Abstract

Fig (*Ficus carica* L.) fruit undergoes rapid softening during ripening, a process that involves changes in the solubility and molecular size of the cell wall polysaccharides in both the receptacle and drupelet tissues. In this study we report on the isolation and characterization of the expression patterns of eleven genes encoding a collection of cell wall modifying enzymes during ripening of the fig fruit. The genes studied include those encoding *endo*-polygalacturonases (PGs), *endo*-glucanases (EGases), β-galactosidases (β-Gals), xyloglucan endotransglycosylases (XTHs,), expansins (Exps) and α-arabinofuranosidases (Arabfs). The Northern analysis data revealed that the expression patterns of these genes in both tissues during fig fruit ripening could be divided into three categories. The *Fc-Pg1*, *Fc-Pg2*, *Fc-Cel1*, *Fc-Cel2* and *Fc-Gal2* transcripts showed increased accumulation from the ripening onset to the over ripe stage and were clustered into group (I). The *Fc-Exp1*, *Fc-Gal1*, *Fc-Arabf1*, *Fc-XTH1* and *Fc-XTH2* transcripts accumulated at the immature stage and were clustered into group (II). The *Fc-XTH3* transcript accumulated only at the over ripe stage and was the only member of group (III). Other than *Fc-PG2* which was specific to the drupelet tissue, all the other genes were detected in both the receptacle and the drupelets tissue albeit at differing stages of ripening and with different intensity of accumulation. This study suggests that the gene products of the 11 isolated cDNAs putatively encoding cell wall related enzymes are coordinated both in time and amount during fig fruit development and ripening and act together in an interdependent way to achieve softening.