

**Title** Comparative transcriptomic analysis of plum fruit treated with 1-MCP

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### Abstract

Microarray technology has allowed the large scale transcriptomic analysis of fruit ripening and the  $\mu$ PEACH1.0 microarray containing 4,806 probes corresponding to genes expressed in peach fruit tissues has been used in a heterologous fashion in two studies of the ripening behaviour of plums. Gene expression of different cultivars of plums treated with the ethylene antagonist, 1-methylcyclopropene (1-MCP) and stored for short periods at room temperature or for longer periods of cold storage was examined. In the first study, mature fruit of a suppressed ethylene climacteric cv. Shiro and a cv. characterized by a typical increase of ethylene production during ripening (Santa Rosa) were harvested and incubated for 24 h in air (control) or 1-MCP. The fruit were allowed to ripen at room temperature for up to 8 days. Different levels of transcripts of genes implicated in cell wall metabolism, hormone (ethylene and auxin) regulation, stress and defense, and in the transcription/translation machinery, as well as others involved with ripening were identified. In the second study, the effects of 1-MCP on gene expression in relation to the development of chilling injury (CI) in the suppressed ethylene climacteric cv. Ruby Red (RR) and the climacteric cv. October Sun (OS) were followed. The fruit were treated for 24 h at room temperature with 1-MCP prior to storage at 0°C. For RR, there was no significant effect of 1-MCP on the level of chilling injury while for OS 1-MCP significantly reduced CI. Microarray analysis showed that immediately following treatment, 186 and 134 genes were differentially expressed between the control and 1-MCP-treated fruit of these cvv., respectively: after 4 weeks cold storage, 311 and 52 genes for RR and OS, respectively, were differentially expressed between control and treated fruit. Thus, for OS, the number of differentially expressed genes reduced during storage while the number increased in RR. Comparisons of the data with those obtained from peaches and nectarines suggest that transcript profile is more altered by 1-MCP in plums than peaches. These studies, carried out within an international collaborative network, will increase our understanding of the regulation of pathways involved in plum fruit ripening and in metabolic processes related to storage and shelf life.