EXPRESSION OF THE 4-COUMARATE: CoA LIGASE GENE FAMILY IN COMPATIBLES AND INCOMPATIBLES *Prunus* GRAFTS

I.S. Pereira¹, J.C. Fachinello¹, L.E.C. Antunes², P. Errea³, R.S. Messias², and A. Pina³*

¹Departamento de Fruticultura, Universidade Federal de Pelotas (UFPel), Brazil

²Departamento de Fitotecnia e Fruticultura, Embrapa Clima Temperado (CPACT), Brazil

³Unidad de Fruticultura, Centro de Investigación y Tecnología Agroalimentaria de Aragón (CITA), Zaragoza. Spain

Graft incompatibility is actually an important problem for development of new Prunus rootstocks. Recently, several authors have reported that the phenylpropanoid metabolism is related with this phenomenon. In plants, this pathway is constituted for three key enzymes, phenylalanine ammonia-lyase (PAL), cinnamate 4-hydroxylase (C4H), and 4-coumarate: CoA ligase (4CL). The 4CL family is especially important in this pathway, as they catalyze the conversion of the hydroxylated cinnamic acids to their respected thioesters. These cinnamyl CoA esters are used for biosynthesis of several phenolic compounds required for various physiological functions and adaptation to environmental perturbations. The aim of the present work was to analyze the gene expression patterns of the 4-Coumarate:CoA genes in compatibles and incompatibles graft combinations two years after grafting. The relationship of Prunus 4CLs with other plants was also studied. To perform this study different graft combinations were evaluated: three rotstocks cultivars, 'Capdeboscq' (Prunus persica L. Batsch), 'Tsukuba 1' (P. persica L. Batsch) and 'Umezeiro' (P. mume Sieb. et Zucc.) grafted into a peach cultivar, 'Chimarrita' (P. persica L. Batsch). Transcript abundance was analysed by qRT-PCR using gene-specific primers designed to amplify the three 4CL genes identified in the assembled peach genome. The results showed that the three 4CL transcripts are expressed in all combinations examined, although the quantitative levels of 4CL mRNA were higher in 'Umezeiro', the incompatible combination. 4CL3 gene was the most highly expressed in the incompatible combination; and it is also the most divergent isoform in the phylogenetic analysis. Based on these results, it seems to be clear the involvement of the phenylpropanoid pathway and especially 4CL enzymes in the incompatibility scion-stock interaction.