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Development of a genetic stock carrying multiple rust and powdery mildew resistance genes.

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Yellow or stripe rust is one of the important rust diseases causing considerable yield loss in India, particularly in the North Western Plains and the Northern and Southern Hill regions. The *T. turgidum* subsp. *dicocoides*-derived yellow rust-resistance gene *Yr15*, present in the Israeli stock V763-2312, confers high degree of resistance against widely prevalent races in India, especially races 78S84 (virulent on *Yr9*), 46S119 (virulent on PBW 343), and I (Southern Hills) (Vinod et al. 2006). The line V 763-2312 is used widely as donor for the development of resistance lines at IARI, Regional Station, Wellington, India. The Australian stock Cook, carrying the *Th. ponticum*-derived, linked genes *Lr19* + *Sr25* and *T. timopheevii*-derived, linked genes *Sr25* + *Pm6*, confers a high degree of resistance against most prevalent races of the leaf and stem rust and powdery mildew pathotypes in India, although a new pathotype is reported virulent on *Lr19*. This stock is used effectively in developing several NILs of popular Indian bread wheat cultivars at the IARI, Regional Station, Wellington.

The availability of stocks carrying these genes in a spring wheat background will immensely help the breeders develop lines resistant to these pests. V763-2312 was crossed to Cook and the line HW 6001, which is resistant to leaf, stem, and yellow rust and powdery mildew, was obtained at the BC_3F_4 stage. The gene *Sr36* confers a very high degree of resistance against the widely occurring stem rust pathotypes in India and also to race Ug99, which is virulent on *Sr31* and becoming a threat to wheat production worldwide. Therefore, this stock with resistance genes *Lr19* + *Sr25*, *Sr36* + *Pm6*, and *Yr15* developed at Wellington will be very useful for the breeders in wheat-improvement programs for developing resistant wheat cultivars (Table 1).

Table 1. Characteristics of parental lines and HW 6001, a genetic stock with multiple rust and powdery mildew resistance genes.

Line/Cultivar	Black rust	Brown rust	Yellow rust	Powdery mildew
V763-2312	R	80S	R	2 (0–4 scale)
Cook	R	R	F (undesignated)	R
New line HW 6001 with *Lr19*+*Sr25*, *Sr36*+*Pm6,* and *Yr15*	R	R	R	R

Reference.

Vinod, Sivasamy M, Prashar M, Menon MK, Sinha VC, and Tomar SMS. 2006. Evaluation of stripe rust resistance gene and transfer of *Yr15* into Indian wheats (*Triticum* species). Ind J Agric Sci *76*(6)362-6.

ITEMS FROM ITALY

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Molecular characterization of Italian soilborne cereal mosaic virus isolates.

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A mosaic disease of winter wheat was first described in the USA by McKinney in 1925 and subsequently in many other wheat-growing countries. Until recently, the disease was associated worldwide to wheat soil-borne mosaic virus (WSBMV). Results of sequence analysis by German and Chinese researchers, however, have prompted the International Committee on Taxonomy of Viruses to approve a taxonomic proposal to divide American, European, and Chinese isolates into different species within the genus *Furovirus*. The novel species have been denominated wheat soil-borne mosaic virus, cereal soilborne mosaic virus (CSBMV), and wheat Chinese mosaic virus (WCMV). On the basis of the new classification, the wheat mosaic disease is believed to be generally caused by WSBMV in United States, Brazil, and Canada; by CSBMV in Europe; and by WCMV in Asia. Twenty-four wheat samples showing typical Furovirus symptoms were collected from farmers in fields northern, central, and southern Italy to study their degree of genetic diversity. SsRNA was extracted, and the nucleotide sequence of a viral coat protein gene was determined for each sample. Nucleotide and amino-acid sequences alignment between the sequences obtained and the published RNA2 CP sequences of CSBMV, WSBMV, and WCMV isolates was generated applying the Clustal V method, and phylogenetic distance trees were constructed. Branching orders identified three major phylogenetic groups. In the first group, all the Italian isolates clustered closely together along with French, English, and German isolates (SBCMV species), whereas the second group included the American isolates, and the third ascribed the Asian isolates. Sequence data analysis revealed a high degree of genetic identity among Italian isolates (96.6 to 100.0 %) and between Italian isolates and SBCMV accessions from the United Kingdom, France, and Germany (88.7 to 99.6 %). Sequence divergences from 29.6 to 45.9 % were observed between Italian SBCMV isolates and SBWMV or CWMV isolates. Amino-acid sequence analysis of CP cistron revealed few nonspecific exchanges as well as a high degree of sequence identity (97.7 to 100%) among CSBMV isolates from Italy and other European countries. Amino-acid sequence similarity between Italian and Asian or American isolates ranged from 71.0 to 81.2 %. Eventhough all the Italian isolates so far analyzed belong to the novel CSBMV species, the presence of SBWMV in this country cannot be excluded.

Reaction of 34 durum wheat cultivars to cereal soilborne mosaic virus.

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Cereal soilborne mosaic virus (CSBMV) in Italy was first detected in the Po Valley in 1960 and is now known be widespread throughout most of the country, particularly in the northern and central regions. Thirty-four durum wheat cultivars were grown during 2006–07 in a field with SBCMV at Cadriano, near Bologna, and evaluated for resistance to CSBMV on the basis of symptom severity, DAS-ELISA readings, and agronomic performance. Seventeen of these cultivars (marked with asterisks in Table 1, p. 72) had never been tested for CSBMV resistance. The cultivars, planted 6 November, 2006, were grown in 10-m^2, solid-seeded plots distributed in the field according to a randomized block design