

Genetic analysis of Southern corn rust resistance (*Puccinia polysora* Underw.) in maize

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Maize (*Zea Mays* L.) is prone to as many as 112 diseases in different parts of the world, incited by fungi, bacteria, viruses, and nematodes, leading to extensive damage to the crop. In India, about 61 diseases have been reported to affect the maize cultivation, which leads to reduction in the yield and quality of the produce [1]. The foliar diseases like *Turcicum* leaf blight, *Maydis* leaf blight, common rust, southern corn rust (*Polysora* rust) and Northern leaf blight are more important [2]. The southern rust caused by *Puccinia polysora* Underw. is most important causing an estimated yield losses of 45-50% [3]. *Polysora* rust is becoming a major threat to maize crop in recent years, especially in southern Karnataka and adjoining states like Aridhra Pradesh and Tamil Nadu. Thus, there is an urgent need to identify sources of resistance and understand the inheritance pattern of resistance to *Polysora* rust of maize for initiating effective breeding programme.

One hundred thirty-four inbred lines along with two checks maintained at Agricultural Research Station, Naganahally, Mysore, Karnataka were screened in the National Screening Nursery during 2007 and 2008 *Kharif* for identifying resistance sources. Each genotype was planted in two rows of five meter row length with a spacing of 70 cm between plants and replicated twice in Random Complete Block Design. Artificial epiphytotic condition for uniform disease development was created. Inoculation for *Polysora* rust was made at 6-8 leaf stage by applying at a spore suspension of 50,000 uredinospores/ml in the late afternoon. In addition, two lines of susceptible maize inbred line NAI-124 was sown as border rows around the screening plots to spread the disease. The disease severity of each genotype was averaged to calculate the mean disease severity. The genotypes were classified according to their disease

reaction as resistant (0-10%), moderately resistant (11-25%) and susceptible (26-100%).

For unraveling the genetics of resistance, the experimental material consisted of three *Polysora* rust resistant inbred lines (NAI-137, SKV-50, NAI-142) and one susceptible inbred line (NAI-124). The four selected lines were sown during *kharif* season of 2008. The crosses were made in all possible combinations. The parents and all the F_1 s were sown in Randomized Complete Block Design with three replications during *Kharif* 2009. Each treatment was sown in two rows of 4m length with a spacing of 60cm between rows and 20cm between plants. Artificial epiphytotic condition for uniform disease development was created as described above. The *Polysora* rust severity data was recorded on individual plants at dough stage on PLAC basis [4], and subjected for diallel analysis (Model I and Method I) [5]. Out of 134 inbred lines tested, 78 showed resistant reaction, 39 were moderately resistant and 17 were susceptible. The reaction of genotypes to *Polysora* rust infection was consistent over two years. Several workers also have reported resistance sources to *Polysora* rust [6-8]. The variances due to GCA as well as SCA were highly significant for disease severity and the estimates of SCA were higher than GCA. The ratio of GCA and SCA variance indicated the importance of both additive and non-additive types of gene action involved in the inheritance of this character. However, non-additive gene effects seemed to be more important than additive ones. Earlier reports [8-11] revealed the presence of single dominant, resistant gene whereas, Paterniani *et al.* [7] reported the predominance of additive gene action with high heritability. The resistance in NAI-137, SKV-50 and NA1-142 will be effective in hybrid combination (F_1 progeny) and, thus, probably has higher value in

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commercial maize.

The general combining ability (GCA) effects revealed that the resistant genotypes NAI-142 (-10.31), NAI-137 (-10.31) and SKV-50 (-10.31) recorded GCA effects in desirable direction (Table 1) while the susceptible genotype NAI-124(30.94) had GCA effect in undesirable direction. Shieh *et al.* [12] also reported high general combining ability in resistant parents. The SCA effects of six crosses in respect of disease severity are presented in Table 2. All the six crosses showed significant SCA effects and three crosses recorded highly significant SCA effects in undesirable direction for disease severity. The resistant parents NAI-142, NAI-137 and SKV-50 recorded negative and significant GCA effects and it is a desired feature in disease resistance breeding. Whereas, the susceptible parent with positive and significant GCA effect appeared to favour disease development. The six crosses showed significant SCA effect for disease severity. The reciprocal crosses NAI-124 x NAI-142, NAI-124 x NAI-137 and SKV-50 x NAI-124 exhibited significant reciprocal differences there by indicating importance of cytoplasmic effects in governing resistance to *Polysora* rust (Table 2). Preponderance of non-additive genetic variance reflected or, the utility

Table 1. Estimates of general combining ability (gca) effects of 4 parents for disease severity in a 4x4 diallel study of maize.

Parents	Disease severity
NAI-142	-10.31**
NAT-137	-10.31**
NAI-124	30.94**
SKV-50	-10.31**
CD at 5%	2.98
CD at 1%	4.12

**Significant at 1 per cent level.

Table 2. Estimates of specific combining ability and reciprocal effects for disease severity in a 4x4 diallel study of maize.

Crosses	SCA effects	Reciprocal effects
1x2 NAI-142xNAI-137	-0.94*	0.00
1x3 NAM42xNAI-124	0.31**	20.00**
1x4 NAI-142x SKV-50	-0.94*	0.00
2x3 NAI-137xNAI-124	0.31**	20.00**
2x4 NAI-137x SKV-50	-0.94*	0.00
3x4 NAI-1 24 x SKV-50	0.31**	-20.00**
CD at 5%	2.37	3.00
CD at 1%	3.28	4.15

*,**Significant at 5 and 1 per cent level, respectively.

of heterosis breeding method to develop resistant and high yielding hybrids and breeding efforts towards development of resistant inbreds needs to be cautious while initiating crossing of selected parents to generate desired recombination.

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