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Inheritance of resistance to cereal soilborne mosaic virus in a durum wheat population of lines derived from the cross ‘ Meridiano / Claudio’: results of a two-year study.

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Only a few of the nearly 200 durum wheat cultivars assayed in Italy for resistance to cereal soilborne mosaic virus (CSBMV) have shown to express very mild symptoms as well as a low virus concentration under severe disease pressure, and none of them has proven completely resistant to either CSBMV symptom expression or infection. Indeed, most of the cultivars tested so far exhibit a consistent array of intermediate reactions, suggesting that their reaction to CSBMV is governed by numerous genes.

Table 1. Symptom severity score frequency (%) distribution at four sampling dates in 2008 for 184 lines from a ‘Meridiano/Claudio’ population assayed during 2007–08 in a field with natural inoculum sources of CSBMV at Cadriano (Bologna), Italy.

Symptom severity interval	Frequency (%)			
	3 March	11 March	25 March	10 April
0.00–0.10	44.6	13.0	32.1	13.6
0.11–0.20	2.7	4.9	7.1	9.2
0.21–0.30	7.6	4.9	4.9	6.5
0.31–0.40	3.3	4.3	3.3	7.1
0.41–0.50	4.9	2.7	2.2	7.1
0.51–0.60	0.0	0.5	0.0	0.5
0.61–0.70	2.7	1.6	1.1	2.2
0.71–0.80	3.3	3.3	1.1	3.3
0.81–0.90	2.7	3.3	0.5	1.1
0.91–1.00	3.3	3.8	0.0	0.5
1.01–1.10	0.0	0.0	0.5	0.0
1.11–1.20	2.2	1.6	1.1	0.5
1.21–1.30	3.8	2.7	0.5	0.5
1.31–1.40	2.7	0.5	0.5	1.1
1.41–1.50	3.3	1.6	0.0	0.0
1.51–1.60	0.0	0.0	0.0	0.0
1.61–1.70	4.9	0.5	1.1	1.1
1.71–1.80	2.7	1.6	0.5	1.6
1.81–1.90	1.1	1.1	1.1	1.1
1.91–2.00	0.5	1.6	2.2	1.1
2.01–2.10	0.0	0.0	0.0	0.0
2.11–2.20	1.1	1.1	2.2	0.5
2.21–2.30	1.6	2.2	1.6	1.1
2.31–2.40	0.0	3.3	4.9	3.8
2.41–2.50	0.5	2.7	4.3	2.7
2.51–2.60	0.0	0.0	0.0	0.0
2.61–2.70	0.0	4.9	2.7	5.4
2.71–2.80	0.0	4.3	7.1	4.9
2.81–2.90	0.5	2.2	6.0	7.6
2.91–3.00	0.0	8.2	3.3	9.2
3.01–3.10	0.0	0.0	0.0	0.0
3.11–3.20	0.0	4.3	5.4	4.3
3.21–3.30	0.0	4.9	1.6	2.2
3.31–3.40	0.0	4.3	0.5	0.0
3.41–3.50	0.0	2.7	0.0	0.0
3.51–3.60	0.0	0.0	0.0	0.0
3.61–3.70	0.0	0.0	0.0	0.0
3.71–3.80	0.0	1.1	0.0	0.0
3.81–3.90	0.0	0.0	0.0	0.0
3.91–4.00	0.0	0.0	0.0	0.0

A population consisting of 184 RILs obtained via single-seed descent by Produttori Sementi Bologna S.p.A., Italy, from a cross between the durum wheat cultivars Meridiano (resistant) and Claudio (moderately susceptible) was assayed during 2006–07 and 2007–08 in a field with natural inoculum sources of CSBMV at Cadriano (Bologna). In each season, the RILs, parents, and the cultivar Grazia (a susceptible control inserted at regular intervals) were evaluated for resistance on the basis of symptomatology on four dates and ELISA absorbance on two dates. The plants were grown in 2.4-m^2, solid-seeded plots distributed according to a randomized block design with two replicates. Symptoms were scored on a 0–4 scale. Virus concentration was estimated by DAS-ELISA, on leaf samples. Grain yield, kernel weight, and test weight also were measured. The data from the first season were reported (Ann Wheat Newlsett 54:76), those obtained in the 2007–08 trial are summarized in Table 1 and

Table 2. Disease pressure was severe in both seasons, as testified by the mean symptom scores (3.8 in 2007 and 3.6 in 2008) recorded for Grazia at the time of maximum symptom expression.

