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### *Genetic basis of stripe rust seedling resistance of Cappelle-Desprez and Mega.*

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**Introduction.** Wheat is grown under diverse environments and different agroecological systems. Apart from the inherent yield potential both biotic and abiotic stresses also determine the realized yield of cultivars. Stripe rust or yellow rust of wheat is an important cereal rust disease in many wheat-growing regions of the world, especially in areas with cool and wet environmental conditions (Roelfs et al. 1992). Rust diseases can be managed effectively and economically in a eco-friendly manner through cultivation of resistant cultivars (Line and Chen 1995). Understanding the genetic basis of resistance is of prime importance for their use in breeding program and not only generates information about the nature and number of genes in the donor parents but also helps in formulating efficient strategy for the incorporation of rust resistance. The present investigation was initiated with the objectives of understanding the genetic basis of stripe rust resistance of some the very important winter wheat cultivars. The results of genetic analysis of stripe rust resistance of Cappelle-Desprez and Mega is discussed.

**Materials and Methods.** The experimental material comprised Cappelle-Desprez, Mega, UP2338, and Agra Local and the $F_1$s, $F_2$, and $F_3$ families of the crosses between Agra Local and Cappelle Desprez and UP2338 and Mega. The $F_2$ population of the cross 'Cappelle-Desprez/Mega' was studied for an allelism test.

The $F_2$ and $F_3$ seedlings were raised in the aluminum bread trays consisting of ten rows; the seventh row of each tray a susceptible check (Agra Local). Inoculations were done as per Nayar et al. (1997). Seedlings were kept in a temperature-controlled glass house at 16°C. Infection types (IT) were recorded 14 days-after-inoculation and plants with zero fleck, fleck, or small pustules with a necrotic area classified as a resistant reaction and large pustules with or without chlorosis were considered susceptible. Pathotype 46S119 (avirulent on *Yr1, 5, 10, 15, 27, SP, Su,* and *CV* and virulent on *Yr2, 3, 4, 6, 7, 8, 9, 22, 23, 25*) was used for inheritance study. A chi square test was used to check the expected ratios in the segregating generations.

**Results and Discussion.** Seedling infection of the parents and other lines with known resistance genes (McIntosh et al. 1995, 2005; Nayar et al. 2001) are presented in Table 1. The IT of Mega was fleck, whereas Cappelle-Desprez varied from ;1 to ;2. UP2338 and Agra Local were fully susceptible (3+) against pathotype 46S119.

**Table 1.** Rust response of some *Yr* genes against yellow rust pathotypes. * adult-plant resistance based on terminal disease severity of the flag leaf under controlled condition; R = free from disease symptoms.

| | | Pathotype | | | | |
|---|---|---|---|---|---|---|
| Cultivar/Line | Genes | 47S102 | 70S69 | 46S119 | 78S84 | 46S119* |
| UP2338 | *Yr9* | 0; | 0; | 3+ | 3+ | 100S |
| Vilmorin23 | *Yr3* | 3+ | 3+ | 3+ | 3+ | 100S |
| Hybrid46 | *Yr3, Yr4* | 3C | 2+3- | 3C | ;- | 80S |
| Maris Huntsman | *Yr2, Yr3, Yr4, Yr13* | 0; | 0; | 0; | 3+ | 80S |
| Agra Local | — | 3+ | 3+ | 3+ | 3+ | 100S |
| **Cappelle-Desprez** | ***Yr3, Yr4, Yr16*** | **0;** | **;1–;2** | **;1–;2** | **;-** | **R** |
| **CD-Mara-2D** | ***Yr3, Yr4*** | **0;** | **;1–;2** | **;1–;2** | **0;** | **R** |
| Mega | *Yr3, Yr4, Yr12* | 0; | 0; | 0; | 0; | R |

The $F_1$s from 'UP2338/Mega' were susceptible. Forty-nine seedlings were resistant and 185 were susceptible, which was good fit to a 1 resistant : 3 susceptible ratio (P = 0.14) (Table 2). Among the 112 $F_3$ families, 61 segregated, 24 were homozygous susceptible, and 27 were homozygous resistant, which was good fit to a 1 resistant : 2 segregating : 1 susceptible ratio (P = 0.59). The $F_2$ and $F_3$ data were in compliance with a single recessive gene for resistance against pathotype 46S119.

