

RISKS TO STYLOSANTHES CULTIVARS FROM ANTHRACNOSE DISEASE

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In Australia, *Colletotrichum gloeosporioides*, the fungus causing anthracnose, is a serious threat to stylo cultivars as its four races may change to infect existing/newly released resistant cultivars. Threat can also come from virulent races accidentally introduced from the centre of diversity of the fungus in South America. This research aims to assess these risks and develop plant improvement strategies to reduce the probability of new races causing damage.

MATERIALS AND METHODS

C. gloeosporioides isolates were collected from surveys in north Queensland and their virulence spectrum was established from glasshouse bioassays using six stylo accessions and cultivars. Data were analysed using multivariate statistical techniques to monitor frequencies of the four races over three years at Calliope. Diversity in 11 Australian and 79 South American isolates was studied in an ACIAR-funded project using Random Amplified Polymorphic DNA (RAPD).

RESULTS AND DISCUSSION

There were five virulence groups among 182 Australian isolates collected over the last 15 years. Groups 1 (race 1, only virulent on cv. Fitzroy) and 3 (race 3, virulent on cv. Seca) were clearly separated. As before (1), separation of groups 4 and 4a was not clear and a majority of isolates were in this group. The fifth group had four weakly pathogenic isolates. The frequency of race 3 isolates at Calliope increased from 26% to 49% over the three years. Whether this may lead to the selection of isolates more damaging on Seca, needs further detailed study to take into account possible variation in Seca as the area under Seca continues to expand.

RAPD analysis using 10 primers showed less than 2% dissimilarity among Australian isolates from hosts other than *Stylosanthes guianensis*. The dissimilarity was over 80% for the overseas isolates from these hosts. Compared with the genetic diversity at centre of origin, there is only a limited diversity in the Australian population of *C. gloeosporioides*. Of the 3-4 major clusters, the Australian isolates form part of a large cluster containing isolates from Brazil, Thailand, Africa and the Philippines. The work endorses the currently adopted management strategies based on host diversity such as the use of genotype mixtures and quantitative resistance (2) to combat the variable pathogen. It highlights the need to better establish the risk of serious damage from new virulence groups accidentally introduced into Australia and/or any that may evolve locally.

REFERENCES

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