

COMPARATIVE PROTEOMICS OF CARICA PAPAYA

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Papaya or papaw (*Carica Papaya L.*) is a soft-wooded plant that is cultivated worldwide in tropical areas. The long-term conservation of papaya species is not possible through seed storage as the seeds can only be stored for a few years. Additionally, several wild type varieties are only available through field collections, which are then vulnerable to insect attack, disease and natural disasters. Therefore, developments of in-vitro conservation techniques are important [1]. Furthermore, the cultivated papaya species have a narrow gene pool and are prone to a number of diseases that rapidly spread throughout plantations. Papaya ring-spot virus (PRSV) has become the limiting factor for commercial production internationally, and several hybrids have been cloned at Griffith University that show specific resistance to PRSV [2].

Here we report a comparative proteomics approach with two specific aims (1) to identify any protein modification and damage associated with the cryopreservation procedures, and to modify and optimise these protocols accordingly, and (2) to discover the unique proteins that are present in the virus resistance species of papaya. The papaya cryopreservation protocols involve several stages of shoot tips incubations in buffers and media including a one-hour incubation in liquid nitrogen prior to the plating of the shoot tips in a solid regeneration medium [1]. For these studies, leaves from papaya plants after each cryopreservation step, and also from disease resistant hybrids are collected. The proteins from these papaya plant leaves are extracted based on adapted procedures [3]. The proteins are then purified by gel electrophoresis and identified by mass spectrometry. This presentation will describe our comparative proteomics approach in discovery of virus resistance proteins and also for the evaluation of papaya plants after cryopreservation.

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