Breeding for yield stabilization in mustard (*Brassica juncea*) in India

Vibha Gupta, Centre for Genetic Manipulation of Crop Plants (CGMCP), University of Delhi South Campus, Benito Juarez Road, New Delhi – 110021, India

Contacts: vibg@hotmail.com, phone : 91-11-24115203

Oilseed mustard (*Brassica juncea*) is a major oilseed crop of the north western parts of India and is grown in around six million hectares of land mostly under rainfed and low irrigation conditions. The average national productivity range from 900-1150 kg/ha which is quite low when compared with the attainable yield of around 2200 kg/ha for pure line varieties and 2800 kg/ha for hybrids. One of the major bottlenecks in obtaining higher productivity is reduction in yields due to diseases and pests which cause damage to this crop at different stages and can result in yield losses ranging from 10-90%.

Of the various diseases, Alternaria blight (*Alternaria brassicae*) causes the maximum damage followed by white rust (*Albugo candida*), Stem rot (Sclerotinia sclerotiorum) and powdery mildew (*Erysiphe cruciferarum*). All the released Indian mustard varieties are susceltible to these diseases. There are no usable sources of resistance available for any of these diseases within *B. juncea* germplasm except for white rust, wherein some of the eastern european lines of *B. juncea* have been found to be resistant to white rust. Resistance to white rust is controlled by single dominant gene. Our studies have identified two independent loci conferring resistance to white rust in east european lines Donskaja and Heera. These resistant loci have been mapped by molecular markers to the linkage group A4 in Heera and A5 in Donskaja. These loci are currently being introgressed into different Indian pure line varieties and hybrids using marker assisted backcross breeding.

For Alternaria blight, a resistance source has been identified in Arabidopsis and a major QTL conferring resistance against Alternaria blight has been mapped to chromosome 2 of Arabidopsis. The region has been narrowed down to 1MB through fine mapping using molecular markers. Efforts are being made to identify the candidate gene in Arabidopsis through map base and transgenic approaches. Resistance gene will then be transferred to *Brassica juncea* to develop resistance to Alternaria. In the absence of any resistance source for resistance against stem rot transgenic approach is being followed.