

Genetics of gall midge (*Orseolia oryzae* Wood Mason) resistance in some new donors of rice (*Oryza sativa* L.)

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SUMMARY

The present study was undertaken with the objectives to study inheritance of gall midge resistance in some new donors of rice and to study the allelic relationships of gene(s) for gall midge resistance possessed by them in context of already known genes. Inheritance study revealed, presence of single dominant gene for gall midge resistance in five new donors, INRC 202, Tellarigarikasunjavari, ARC 15831, JGL 384 and Bhumansan. Allelic study revealed that the resistant gene present in donor ARC 15831 was allelic to the *Gm 2* gene present in differential Phalguna.

Key words : Rice, Gall midge, Inheritance of resistance, Allelic relationship.

Rice (*Oryza sativa* L.) is the principle food crop of more than half of the world's population. It is grown in 115 countries over an area of 1.5 billion hectares. In Asia alone 90% of the world's rice is produced and consumed. Rice plant is the host of more than 85 insects and diseases. Several studies have reported major yield losses to rice crop by insect pest infestation. Among the various insects attacking rice, the dipteran pest gall midge (*Orseolia oryzae* Wood Mason) alone is responsible for loss of more than US \$ 550 million annually (Herdt, 1991). Based on estimates available from eastern (Widowsky and O' Toole, 1996) and southern states of India (Ramaswamy and Jatileksono, 1996) gall midge damage causes an annual yield loss of about 477 thousand tonnes of grain amounting to Rs. 330 crores or US \$ 80 million.

Existence of two species of gall midge *i.e.* Asian rice gall midge (*Orseolia oryzae* Wood Mason) and African rice gall midge (*Orseolia oryzivora* Harris and Gagne) has been reported (Ukwungwu and Joshi, 1992; Taylor *et al.*, 1995).

Formation of "silver shoot", clustering of leaf blade at flowering, infestation of terminal shoot apices, tender grains in panicle just at flowering etc are some of the characteristic symptoms of the gall midge (*Orseolia oryzae* Wood Mason) (Chiu Shin foon, 1980; Rajamani *et al.*, 1979).

Insect being endo-parasitic, chemical control has not been found very effective. Therefore, developing rice varieties with in-built resistance to gall midge is one of the most effective way of controlling this pest. The success of resistance breeding programme lies in the identification of diverse sources of resistance and sound knowledge of genetic behavior of resistant gene(s)

present in these donors. This enables the breeder to systematically handle the segregating generations.

Emergence of new biotypes enables the insect to overcome the resistance of existing varieties with particular source of resistance. The occurrence of biotypes in gall midge was first suspected by Shastry *et al.* (1972), has been confirmed now. Six biotypes of gall midge are known to exist in different parts of India. In order to efficiently overcome the threat of emergence of new biotypes, it is essential for the breeder to identify as many non-allelic genes as may be possible and use them under various combinations as gene pyramids whenever necessary.

MATERIALS AND METHODS

The study was carried out at the Research farm of Indira Gandhi Agricultural University, Raipur (Chhattisgarh) during *kharif* 2001, *rabi* 2001, 2002 and *kharif* 2002.

The experimental material consisted of 16 genotypes including five new donors (INRC 202, Tellarigarikasunjavari, ARC 15831, JGL 384 and Bhumansan), eight differentials (Samridhi, Phalguna, RP 2068-18-3-5, Abhaya, ARC 5984, RP 2333-156-8, Jhitpiti and Madhuri line 9) with known genes for gall midge resistance, three known susceptible lines (Kranti, TN 1 and Annada) and F_1 and F_2 population of crosses between five new donors with susceptible lines as well as with differentials possessing the known genes for gall midge resistance.

Parental strains included in the study were screened for gall midge infestation during *kharif* 2001 and also during *kharif* 2002 along with F_1 and F_2 populations. Parents and F_1 plants of each cross were grown in single rows. F_2 populations were grown family wise as a produce

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