

Inheritance of resistance to the cowpea aphid in cowpea

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Summary. Inheritance of resistance to cowpea aphid, Aphis craccivora Koch, in three resistant cultivars of cowpea, Vigna unguiculata (L.) Walp, was studied. The parents, F1 and F2 population were grown in an insectproof screenhouse. Each 3-day-old seedling was infested with 10 apterous adult aphids. Seedling reaction was recorded when the susceptible check was killed. The segregation data revealed that the resistance of ICV11 and TVU310 is governed by single dominant genes. All the F_2 seedlings of the cross ICV10×TVU310 were resistant, indicating that they have the same gene for resistance. However, the F_2 populations from the crosses ICV10×ICV11 and ICV11×TVU310 segregated in a ratio of 15:1, indicating that the dominant genes in ICV11 and TVU310 are non-allelic and independent of each other. The resistance gene of ICV10 and TVU310 is designated as Ac_1 and that of ICV11 as Ac_2 .

Key words: Aphis craccivora Koch – Resistance genetics – Insect resistance – Vigna unguiculata (L.) Walp.

Introduction

The distribution of the cowpea aphid, *Aphis craccivora* Koch has been reported by Singh and van Emden (1979) to be worldwide. Damage by the aphid is more severe in areas with marginal rainfall. The cowpea aphid also transmits numerous virus diseases in a range of host plants (Dubey and Nene 1974). The most serious virus of cowpea transmitted by the aphid is aphid-borne mosaic virus (CAMV).

The cowpea aphid is an important pest at the flowering stage in Kenya (Muruli et al. 1980). It is known to achieve its peak population density at the pod formation stage in Assam (Saharia 1980). Heavy aphid population may result in the death of the plant and thus complete failure of the crop. Singh and Allen (1980) estimated yield losses of 20% to 40% in cowpea due to *A. craccivora* infestation in Asian continent and up to 35% in Africa.

Screening work in Southeast India (Chari et al. 1976) and Nigeria (Singh 1979) led to identification of several sources of resistance to *A. craccivora*. Recently, Pathak (1983) reported high levels of resistance in two cowpea cultivars, ICV11 and ICV12, obtained by induced mutations. In the available literature on the genetics of resistance to cowpea aphic, only two reports are known. International Institute of Tropical Agriculture (IITA) (1982) reported resistance as dominant to susceptibility, and F_2 population segregated in a ratio of 3 resistant: 1 susceptible. Similar results were reported at the International Centre of Insect Physiology and Ecology (ICIPE) (Pathak 1984).

Three biotypes of *A. craccivora* have been identified; biotypes A and B occur in Nigeria and biotype K in Upper Volta (IITA 1981). This study was undertaken to determine the mode of inheritance of resistance to *Aphis craccivora* in a local cultivar (ICV10), an exotic cultivar (TVU310) and a mutant cultivar (ICV11).

Materials and methods

Three resistant (ICV10, ICV11 and TVU310) and one susceptible (ICV1) cultivars were utilized in the study. Resistant cultivars ICV11 and TVU310 were crossed with susceptible cultivar ICV1 and the F_1 and F_2 populations were evaluated for reaction to the aphid. A backcross (Bc₁) population of the cross ICV1×ICV11 was also studied. Three crosses amongst the three resistant cultivars (Table 1) were also studied. Crosses were made in an insect-proof screenhouse at the

| Cross/progeny | No. of plants | | $\chi^{2}3:1 \text{ or}$ | Р | Remarks |
|------------------|---------------|-------------|---------------------------------------|-------------|------------------------|
| | Resistant | Susceptible | 1:1 or 15:1 | | |
| 1. ICV 1 | | 23 | · · · · · · · · · · · · · · · · · · · | | |
| TVU 310 | 23 | - | | | |
| \mathbf{F}_{1} | 24 | _ | | | |
| F ₂ | 112 | 43 | 0.099 | 0.80-0.95 | Good fit to 3:1 ratio |
| 2. ICV 1 | _ | 20 | | | |
| ICV 11 | 22 | _ | | | |
| F ₁ | 21 | - | | | |
| F_2 | 140 | 49 | 0.087 | 0.70-0.80 | Good fit to 3:1 ratio |
| Back-cross | 10 | 11 | 0.048 | 0.80-0.90 | Good fit to 1:1 ratio |
| 3. ICV 10 | 29 | _ | | | |
| ICV 11 | 24 | | | | |
| F ₁ | 9 | _ | | | |
| F ₂ | 179 | 12 | 0.00035 | 0.98-0.99 | Good fit to 15:1 ratio |
| 4. ICV 11 | 21 | | | | |
| TVU 310 | 20 | _ | | | |
| F ₁ | 21 | | | | |
| F_2 | 73 | 7 | 0.853 | 0.30 - 0.50 | Good fit to 15:1 ratio |
| 5. ICV 10 | 24 | _ | | | |
| TVU 310 | 22 | - | | | |
| F ₁ | 20 | | | | |
| F_2 | 75 | | | | No segregation |

Table 1. Segregation ratios in cowpea for resistance to the cowpea aphid, Aphis craccivora Koch

International Centre of Insect Physiology and Ecology (ICIPE), Mbita Point Field Station, South Nyanza, Kenya.

The F₁, F₂ and backcross populations, and the parents were planted in the screenhouse on a well prepared and irrigated soil bed to ensure uniform germination. Nitrogenous fertilizer at the rate of 20 kg N/ha was applied before planting. One row each of parents F_1 and Bc_1 and eight rows each of the F₂ were planted on 14th May 1985. Each row contained 25 plants with 20 cm between rows and 10 cm between plants in a row. The F_2 of the cross ICV11×TVU310 contained five rows while the cross ICV10×TVU310 contained four. The number of rows planted depended upon the availability of seeds. Aphids were collected from cowpea fields and cultured on potted cowpea plants in the screenhouse. Then 3-day old seedlings were infested with 10 apterous adult aphids per seedling using a camel hair-brush. The seedling reaction was recorded 10 days after infestation, when the seedlings in the susceptible rows were dead or seriously injured. Counts of susceptible (dead) and resistant (surviving) seedlings in each progeny were taken.

Results and discussion

The F_1 of all the crosses were resistant, indicating complete dominance of resistance. The segregation ratio in the F_2 populations of the two crosses involving the susceptible cultivar, ICV1, and resistant parents, TVU310 and ICV11 gave a good fit to the 3 resistant: I susceptible ratio expected for a single dominant gene control (Table 1). These results were further confirmed by the good fit to the 1 resistant: I susceptible ratio observed in the backcross population ICV1×(ICV1× ICV11). The F_2 populations of the crosses between resistant parents, ICV10×ICV11 and ICV11×TVU310 segregated in a ratio of 15 resistant: 1 susceptible (Table 1). These results indicate that the resistance genes in these parents are non-allelic. All the F_2 seedlings of the cross ICV10×TVU310 were resistant, indicating that the resistance in these parents is governed by the same gene.

The resistance gene in the cultivars ICV10 and TVU310 is designated Ac_1 (*Aphis craccivora* resistance) and that of ICV11 is designated Ac_2 . The resistance gene Ac_2 found in ICV11 is the result of induced mutation in the susceptible cultivar ICV1 (Pathak 1983). Among the materials used in the present study, resistant cultivar ICV10, TVU310 or ICV11 may be utilized in a breeding programme to develop resistant varieties with acceptable agronomic characters.

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