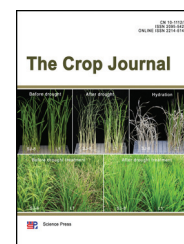
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Weedy red rice has novel sources of resistance to biotic stress[☆]

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ABSTRACT

Weedy red rice (*Oryza sativa*; WRR), a close relative of cultivated rice, is a highly competitive weed that commonly infests rice fields and can also naturally interbreed with rice. Useful genes for biotic stress have been maintained in WRR and can be explored for breeding. Here we describe genetic and physiological traits of WRR that can be beneficial in preventing major rice diseases. Rice blast, caused by the hemibiotrophic fungal pathogen *Magnaporthe oryzae*, and sheath blight disease, caused by the necrotrophic pathogen *Rhizoctonia solani*, are the two most damaging biotic stresses of rice. Many major and minor resistance genes and QTL have been identified in cultivated and wild rice relatives. However, novel QTL were recently found in the two major U.S. biotypes of WRR, blackhull-awned (BH) and strawhull-awnless (SH), suggesting that WRR has evolved novel genetic mechanisms to cope with these biotic stresses. Twenty-eight accessions of WRR (PI 653412–PI 653439) from the southern USA were characterized and placed in the National Small Grains Collection, and are available for identification of novel genetic factors to prevent biotic stress.

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1. Introduction

Rice is one of the most important food crops. It feeds half of all human beings and has been grown in diverse ecological systems for more than a thousand years [1, 2]. The United Nations estimates that by 2030, the world population will grow by an additional 1.2 billion people (<http://www.un.org/en/sections/issues-depth/population/index.html>). Thus, a demand for additional rice needed to meet increased human consumption is recognized worldwide. Long before there were organized rice breeding efforts, rice plants that survived after each disease epidemic were selected and used as parents for

subsequent seed production (a process known as “selection” breeding). Such selection after epidemics over the history of rice domestication and cultivation has created a genetic bottleneck for genetic resistance to other strains or other diseases in cultivated rice. In contrast, a highly competitive weedy relative of rice, weedy red rice (WRR, *Oryza sativa*) that commonly infests rice fields has not been selected by humans, but has survived through stochastic introduction and de-domestication [3].

Rice, a monocot, is a self-pollinated species, and its genetic diversity is often limited in comparison with that of outcrossing crop species such as maize [1]. During rice

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domestication, some resistance (R) genes were introgressed into cultivated rice, and some of them were lost owing to the absence of selection pressures from pathogens and environments. In theory, genes for resistance to all races of rice pathogens are present in different rice varieties. Temporal and spatial mismatching of host R genes to pathogen races is a common cause of disease epidemics. *Oryza* and its pathogens represent one of the best models to elucidate genetic and physiological mechanisms of host–pathogen interactions, not only because rice is an essential food for humanity, but also because the rice genome is one of the smallest among cereal crops, with a complete genome sequence available since 2002 [4] as well as genome sequences of rice pathogens [5]. There are two cultivated rice species, Asian rice (*O. sativa*) and African rice (*O. glaberrima*). Cultivated Asian rice is thought to have originated from *O. rufipogon* and *O. nivara* in Asia and cultivated Africa rice from *O. barthii* in Africa, respectively. Asian rice has two major subgroups, Geng (*japonica*) and Xian (*indica*) [6]. The Geng subgroup consists of tropical Geng, temperate Geng, and aromatic rice, and the Xian subgroup consists of Aus and Xian [7].

WRR is one of the major rice weeds, reducing both the quantity and quality of the rice crop and adapted to a wide range of environments. WRR is a troublesome weed in rice in the southern USA (where primarily tropical Geng cultivars are

grown), and throughout the world, especially where direct seeding methods are employed (Fig. 1) [8]. The diversity of biotypes of red rice creates a challenge for management of this weed, but also creates a unique opportunity for detailed biological and genetic studies of adaptive traits that have been lost in domesticated rice and are not found in wild rice relatives (Fig. 2).

2. Major biotic stress

In the USA and worldwide, major biotic stresses of rice are rice blast and sheath blight disease. Cultivated rice has been constantly challenged by the ascomycete filamentous fungus *Magnaporthe oryzae* (synonym of *Pyricularia oryzae*) causing rice blast disease. At present, rice blast disease is the most damaging rice disease worldwide, responsible for an estimated annual 30% crop loss corresponding to food for 60 million people [9]. In the USA, where approximately 2% of the world's rice is produced, rice farmers spend US\$69 million per year to prevent crop loss due to blast disease [10].

M. oryzae, a highly adaptive fungus, is a polycyclic pathogen that can reproduce three to five times during a single crop season [11]. For each life cycle, asexual spores begin to germinate in water within minutes, and germinated

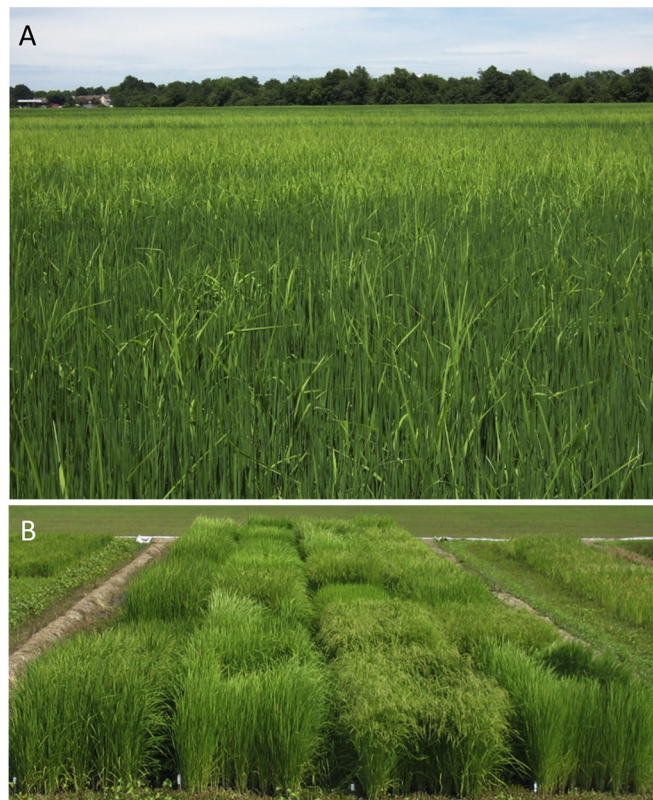


Fig. 1 – Photographs of red rice in a commercial rice field in Arkansas (A) and in an experimental field (B), Stuttgart, Arkansas, showing the diverse weedy red rice lines submitted to the GRIN (Germplasm Resources Information Network) collection. In (A), the taller plants with light green-colored leaves are red rice and the others are cultivated rice. In (B), there are 28 nine-row plots containing individual weedy red rice biotypes. Plots are arranged four wide by seven deep, but individual plots are less clearly differentiated toward the top of the photograph.

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