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World population structure of the rice blast fungus, *Magnaporthe oryzae*.

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Magnaporthe oryzae is a heterothallic fungus reproducing clonally in the field. The diversity and structure of populations of this pathogen of rice was described in many countries during the last 20 years. The expected clonal structure of the populations has been illustrated in various studies. But, relationships between the different populations was hardly testable mainly due to the choice of molecular markers.

We recently developed a set of 18 microsatellite markers for population studies (Adreit et al. 2007). We used these markers to genotype more than 1,700 isolates from 40 countries. This sample included reference isolates from previous studies and real populations (1 site, 1 year).

The world population structure show evidence for some geographic structuration. However, local adaptation and intercontinental migration are (or were) also common. A structure in three major genetic groups is observed. Two groups correspond to isolates of mating type Mat1.1 and Mat1.2 respectively. The third group gathers isolates of both mating types. Diversity is higher in Asia and more precisely in the countries of the Himalayan foothills. This area is the only one where female fertile isolates (able to produce perithecia and ascospores in vitro) were identified. Both mating types are also present in these populations. Whether sexual reproduction is (was) taking place in this region will be tested. The area of the Himalayan foothills is a center of diversity and is a good candidate for the center of origin of the rice blast fungus.