

The first report on identification of faba bean host differentials for assessing variation on *Uromyces viciae-fabae* populations and pathotype nomenclature system in Australia

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Abstract

Faba bean rust caused by *Uromyces viciae-fabae* (Pers.) J. Schrt.) is an important disease limiting faba bean production globally. The development of rust resistant cultivars provides economical and viable solution to overcome this disease. Different sources of resistance have been identified, but there is a lack of understanding on the pathotype variation. Faba bean rust is an obligate parasite exhibiting all five spore forms in its life cycle on a single host allowing sexual recombination and variation in the pathogen population. However, neither continuous surveillance for the pathogen variation has been conducted nor a host differential set to assess the variation has been developed. This study examined differences in the virulence of Australian *U. viciae-fabae* isolates by developing a differential set of faba bean genotypes collecting isolates from major faba bean growing states in Australia; South Australia (SA), New South Wales (NSW) and Queensland (Qld). A single spore culture was generated from each isolate and multiplied in isolation on susceptible cultivar Fiord, under greenhouse conditions. In the absence of a differential set, these pathogen isolates were used for assessing virulence on 40 diverse faba bean genotypes. Based on the host-pathogen interactions, 12 putative host genotypes were identified that displayed variation in the rust isolates. These genotypes have been proposed as a differential set for assessing pathotype variability in the future.

We found a variation in the pathogen, but there was no system of naming the pathogen isolates. For the first time, a nomenclature system was developed using the binary pathotype naming system similar to developed for common bean rust. Each isolate was given a two-digit code separated by a hyphen. The differential set genotypes were ranked (1 to 12) on the basis of resistance; genotypes showing resistance against most isolates were arranged first followed by the genotypes with resistance on fewer isolates. Each susceptible reaction of a differential genotype was attributed a binary value. In this arrangement, the genotypes were separated in two groups (genotype 1 to 6 and 7 to 12) and the name of each pathotype was assigned by the concatenation of the corresponding binary values attributed to the susceptible reaction of the differential lines within each group. Nine virulence patterns on the differential set were detected and the isolates were named using the new nomenclature system.

SA pathotypes were the least virulent, NSW moderately virulent and Qld highly virulent. This fits well with the development of rust in these regions. The pathotype 63-63 from the southern Qld was highly virulent and overcame all host differentials posing a risk of rust outbreak in the region. This is the first report of the well characterised *U. viciae-fabae* pathotypes based on differential set in Australia. The differential set will allow to detect any new variation in pathotypes before it becomes epidemic in the region. This information will facilitate breeding for rust resistance in faba bean according to the prevalence of pathotypes in the target region and monitor the breakdown of resistant genes.

