

## Stripe rust resistance in *Aegilops tauschii* and its genetic analysis

Dengcai Liu · Lianquan Zhang · Zehong Yan ·  
Xiujin Lan · Youliang Zheng

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**Abstract** *Aegilops tauschii* Coss., the D-genome progenitor of common wheat (*Triticum aestivum* L.) includes two subspecies, *tauschii* and *strangulata* (Eig) Tzvel. Subspecies *tauschii* has a wide geographic distribution spreading westwards to Turkey and eastwards to Afghanistan and China, while ssp. *strangulata* has a narrower distribution occurring only in two disjointed regions, southeastern Caspian Iran and Transcaucasia. A collection of 56 *Ae. tauschii* accessions was screened at adult stage against a mixture of pathotypes of stripe rust prevalent in the current wheat production in China. The results for three crop seasons indicated that among the 38 ssp. *tauschii* accessions, 37 were susceptible and only one was resistant, while all the 18 ssp. *strangulata* accessions were resistant. These results indicated that stripe rust resistance was related to taxonomic origin. Further genetic analysis revealed

the resistance of stripe rust in ssp. *strangulata* accession AS2388 was conferred by a single dominant gene.

**Keywords** *Aegilops tauschii* · Bread wheat · Stripe rust

### Introduction

*Aegilops tauschii* Coss. (syn. *Ae. squarrosa* auct. non L.,  $2n = 2x = 14$ , genome DD) is the D-genome progenitor of common wheat (*Triticum aestivum* L.,  $2n = 6x = 42$ , genome AABBDD) (Kihara 1944; McFadden and Sears 1944). This species includes two subspecies, i.e. ssp. *tauschii* and *strangulata* (Eig) Tzvel. Within its distribution range, *Ae. tauschii* is adapted to diverse environments including sandy seashore, margins of deserts, stony hills, steppe, wastelands, roadsides and humid temperate forests (Van Slageren 1994). It also grows as a weed in wheat and barley fields. As genetic variability within the D genome of *Ae. tauschii* is much higher than within the D genome of wheat, the wild species offers great potential for wheat improvement. Utilization of the species for wheat improvement is further aided by the ability of the chromosomes of *Ae. tauschii* and the D genome chromosomes of wheat to recombine naturally. Therefore, *Ae. tauschii* has been extensively exploited by various groups around the world for wheat improvement (see review by Ogonnaya et al. 2005).

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D. Liu (✉)  
Northwest Plateau Institute of Biology, Chinese Academy  
of Science, 810001 Qinghai, China  
e-mail: dcliu7@yahoo.com

D. Liu · L. Zhang · Z. Yan · X. Lan · Y. Zheng  
Triticeae Research Institute, Sichuan Agricultural  
University, Wenjiang of Chengdu city, 611130 Sichuan,  
China

D. Liu · L. Zhang · Z. Yan · X. Lan · Y. Zheng  
Key Laboratory of Crop Genetic Resources and  
Improvement, Ministry of Education, Sichuan  
Agricultural University, Yaan, 625014 Sichuan, China

Stripe (yellow) rust, caused by *Puccinia striiformis* f. sp. *tritici* (PST), is a major disease of common wheat (*Triticum aestivum* L.) in many cool and temperate regions of the world (Stubbs 1988). This disease occurs on many grasses and cereal crops, including wheat, barley, triticale, and rye. China has the largest stripe rust epidemic region in the world in terms of wheat acreage with more than 20 million ha of wheat affected by the disease and stripe rust has been considered the most important disease of wheat (Wan et al. 2004, 2007). Breeding for resistance has always faced the challenge of rapid resistance breakdown in released resistant cultivars due to the rapid mutation and development of new races in this country. The recent destructive epidemic in 2002 was caused by a new Chinese PST isolate CYR32 (Chinese Yellow Rust), which resulted in yield losses of 1.3 million tones (Wan et al. 2004, 2007). Among the identified resistance genes (*Yr1-Yr41*) and many other provisionally designated genes (McIntosh et al. 2008), most have lost their effectiveness in China (Wan et al. 2007).

In China the stripe rust usually infects bread wheat cultivars at their adult stage in early spring. Noticeably, the infection of adult plants causes much more serious yield losses than the infection of seedlings due to shrivelness obviously occurs at this stage. *Ae. tauschii* accessions resistant to stripe rust have been previously reported (Valkoun et al. 1985; Yildirim et al. 1995; Knaggs et al. 2000). The objective of this study was: (1) to screen the adult-plant resistance resources to currently Chinese

prevailing races in *Ae. tauschii* germplasm; (2) to analyze the resistant inheritance.

## Materials and methods

This study included 56 *Ae. tauschii* accessions originated from different regions and belonging to two subspecies, ssp. *tauschii* and *strangulata* (Table 1) as well as the bread wheat check SY95-71, which is a good stripe rust spreader and has been widely used in the resistant identification of wheat cultivars in Sichuan province, China (Shu et al. 1999).

Field evaluation for resistance to stripe rust was carried out at the experimental station of Triticeae Research Institute in Dujiangyan, Chengdu city, Sichuan province, China, a favorable environment for stripe rust development. The 56 *Ae. tauschii* accessions were evaluated in three crop seasons, i.e. 2006–2007, 2007–2008, and 2008–2009. They were planted into plots of two rows with 2.0 m long and 0.3 m apart. The hybrid F<sub>1</sub> and F<sub>2</sub> populations between ssp. *strangulata* AS2388 and ssp. *tauschii* AS87 were evaluated in 2008–2009 crop seasons for genetic analysis. These materials were grown as individual plants spaced 10 cm apart within rows and 30 cm between rows with 2 m long. The highly susceptible spreader variety, SY95-71, was planted at both sides of each experimental row.