Analysis of symptom score and ELISA absorbance frequency distributions indicated a complex inheritance of CSBMV-resistance, involving no less than four major genes, various modifiers, and a different timeline of the expression of resistance. Transgressive segregation, moreover, indicated that both the resistant (Meridiano) and the moderately susceptible parents (Claudio) contributed favorable alleles. Despite the favorable genes contributed by the latter cultivar, however, RILs completely resistant to CSBMV were not recovered. Indeed, leaf samples from all the RILs assayed were found ELISA-positive on at least one of the four collection dates, and all except two RILs gave ELISA-positive results on at least two dates. Moreover, the only RIL that remained symptom-free throughout the two seasons (i.e., on eight scoring dates) proved ELISA-positive on two out of collection dates. Eighteen of the 184 RILs assayed had overall mean symptom scores lower than the resistant parent; 15 of these RILs also showed lower overall mean ELISA absorbances; 9 produced higher grain yields; 10 showed higher test weights; and 11 showed higher kernel weights. Two RILs performed better than cultivar Meridiano in regard to all of the five parameters considered. Further trials are being set up to establish whether any of the above 18 RILs are indeed more resistant to CSBMV than cultivar Meridiano.

The RILs also were profiled with molecular markers (158 SSRs), and an association map spanning 2,050 cM was obtained. Preliminary results indicate that at least four QTL accounted for most of the phenotypic variation observed. A major QTL was associated to *Xwmc243* (distal telomeric region of chromosome arm 2BS),with the favorable allele contributed by Meridiano. The additional favorable QTL all located in the distal regions of the short and long arms of chromosome group 5 (particularly in chromosome 5A), were contributed by both parents. The QTL identified in the distal regions of 5AL (*Xwmc524*) and 5BL (*Xbarc243*) could represent the homoeologous copies of the major QTL identified in bread wheat (*Sbm1*).

Table 2. Symptom severity score frequency (%) distribution at four sampling dates in 2008 for 184 lines from a 'Meridiano/Claudio' population assayed during 2007–08 in a field with natural inoculum sources of CSBMV at Cadriano (Bologna), Italy.

Symptom severity interval	Frequency (%)	
	11 March	10 April
0.000–0.050	12.5	21.2
0.051–0.100	2.7	3.3
0.101–0.150	3.3	0.5
0.151–0.200	1.6	1.1
0.201–0.250	1.6	0.5
0.251–0.300	0.5	0.0
0.301–0.350	0.0	0.5
0.351–0.400	1.6	0.0
0.401–0.450	2.2	1.1
0.451–0.500	1.6	0.0
0.501–0.550	2.7	0.5
0.551–0.600	2.2	0.5
0.601–0.650	1.1	0.0
0.651–0.700	1.6	1.1
0.701–0.750	1.1	1.1
0.751–0.800	2.7	0.5
0.801–0.850	1.6	0.5
0.851–0.900	2.2	2.2
0.901–0.950	3.3	2.7
0.951–1.000	1.1	4.9
1.001–1.050	2.7	4.9
1.051–1.100	2.7	0.5
1.101–1.150	1.1	1.1
1.151–1.200	1.1	0.0
1.201–1.250	0.5	1.6
1.251–1.300	1.1	1.1
1.301–1.350	1.6	0.0
1.351–1.400	2.2	0.5
1.401–1.450	1.1	1.1
1.451–1.500	0.5	3.8
1.501–1.550	1.6	0.5
1.551–1.600	3.3	1.1
1.601–1.650	2.2	1.6
1.651–1.700	1.1	0.5
1.701–1.750	0.0	2.2
1.751–1.800	2.7	0.5
1.801–1.850	2.7	0.5
1.851–1.900	1.6	1.1
1.901–1.950	7.1	3.3
1.951–2.000	4.9	6.5
2.001–2.050	8.7	17.9
2.051–2.100	1.6	7.1
2,101–2,150	0.5	0.0

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ITEMS FROM JAPAN

NATIONAL INSTITUTE OF CROP SCIENCE (NICS) – NATIONAL AGRICULTURE AND FOOD RESEARCH ORGANIZATION (NARO)
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A possible transmission route for common wheat to Japan by the distribution of high-molecular-weight glutenin subunit Glu-D1f; two transmission routes to Japan, a direct route via China and one via the Korean peninsula.

Hiro Nakamura.

High-molecular-weight (HMW) glutenin subunits make up a group of seed endosperm proteins of common wheat. This group has been extensively explored during the past 25 years, and its members have an important effect on the quality of bread and/or noodles made from wheat. HMW glutenin alleles, such as *Glu-D1*, are of particular significance for Japanese bread and/or udon products (Nakamura and Fujimaki 2002). The *Glu-D1f* allele has a major influence on Japanese common wheat. It is thus important to understand the genetic diversity of this allele in noodle-culture zones such as Asia compared with bread-culture zones such as Europe, Canada, and the USA (Nakamura 2001, Nakamura and Fujimaki 2001). Common wheat (2n=42, AABBDD) is thought to have originated about 7,000 years ago in the Middle