Journal of Genetics and Genomics

(Formerly *Acta Genetica Sinica*) December 2007, 34(12): 1123–1130



Research Article

Mapping of a Major Stripe Rust Resistance Gene in Chinese Native Wheat Variety Chike Using Microsatellite Markers

Fanghui Liu^{1,3}, Yongchun Niu^{1,2,①}, Hui Deng¹, Genjia Tan³

- 1. Institute of Agricultural Resources and Regional Planning, Chinese Academy of Agricultural Sciences, Beijing 100081, China;
- 2. Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100094, China;
- 3. Plant Protection Academy, Agricultural University of Anhui, Hefei 230036, China

Abstract: Chike (accession number Su1900), a Chinese native wheat (Triticum aestivum L.) variety, is resistant to the currently prevailing physiological races of *Puccinia striiformis* Westend, f. sp. tritici in China. Genetic analysis indicated that resistance to the physiological race CY32 of the pathogen in the variety was controlled by one dominant gene. In this study, BSA (bulked segregant analysis) methods and SSRs (simple sequence repeats) marker polymorphic analysis are used to map the gene. The resistant and susceptible DNA bulks were prepared from the segregating F2 population of the cross between Taichung 29, a susceptible variety as maternal parent, and Chike as paternal parent. Over 400 SSR primers were screened, and five SSR markers Xwmc44, Xgwm259, Xwmc367, Xcfa2292, and Xbarc80 on the chromosome arm 1BL were found to be polymorphic between the resistant and the susceptible DNA bulks as well as their parents. Genetic linkage was tested on segregating F2 population with 200 plants, including 140 resistant and 60 susceptible plants. All the five SSR markers were linked to the stripe rust resistance gene in Chike. The genetic distances for the markers Xwmc44, Xgwm259, Xwmc367, Xcfa2292, and Xbarc80 to the target gene were 8.3 cM, 9.1 cM, 17.2 cM, 20.6 cM, and 31.6 cM, respectively. Analysis using 21 nulli-tetrasomic Chinese Spring lines further confirmed that all the five markers were located on chromosome 1B. On the basis of the above results, it is reasonable to assume that the major stripe rust resistance gene YrChk in Chike was located on the chromosome arm 1BL, and its comparison with the other stripe rust resistance genes located on 1B suggested that YrChk may be a novel gene that provides the resistance against stripe rust in Chike. Exploration and utilization of resources of disease resistance genes in native wheat varieties will be helpful both to diversify the resistance genes and to amend the situation of resistance gene simplification in the commercial wheat cultivars in China.

Keywords: wheat; native variety; Puccinia striiformis; resistance gene; microsatellite marker; gene mapping

Stripe rust (yellow rust), caused by *Puccinia striiformis* Westend. f. sp. *tritici*, is one of the most important diseases of wheat (*Triticum aestivum* L.) worldwide. In China, stripe rust prevailed for several times in large wheat-growing areas and this caused serious yield losses. The use of resistant cultivars is the most economical, effective, and environment-friendly method to reduce damage and loss cau-

sed by stripe rust. However, resistance of most commercial wheat cultivars will "breakdown" after continual growing for several years because of the appearance and development of novel races of the stripe rust pathogen. In the past decades, most of the resistant resources used for the breeding of wheat were brought from abroad. Simplification of resistance genes in the commercial wheat cultivars has

Received: 2007-04-17; Accepted: 2007-05-31

This work was supported by the National Natural Science Foundation of China (No. 30571157) and the National Basic Research Program (973 Program) (No. 2006CB100203).

① Corresponding author. E-mail: niuyongchun@yahoo.com.cn; Tel: +86-10-6891 8647

become the latent basis for stripe rust epidemic in several areas. Therefore, it is vital to breed and use novel wheat cultivars with effective and diverse resistance genes that provide protection against stripe rust.

Native wheat varieties are abundant in China, but they were often ignored in wheat breeding because of their poor agronomic traits. Native wheat varieties are the outcome of both natural and artificial selection through long evolutionary processes, and they have high adaptability even in unfavorable environment. There may be valuable gene resources that provide resistance against stripe rust in these varieties. The study, exploration, and utilization of resistance gene resources in native wheat varieties are significant to change the simplification of stripe rust resistance genes in the commercial wheat cultivars in China [1].

Chike (accession number Su1900), a Chinese native wheat variety, is resistant to several physiological races of *P. striiformis* f. sp. *tritici*, which are currently prevalent in China. On the basis of genetic analysis, a major stripe rust resistance gene in Chike was mapped using microsatellite (simple sequence repeat, SSR) polymorphic analysis in this study. The results will facilitate the effective, reasonable utilization of the resistant germplasm resource, and it will also provide the scientific basis for the exploration of novel resistance genes in native wheat varieties and the selection of resistance genes in wheat breeding.

1 Materials and Methods

1.1 Materials

1.1.1 Plant materials

Seeds of the Chinese native wheat variety Chike and the susceptible variety Taichung 29 were collected and preserved by the Institute of Plant Protection, Chinese Academy of Agricultural Sciences (CAAS), China. Before analysis, the plants of Chike were self-pollinated for three generations and purified

for agronomic traits and resistance to stripe rust through selection. Taichung 29, as maternal parent, was crossed with Chike, as paternal parent, to obtain F_1 seeds. F_1 plants were self-pollinated to obtain F_2 seeds, and backcrossed with the female parent Taichung 29 to obtain BC_1 seeds. F_2 plants were self-pollinated to obtain F_3 seeds.

The wheat varieties Clement and Lovrin10, the carrier of stripe rust resistance gene *Yr9*, were collected and preserved by the Institute of Plant Protection, CAAS, China. The varieties Vilmorin 23, Hybrid 46, Lemhi, Lalbahadur, the carriers of stripe rust resistance genes *Yr3a*, *Yr3b*, *Yr21*, *Yr29*, respectively, and disomic and the nulli-tetrasomic Chinese Spring lines were provided by Dr. X. M. Chen of Washington State University.

1.1.2 Strain of P. striiformis f. sp. tritici

Tested single-spore strain of physiologic race CY32 of Chinese wheat stripe rust was preserved at the Institute of Plant Protection, CAAS, China. Fresh uredospores of CY32 were prepared by propagating it on seedlings of susceptible variety Mingxian 169 in advance of use.

1.2 Assessment of resistance

Seeds of tested wheat materials were sown in pots of 10 cm in diameter with 15 plants per pot and then cultivated in greenhouse. When the first leaves were fully spread out, the seedlings were inoculated with fresh spores of CY32 using the brush method. Inoculated plants were placed in dew chambers at 10°C for 24 h and then incubated at 18/12°C (day/night) with a photoperiod of 12–14 h of light per day in an air-conditioned greenhouse. Infection types (ITs) were recorded 15 days after inoculation when the susceptibility of the check, Taichung 29, was fully expressed. Infection types were scored on a common 0–4 scale. Infection types in the range of 0–2 were considered to be resistant, and the infection types in the range of 3–4 were considered to be susceptible.

Download English Version:

https://daneshyari.com/en/article/2788200

Download Persian Version:

https://daneshyari.com/article/2788200

Daneshyari.com