previously resistant was ineffective producing a susceptible tan reaction at the seedling stage. A positive correlation between mean lesion density at the seedling stage and adult plant severity indicated that using field isolates to screen for seedling resistance can be a useful breeding approach to extrapolate resistance in adult plants. Overall, these results emphasise the relevance of using field isolates from the target areas to evaluate lines for soybean rust resistance. Soybean genotypes Maksoy 3N, UG5, G7955 and GC00138-29 were identified as ideal sources resistance to soybean rust that can be used across the selected sites.

The impact of soybean rust (*Phakopsora pachyrhizi*) on soybean yields has been extensively studied. However, few studies have evaluated early generation segregating material under field conditions for soybean rust resistance to facilitate selection. The objective of the second study was to estimate combining abilities for soybean rust resistance in the F<sub>2</sub> and F<sub>3</sub> populations at MUARIK and F<sub>3</sub> populations simultaneously across five locations. Combining ability for soybean rust resistance was estimated from a half diallel cross of eight soybean lines using disease severity and sporulation rates as indices for resistance. A consistent contribution of additive gene action was observed at MUARIK across F<sub>2</sub> and F<sub>3</sub> despite high environment contribution to both severity and sporulation rate. The simultaneous evaluation of F<sub>3</sub> populations in five diverse locations produced similar results with significant GCA effects for both traits. There were, however, greater genotypic effects compared to environmental effects for soybean rust severity and sporulation across the five test environments, although genetic systems of severity and sporulation rate acted independently. Additive and complementary additive gene effects were the most common form of GCA controlling resistance. Specific combining ability did not always contribute to soybean rust resistance. The positive correlation between parental severity, sporulation rate performance and GCA estimates suggested that selection of parents for soybean rust resistance breeding can be based on parental performance. Parental line UG 5 was the most outstanding producing the greatest number of resistant populations. This study underscores the importance of additive gene effects in the control of soybean rust severity and sporulation rate.

The problem of soybean rust is compounded by its high pathogenic variability which overcomes single gene resistance present in most cultivars. Few studies have, however, been undertaken to use mapped simple sequence repeat markers for gene pyramiding to enhance rust resistance. The

study validated use of identified simple sequence repeat markers for gene pyramiding and determined the most effective pair wise gene combination for three independent resistance genes; *Rpp2*, *Rpp3* and *Rpp4*. Markers Satt460 and AF162283 were polymorphic for three resistance genes between the parents and therefore used in F<sub>2</sub> and F<sub>2:3</sub> family selection. In the F<sub>2</sub> generation, soybean plants (homozygous or heterozygous at both loci) with two gene combinations had relatively lower disease severity and sporulation than the parents suggesting complementary epistatic gene action for resistance. Homozygous F<sub>2:3</sub> families similarly showed lower severity, lesion density and sporulation. Gene *Rpp3* interacted and contributed positively to resistance with various genetic backgrounds for most parameters measured compared to *Rpp2* and *Rpp4* resistance genes. Overall, the results suggest that marker gene pyramiding is feasible and can substantially increase resistance to soybean rust through reduced severity and reduced frequency of uredinia with sporulating lesions.

High potential genotypes UG5, Maksoy 3N, G7955 and GC00138-29 are ideal sources of soybean rust resistance in Uganda. These findings also imply that breeding for soybean rust has to focus on other strategies such as partial resistance and tolerance that are polygenic and have broad ASR effectiveness.