B-38: A molecular approach to distinguish the *Corynespora cassiicola* isolates

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The fungus *Corynespora cassiicola* is the most recognised cause of devastating leaf disease of plantation rubber trees (*Hevea brasiliensis*). Although *C. cassiicola* as a species has wide host range, a large number of host-specific strains have been identified.

Genetic variability among *C. cassiicola* isolates collected from different host plants were assessed using RAPD-PCR profiles generated by 8 decamer

primers. Based on degree of sharing of common bands, isolates collected from rubber plants could be divided into 3 different genetically identical groups whereas papaw isolates fall into one group. All the other isolates from different host plants could be distinguished from each other and from papaw and rubber isolates by their unique banding patterns obtained with each of the primers. The isolates collected from the same host plant from different geographical origin could not be identified using this method.

RAPD-PCR technique could effectively be employed to identify the *C. cassiicola* isolates collected from different host plants.

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