Mode of inheritance and genetic relatedness of new sources of cowpea resistance found in Ghana.

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Project overview

A screen for seedling reaction to aphid infestation conducted at CSIR-SARI previously identified the five lines IT97K-556-6, KvX-295-2-124-99, 58-77, CB27 and SARC1-57-2 as potential donors of resistance. Our aim was to determine the mode of inheritance of the aphid resistance carried by CB27, KvX-295-2-124-99 and 58-77 and to define the allelic relationship of the genes responsible with those present in SARC1-57-2 and IT99K-556-6. F2:3 populations were developed from crosses between KvX-295-2-124-99, 58-77 and CB27 and the susceptible variety Apagbaala, with the resistant varieties SARC 1-57-2 and IT99K-556-6, and with one another. The populations were subjected to artificial aphid infestation and were also genotyped using a number of molecular markers. Progenies were scored as homozygous resistant, heterozygous, or susceptible. A chi-squared goodness of fit test was used to analyse segregation ratios. The analysis demonstrated that the aphid resistance present in KvX-295-2-124-99, 58-77 and CB27 is controlled by a single dominant gene. The genes controlling aphid resistance in CB27, SARC1-57-2 and KvX-295-2-124-99 are allelic with one another but are non-allelic to the genes present in 58-77 and IT99K-556-6. The latter two varieties carry the same gene. For this work Ms Mensah was awarded her MSc in 2019.

Young plants of IT97K-556-6, SARC-57-2 and Apagbaala showing symptoms of aphid damage (i); segregation of aphid resistance in F2:3 families derived from the cross KvX-295-2-124-99 x 58-77, indicating that these two varieties carry a different gene for resistance (ii); Ms Mensah tagging plants of her mapping population (iii).