Evaluation of resistance to stripe rust at seedling stages was done by inoculating spreader SY95-71 and

**Table 1** The stripe rust infection types (ITs) of *Ae. tauschii* accessions at adult-plant stage

ITs	Accessions <sup>a</sup>	Note
7–9	AS60 (Iran), AS61, AS62, AS64, AS65, AS67 (Iran), AS68, AS69, AS71 (Xinjiang, China), AS72 (Xinjiang, China), AS74 (Shannxi, China), AS75 (Shannxi, China), AS76 (Shannxi, China), AS77 (Henan, China), AS78 (Henan, China), AS79 (Henan, China), AS80 (Henan, China), AS81 (Henan, China), AS82 (Henan, China), AS84, AS85, AS86, AS87, AS88, AS89, AS90, AS91, AS92, AS93, AS94, AS95, AS96, AS2389 (Astara, Iran), AS2390, AS2392, AS2410, AS2564	All the 37 accessions belong to ssp. <i>tauschii</i>
0–2	AS63, AS66, AS2386 (Behshahr, Iran), AS2387 (Behshahr, Iran), AS2388 (Gorgan, Iran), AS2393, AS2394, AS2395, AS2396, AS2397, AS2398, AS2399, AS2402, AS2403, AS2404, AS2405, AS2406, AS2407, AS2409	Among the 19 accessions, AS63 belongs to ssp. <i>tauschii</i> , the others belong to ssp. <i>strangulata</i>

AS is the code of Triticeae Research Institute of Sichuan Agriculture University

<sup>a</sup> The known origins of *Ae. tauschii* accessions are indicated in brackets

the *Ae. tauschii* accessions, 6 weeks after planting, with the mixed urediospores of CYR32, CYR31, CYR30, SY11-14, SY11-4, and HY46-8, provided by Research Institute of Plant Protection, Gansu Academy of Agricultural Sciences. These mixed urediospores were isolated from infected wheat plants, which are epidemic physiological races or pathotypes in current wheat production of China (Wan et al. 2007). Stripe rust infection type was recorded three times at 10-day intervals. Disease notes were taken when the susceptibility of flag leaves of the susceptible check SY95-71 was fully expressed. For each plant, infection type (IT) was recorded on a 0- to 9-scale (McNeal et al. 1971). Chi-square tests were used to analyze inheritance of stripe rust resistance in the F<sub>2</sub> population.

## Results and discussion

The tests for stripe rust resistance in the three crop seasons showed similar results. Among the 38 *ssp. tauschii* accessions, 37 were susceptible (infection type 7–9) and only one was resistant (infection type 0–2). The resistant accession AS63 showed the typical taxon characters for *Ae. tauschii ssp. tauschii*. All the 18 *ssp. strangulata* accessions were resistant (infection type 0–2).

All the observed 40 hybrid F<sub>1</sub> plants between resistant *ssp. strangulata* accession AS2388 and susceptible *ssp. tauschii* accession AS87 were resistant. Among the 176 F<sub>2</sub> plants between AS2388 and AS87, 130 plants were resistant (infection type 0–1) and 46 were susceptible (infection type 7–9). Segregation of resistant and susceptible plants fit 3R:1S ratio ( $\chi^2 = 0.068$ ,  $P > 0.75$ ). Therefore, the resistance of stripe rust in AS2388 was conferred by a single dominant gene.

Subspecies *tauschii* has a wide geographic distribution spreading westwards to Turkey and eastwards to Afghanistan and China, while *ssp. strangulata* occurs only in two disjointed regions, southeastern Caspian Iran and Transcaucasia (Kihara et al. 1965; Yen et al. 1983; Jaaska 1995). In this study, only one *ssp. tauschii* accession was resistant to stripe rust, while all the *ssp. strangulata* accessions were resistant. An evaluation of resistance to stripe rust carried out by Knaggs et al. (2000) revealed that all five of the tested *ssp. strangulata* and only two of the 49

tested *ssp. tauschii* accessions showed resistance to the prevailing natural population of stripe rust infection. Yildirim et al. (1995) evaluated the seedling resistance by inoculating *Ae. tauschii* with four different races of stripe rust that represent all known virulences in the Pacific Northwest. A much higher frequency of *ssp. strangulata* than *ssp. tauschii* accessions was resistant to stripe rust at seedling stage. These results indicated that the stripe rust resistance was related to taxonomic subspecies.

The subspecies *strangulata* provides good resistance to stripe rust for wheat resistance breeding. The stripe rust resistance in *Ae. tauschii* can be easily transferred into hexaploid wheat via homologous chromosome recombination. However, the stripe rust resistance in *Ae. tauschii* is not expressed in some hexaploid wheat backgrounds possessing suppressors on A or B genomes. Therefore, recipient parents without suppressor genes should be used in order to exploiting *Ae. tauschii* resources for wheat stripe rust breeding (Ma et al. 1995; Yang et al. 2003; He et al. 2007). The transfer of the resistance to stripe rust originated from *ssp. strangulata* into Chinese common wheat cultivars, using diverse recipient parents, is in progress in Sichuan and Qinghai provinces.

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