**Table 2.** Segregation of the $F_2$ and $F_3$ generations in the seedling test against pathotype 46S119.

| | Number of seedlings/family | | | | | |
|---|---|---|---|---|---|---|
| Cross | Resistant | Segregating | Susceptible | Expected ratio | $X^2$ value | P value |
| Agra Local / Cappelle-Desprez | | | | | | |
| $F_2$ | 12 | | 216 | 1R:15S | 0.54 | 0.46 |
| $F_3$ | 11 | 105 | 99 | 1R:8SEG:7S | 0.76 | 0.68 |
| UP2338 / Mega | | | | | | |
| $F_2$ | 49 | | 185 | 1R:3S | 2.17 | 0.14 |
| $F_3$ | 27 | 61 | 24 | 1R:2SEG:1S | 1.05 | 0.59 |
| Mega / Cappelle-Desprez | | | | | | |
| $F_2$ | 158 | | 21 | 1R:0S | ∞ | <0.0 |

The $F_1$s of the cross between Agra Local and Cappelle-Desprez were susceptible. In the $F_2$, 12 seedlings were resistant and 216 were susceptible, which fit a 1 resistant : 15 susceptible ratio (P = 0.46) (Table 2). In the $F_3$ families, 105 segregated, 99 were homozygous susceptible, and 11 were homozygous resistant (Table 2). The $F_3$ family segregation was good fit to 1 resistant: 8 segregating : 7 susceptible ratio (P = 0.68). The $F_2$ and $F_3$ data indicated presence of two recessive genes for resistance to pathotype 46S119. The $F_2$ population of the cross 'Cappelle-Desprez/Mega' segregated, which confirmed that different genes were involved in the resistance against pathotype 46S119 in these cultivars.

The $F_2$ segregation and the $F_3$ family analysis confirmed presence of a single recessive gene in Mega for stripe rust resistance against the pathotype 46S119. Although the $F_2$ and $F_3$ data indicated that two recessive genes governed resistance to pathotype 46S119 in Cappelle-Desprez, we could not be explained why immune-type (seedling reaction 0;) lines were recovered in the $F_3$ and other advanced generations not only from the cross 'Agra Local/Cappelle-Desprez' but also from 'UP238/Cappelle-Desprez' (data not presented). Cappelle-Desprez may have suppressors of seedling resistance. Furthermore, why the seedlings of Cappelle-Desprez showed a high infection type (;2) and the adult plants were completely devoid of disease symptoms is difficult to explain. Obviously, it is not due to *Yr16,* because the seedling and adult-plant reaction of Cappelle-Desprez and the Cappelle-Desprez-Mara 2D substitution line were identical. Adult-plant resistance genes other than *Yr16* or suppressors of seedling resistance may be present. Either of these possibilities can not be ruled out from this study. The genes governing resistance in Mega and Cappelle-Desprez against pathotype 46S119 are likely to be different from the other documented genes in these cultivars, namely *Yr3a* and *Yr4a* in Cappelle-Desprez and *Yr3, Yr4*, and *Yr12* in Mega (McIntosh et al. 1995), because other cultivars/lines carrying *Yr3a*, *Yr4a,* and *Yr12* were susceptible to pathotype 46S119 (Table 1, p. 64).

In addition to a durable, adult-plant stripe rust-resistance gene (Johnson 1984) and *Yr3a* and *Yr4a*, Cappelle-Desprez also possesses additional seedling-resistance genes against the Indian stripe rust pathotype 46S119. Allelism tests and gene action clearly demonstrated that the resistance genes in Mega and Cappelle-Desprez are different. No reports of effective seedling-resistance genes against virulent pathotypes of stripe rust in Cappelle-Desprez or Mega have been made. Both cultivars have seedling resistance against the highly virulent pathotypes 46S119 (avirulent on *Yr1, 5, 10, 15, 27, SP, Su,* and *CV* and virulent on *Yr2, 3, 4, 6, 7, 8, 9, 22, 23, 25*) and 78S84 (avirulent on *Yr1, 5, 10, 15, 25, SP,* and *CV* and virulent on *Yr2, 3, 4, 6, 7, 8, 9, 22, 23, 27,* and *A*). Particularly for Cappelle-Desprez, the resistance is likely to be short lived, because it has not shown seedling resistance elsewhere in the world and the stripe rust pathotypes distributed in India may not be so virulent. Cappelle-Desprez has been grown every year for last 12 years in an experimental plot, and the pathotypes 46S119 (46E151 + *Yr9*) and 78S84 (78E16) are quite virulent, existing since 1996 and 2002, respectively. Therefore, no evidence exists right now that the seedling resistance gene reported in Cappelle-Desprez will be rendered ineffective very soon. However, the effectiveness of the seedling-resistance gene and the role of a suppressor of resistance is more important. Further studies are required to reach any conclusion about a suppressor gene. We have initiated studies to test whether or not Cappelle-Desprez carries suppressors for seedling resistance against stripe rust. For this purpose, the $F_3$ lines that were homozygous for a zero fleck reaction at the seedling stage were advanced to the $F_4$. About 100 seedlings of the $F_4$ families were tested and the resistance was confirmed to be homozygous. One of the derived zero fleck lines was named FLW-CD. In the next step, segregating populations ($F_2$ population and $F_3$ families of 'Agra Local/FLW-CD' and $F_2$ population of 'Cappelle-Desprez/FLW-CD' are being generated. The results are awaited.

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