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Identifying sources of resistance in wild Rice (*Oryza rufipogon*) derivatives for Rice Tungro Virus

D Krishnaveni, Asma Jabeen, V Hemant Kishore, D Ladhalakshmi, S K Mangrauthia, N Sarla and C N Neeraja
Directorate of Rice Research, India

Tungro virus disease is one of the most devastating and widespread diseases of rice. The disease occurs sporadically and causes significant grain yield losses. Tungro disease is reported to be caused by a combination of a spherical picornavirus (RTSV) and a bacilliform DNA pararetro virus (RTBV) and transmitted by green leafhopper (GLH) species *Nephotettix virescens*. As chemicals are not very effective for the control of tungro, host plant resistance has become the most important alternative for the management of this disease. Several donors are known for resistance to virus and vector. However, due to large scale cultivation of rice and shift in the vector population, several of these varieties have become susceptible to tungro as well as vector. For durable resistance to rice tungro disease, the resistance genes for virus and vector are required and many of the donors in cultivated species do not possess the same. Identification of novel genes introgressed from wild rice would help in developing durable and multiple pest resistant varieties to stabilize the rice production in the country. Wild species are an important reservoir of useful genes for tolerance to biotic and abiotic stresses. The wild species of rice such as *O. rufipogon*, *O. alta*, *O. grandiglumis*, *O. latifolia*, *O. glaberrima* and *O. officinalis* expressed high level of resistance to rice tungro disease but very limited efforts have been made to introgress the gene(s) into cultivated variety. In the present study, 120 introgression lines of BPT 5204 x *O. rufipogon* along with T(N)1 (Susceptible check) and Vikramarya (resistant check) were screened for the reaction to RTV in a glasshouse (28±2°C, >95% RH). Initially leafhoppers were provided with an acquisition feeding on RTV infected plants for 12h. Fifteen-day old seedlings were individually capped with a Mylar cage into which 2-3 viruliferous green leafhoppers were released for 24 h and the reaction was scored 15 days later. Tungro disease was recorded by adopting the standard evaluation method (IRRI 1996). Of these 120 lines screened, 6 lines scored as 3 (Resistant BILs # 4B, 5B, 6B, 24B, 25B and 84B), 30 lines scored as 5 (moderately resistant) and the rest of the lines were susceptible. The resistant lines scoring 3 in 1-9 scale were on par with the Vikramarya which scored 3. The allelic variability of the putative candidate gene identified through fine mapping of qRTV-7 was screened in the resistant and susceptible lines. The association of the identified candidate genes in the identified resistant lines will be discussed.

krishnavenid4@gmail.com