MOLECULAR DETECTION AND FUNGICIDE SENSITIVITY OF DOWNY MILDEW PATHOGEN (*Pseudoperonospora cubensis*) IN CUCURBITS

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Cucurbit downy mildew, caused by *Pseudoperonospora cubensis* is one of the most damaging foliar diseases, causing heavy yield losses in all commercially grown cucurbits in Sri Lanka. However, detailed knowledge on morphology, fungicide sensitivity and molecular genetics of *P. cubensis*, is currently lacking. *P. cubensis* isolated from downy mildew infected cucurbits; snake gourd (*Trichosanthes cucumerina*), bitter gourd (*Mormordica charantia*), cucumber (*Cucumis sativus*) and ridge gourd (*Luffa acutangula*) were morphologically characterized, based on the dimensions of sporangia and sporangiophores. Length and width of spores were 28.16±0.01µm and 17.99±0.01µm, respectively. The length of the sporangiophore was 252.32±0.01 µm, while height of the first ramification was 188.32±0.01µ and width of the trunk was 6.95±0.01µm. The length of the longer ultimate branchlets was15.18±0.01 µm, while that of the shorter ultimate branchlets was 5.09±0.01µm. *P. cubensis* isolated from different hosts were morphologically similar. Fungicide sensitivity of *P. cubensis* was evaluated against seven selected fungicides, by modified sporangia germination test. The most effective fungicides were, 'Acrobat' (Dimethomorph 90 g/kg + Mancozeb 600 g/kg WP) and a new fungicide (Azoxystrobin 120g/l + Tebuconozole 160 g/l). Molecular differences were identified by two primer pair sets; one for the ribosomal internal transcribed spacer (ITS4/ITS5) regions and the other for COX II gene (FM35/FM36). The above products of *P. cubensis* differed between hosts: 760 bp in ridge gourd and 800 bp in cucumber. This suggests that molecular genetic diversity exists among *P. cubensis* that infect different host plant species.

Keywords: Cox II gene, Cucurbit downy mildew, Fungicide sensitivity, Morphological characterization, Molecular diversity