Biosynthesis of Chlorogenic Acids in Growing and Ripening Fruits of *Coffea arabica* and *Coffea canephora* Plants

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Chlorogenic acids are major secondary metabolites found in coffee seeds. The accumulation of chlorogenic acids and free quinic acids was studied in *Coffea arabica* cv. Tall Mokka and *Coffea canephora* seeds. Growth stages are specified from I to V, corresponding to rapid expansion and pericarp growth (I), endosperm formation (II), mature (green) (III), ripening (pink) (IV), and fully ripened (red) (V) stages. We detected monocaffeoylquinic acids (3CQA, 4CQA and 5CQA), dicaffeoylquinic acids (3,4diCQA, 3,5diCQA and 4,5diCQA) and a monoferuloylquinic acid (5FQA) in whole fruits (stage I), pericarps and seeds. The most abundant chlorogenic acid was 5CQA, which comprised 50 – 60% of the total of *C. arabica* and 45 – 50% of *C. canephora* seeds. The content of dicaffeoylquinic acid, mainly 3,5-diCQA, was high in *C. canephora*. A high content of 5FQA was found in seeds of stages III to V, especially in *C. canephora*. Total chlorogenic acids were accumulated up to 14 mg per fruit in *C. arabica* and 17 mg in *C. canephora*, respectively. In contrast, free quinic acid varied from 0.4 – 2.0 mg (*C. arabica*) and 0.2 – 4.0 mg (*C. canephora*) per fruit during growth. High biosynthetic activity of 5CQA, which was estimated via the incorporation of [U-^{14}C]phenylalanine into chlorogenic acids, was found in young fruits (perisperm and pericarp) in stage I, and in developing seeds (endosperm) in stages II and III. The biosynthetic activity of chlorogenic acids was clearly reduced in ripening and ripe seeds, especially in *C. canephora*. Transcripts of *PAL1*, *C3′H* and *CCoAMT*, three genes related to the chlorogenic acid biosynthesis, were detected in every stage of growth, although the amounts were significantly less in stage V. Of these genes, *CCoAMT*, a gene for FQA biosynthesis, was expressed more weakly in stage I. The transcript level of *CCoAMT* was higher in seeds than in pericarp, but the reverse was found in *PAL1*. The pattern of expression of genes for the CQA and FQA synthesis is roughly related to the estimated biosynthetic activity, and to the accumulation pattern of chlorogenic acids.

Key words: Caffeoylquinic Acid, Phenylalanine Metabolism, Gene Expression