FIGHTING FUSARIUM WILT THROUGH BREEDING IN COTTON: A SUCCESSFUL STORY IN CHINA

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Abstract

When I was a cotton breeder and geneticist at Huazhong Agricultural University (Wuhan, China), I initiated and directed a project to study the genetic basis of resistance to Fusarium wilt (FW) in the early 1990s (Zhang et al., 1994, 1995; Feng et al., 1996c). The pathogen was identified as race 7 of *Fusarium oxysporum* f. sp. *vasinfectum* (FOV) thought to be originally from the US when Upland cotton was first introduced to China through fuzz seeds in the 1890s and thereafter. Breeding for resistance to FW in cotton was started in the 1950s, resulting in the development of two highly resistant lines- Chuan 52-128 and Chuan 57-681 in Shichuan Province. The two lines were derived from direct selections from susceptible Delfos 531 and Deltapine 15, respectively, selected in FOV heavily infected cotton fields. The two lines became the most important sources for further breeding for resistance to FOV in Upland cotton in China (Feng et al., 1996b; Zhang et al., 1996). Our work confirmed that FW resistance genes were contained in heterogeneous susceptible cultivars, as highly resistant Jianmian 1R and Emian 18R were developed from their original susceptible cultivars through five cycles of repeated selections for FW resistance in FW-infected fields (Feng et al., 2001). As a result of the collective nationwide effort, 13 FW resistant Upland cultivars were released for commercial production from cross breeding using the two major resistant sources, some of which include Shaanmian 4 and Shaanmian 401. In the 1970s, 29 FW resistant cultivars including 86-1 and Lukang 1 were developed. This number in the 1980s was increased to 48 with FW resistant cultivars such as CRI 12 (Zhongmian 12) from a cross of Uganda 4 × Xingtai 6871, which was grown to more than 20% of the cotton acreage in China in the mid-90s. Another release was resistant Shaanmian 1155 from a cross of Zhongchang 1 × Xuzhou 1818. Interestingly, Xuzhou 1818 is FW susceptible and was a direct selection from the susceptible Stoneville 2B, and it gave rise to the susceptible Xintai 6871. Stoneville 2B was used in a cross with Deltapine 14 to produce the susceptible Deltapine 15. In the 1990s, more than 100 FW resistant cultivars were released, many of which were derived from CRI 12 (Zhang et al., 2015; Sanogo and Zhang, 2016). As breeding for FW resistance has been one of the major breeding objectives, FW resistance is required in officially approving releases of cotton cultivars at the provincial and national levels. The cotton acreage grown to FW-resistant cultivars increased from 44% in the early 1990s to more than 80% in the early 2000s. FW is currently no longer a cotton production problem in China.

Representatives of the above major resistance sources were crossed with one another and also with several susceptible lines including T582 and T586 to study the segregating ratios for FW resistance (Feng et al., 1996a, 1998). A typical 3 resistant (R):1 susceptible (S) or 15R:1S were observed, leading to the identification of two major resistance genes to FW- Fw_1 in Chuan 52-128 and Shaan 1155 and Fw_2 in Chuan 57-681 and CRI 12. The two genes appeared to have no deleterious effects on lint yield and fiber quality (Feng et al., 2001). The dominant resistance gene Fw^R mapped on chromosome c17 using molecular markers in CRI 35 (derived from a cross of [Zhong 23021 × (CRI 12 × Chuan 1704)] was likely from CRI 12 and therefore, the same as Fw_2. As a comparison, major FW resistance genes were also identified in *Gossypium arboreum*, *G. herbaceum*, and *G. barbadense* (Table 1; Zhang et al., 2015). The FW resistance was also successfully transferred into several commercial Upland cultivars from *G. arboreum* in China. Also via introgression breeding, the current cotton breeding program at New Mexico State University has transferred FW resistance (race 4) from *G. barbadense* and/or Chinese Upland to NuMex COT 15 GLS released in 2015 (Zhang et al., 2016) and NM 13P1117 (Zhang et al., 2018).

Table 1. Qualitative genetic studies of Fusarium wilt resistance in cotton, *Gossypium* spp. (Zhang et al., 2015).

Species	**Race**	**Major results**	**Country**	**Reference**
G. arboreum	4	1 major gene	India	Based on Jones (1961)
G. herbaceum	4	2 dominant genes with complementary actions	India	Based on Jones (1961)
G. hirsutum	1	1 major recessive genes and modifiers in Delfos 425	US	Jones (1953)
G. hirsutum	1	1 major dominant gene in Cook 307-6	US	Smith and Dick (1960)
G. hirsutum	3	1 dominant gene in Acala SJ-2	Israel	Netzer et al. (1985)
G. hirsutum	6	1 major gene action in IAC17	Brazil	Gridi-Papp et al. (1977)
G. hirsutum	7	1 major dominant Fw1 in Chuan 52-128, Shaan 1155 & 86-1	China	Feng et al. (1998)
G. hirsutum	7	1 major dominant gene Fw2 in Chuan 57-681 and CRI 12	China	Feng et al. (1998)
G. hirsutum	7	1 dominant resistance gene FwR on c17 in CRI 35 [Zhong 23021 × (CRI 12 × Chuan 1704)]	China	Wang et al. (2009)
G. barbadense	3	1 major dominant gene with 1 to a few minor genes	Egypt	Fahmy (1934)
G. barbadense	1	2 dominant genes with additive effects in Seabrook	US	Smith and Dick (1960)
G. barbadense	1	1 major dominant gene FOV1 on c16 in Pima S-7	US	Wang & Roberts (2006)
G. barbadense	4	1 major dominant gene FOV4 on c14 in Pima S-6	US	Ulloa et al. (2013)
G. barbadense	7	1 major gene in HK 237	China	Zhu et al. (2010)

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