AN INOCULATION SCREENING PROTOCOL FOR CYPRESS CANKER IN *CUPRESSUS MACROCARPA*

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Cupressus macrocarpa clones selected for rural woodlots and forest plantations may not always be adequately exposed to populations of the cypress canker disease pathogens prior to release. In order to develop a direct method for testing field selections, wounds made on seedlings of nine families were inoculated with two isolates of *Seiridium unicorne*. Disease severity, as measured by lesion length, varied between fungal isolates and between host families. Higher temperatures (23°C/17°C, day/night) encouraged greater stem infection, and initially more foliage browning, than cooler temperatures (12°C/8°C). Inoculation of side branches suggested a technique for simultaneous screening of cypress clones against multiple pathogen isolates using single plants. Conidia were less effective as inoculum than mycelium in agar. Incidence of plants bearing fruit bodies of *S. unicorne* varied between fungal isolates, and fruitbodies of *S. cardinale* or *Lepteutypa cupressi* appeared on some plants inoculated with *S. unicorne*. A routine inoculation screening procedure may be feasible if consistency between test runs can be demonstrated.

VANILLA MOSAIC VIRUS: A DISTINCT POTYVIRUS SPECIES

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Vanilla mosaic virus (VaMV) was first described in 1984 in French Polynesia on vanilla (*Vanilla tahitensis*) showing leaf mosaic and distortion. It was subsequently shown to be a *Potyvirus* (*Potyviridae*) serologically related to *Dasheen mosaic virus* (DsMV), although there was insufficient characterisation to conclusively show that it was a distinct *Potyvirus* species. As part of a programme to develop specific detection methods for vanilla viruses we have been sequencing VaMV. Nucleic acid was extracted from partially purified virus particles and amplified by the reverse transcriptase-polymerase chain reaction using a selection of degenerate primers for the genus *Potyvirus*. The sequence data obtained for both the CI-6K-N1a region and the NIb-CP region of the genome confirmed that VaMV is a member of the genus *Potyvirus*. Furthermore, low nucleotide homologies to all other *Potyvirus* sequences in GenBank, including DsMV, clearly show that VaMV is a distinct *Potyvirus* species.