



Pyramiding Two Different Sources Of Aphid Resistance Genes Into A Farmers' Preferred Cowpea Variety Using Marker Assisted Backcrossing

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Abstract:

The cowpea aphid (*Aphis cracivora*) is a cosmopolitan insect pest that causes economic damage wherever cowpea is cultivated. Although the pest persists at all the growth stages of the crop, in West Africa, aphids are the only major insect pest which farmers regularly control at the vegetative stage. Thus, deploying aphid resistant cowpea varieties can reduce farmers expenditure on insecticide. The availability of different biotypes of the pest and reports of resistance breakdown necessitates the pyramiding of sources of aphid resistance to develop a more robust and durable resistance. The two aphid resistance genes sourced from SARC-1-57-2 and IT97K-556-6 were stacked into a farmer preferred cowpea variety Zaayura using marker assisted backcrossing. Zaayura had previously been improved with the SARC-1-57-2 aphid resistance source and released as Zaayura Pali. An SSR marker, CP171/172 and an allele - specific SNP marker, SNP1_0912, were used for the foreground selection for the SARC-1-57-2 and IT97K-556-6 aphid resistance genes, respectively. A stepwise backcross approach was used to introgress the Qac-vu7.1 aphid resistance QTL from IT97K-556-6 was introgressed into Zaayura to BC4F1 using the SNP1_0912 as a foreground marker coupled with intermittent screening under artificial aphid infestation. Three heterozygous BC4F1 of Zaayura/IT97K-556-6 were intercrossed to Zaayura Pali to develop intercross F1. Three true ICF1 hybrids were advanced to ICF2 through selfing. Five (5) out of the 48 ICF2 plants that were genotyped with the foreground markers had the two aphid resistance genes fixed in the double homozygous state. Of the 192 allele -specific markers screened, 47 polymorphic markers were identified and used for the iii-background selection and analysis of the pyramided lines. The recurrent parent genome recovery ranged from

72 – 93.8%. ICF2_Zaa/556/SARC-P6 had the highest recurrent parent genome and the least percentage heterozygosity among the 5 improved lines. Seeds of these lines are being multiplied for field testing and further evaluation.

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