

Unequal Contributions of Parental Isolates in Somatic Recombination of the Stripe Rust Fungus

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Abstract : The dikaryotic basidiomycete fungus, *Puccinia striiformis*, causes stripe rust, one of the most important diseases of wheat and barley worldwide. The pathogen is largely reproduced asexually, and asexual recombination has been hypothesized to be one of the mechanisms for the pathogen variations. To test the hypothesis and understand the genetic process of asexual recombination, somatic recombinant isolates were obtained under controlled conditions by inoculating susceptible host plants with a mixture of equal quantity of urediniospores of isolates with different virulence patterns and selecting through a series of inoculation on host plants with different genes for resistance to one of the parental isolates. The potential recombinant isolates were phenotypically characterized by virulence testing on the set of 18 wheat lines used to differentiate races of the wheat stripe rust pathogen, *P. striiformis* f. sp. *tritici* (Pst), for the combinations of Pst isolates; or on both sets of the wheat differentials and 12 barley differentials for identifying races of the barley stripe rust pathogen, *P. striiformis* f. sp. *hordei* (Psh) for combinations of a Pst isolate and a Psh isolate. The progeny and parental isolates were also genotypically characterized with 51 simple sequence repeat and 90 single-nucleotide polymorphism markers. From nine combinations of parental isolates, 68 potential recombinant isolates were obtained, of which 33 (48.5%) had similar virulence patterns to one of the parental isolates, and 35 (51.5%) had virulence patterns distinct from either of the parental isolates. Of the 35 isolates of distinct virulence patterns, 11 were identified as races that had been previously detected from natural collections and 24 were identified as new races. The molecular marker data confirmed 66 of the 68 isolates as recombinants. The percentages of parental marker alleles ranged from 0.9% to 98.9% and were significantly different from equal proportions in the recombinant isolates. Except for a couple of combinations, the greater or less contribution was not specific to any particular parental isolates as the same parental isolates contributed more to some of the progeny isolates but less to the other progeny isolates in the same combination. The unequal contributions by parental isolates appear to be a general role in somatic recombination for the stripe rust fungus, which may be used to distinguish asexual recombination from sexual recombination in studying the evolutionary mechanisms of the highly variable fungal pathogen.

Keywords : molecular markers, *Puccinia striiformis*, somatic recombination, stripe rust

Conference Title : ICFG 2017 : International Conference on Fungal Genetics

Conference Location : Venice, Italy

Conference Dates : June 21-22, 2017