

Update on Coffee Biochemical Compounds, Protein and Gene Expression during Bean Maturation and in other Tissues

P. MARRACCINI¹, C. ALLARD¹, M.-L. ANDRE¹, C. COURJAULT¹, C. GABORIT¹,
N. LACOSTE¹, A. MEUNIER¹, S. MICHAUX¹, V. PETIT¹, P. PRIYONO³,
J. W. ROGERS², A. DESHAYES¹

¹Nestlé Research Center Tours, Plant Science and Technology, 101 Avenue
Gustave Eiffel, B.P. 9716, 37097 Tours Cedex 2, France

²presently at GeneProt Inc. Geneva Branch, Pré-de-la-Fontaine 2,
Case Postale 125, 1217 Meyrin 2 Switzerland

³Indonesian Coffee and Cocoa Research Institute (ICCRI), Jl.P.B. Sudirman
N°90, Jember 68118, Jawa Timur, Indonesia

SUMMARY

Although coffee is an important economic crop, little work has been carried out on the bean during its maturation. Through a limited number of examples, the aim of this presentation is to make an overview about changes of biochemical compounds, protein and gene expression occurring mainly during coffee bean maturation but also during germination and in other tissues.

The kinetic of accumulation of the main compounds present in the mature bean was performed separately on the three main tissues of the cherry (pericarp, perisperm and endosperm) from 15 weeks after flowering (WAF) to maturity. The relative importance of these three tissues varies during maturation principally. For example the perisperm (maternal tissue), which is the main tissue in the early stages of the bean, is progressively replaced by the endosperm. The evolution of the compounds analyzed by HPLC (i.e quinic acids, 3,5CQA, 5CQA, sucrose glucose, fructose...) is different in these three tissues, it looks similar for several genotypes of *C. canephora* provided by ICCRI, although some differences in the grain filling are observed. These results confirmed that major changes occurred during coffee bean maturation and that exchanges occurred between the main tissues of the cherry.

This point is also confirmed by 2-D gel electrophoresis, which shows significant differences in protein composition during maturation. By the 2-D approach, N-terminal sequencing of proteins and database searching, we also identify several coffee proteins, which led us to clone their corresponding cDNAs. Some of them were used as specific probes to check the expression of the corresponding genes during grain maturation and in other coffee tissue.

For example, the *csp1* gene, encoding 11S storage proteins, and the α -galactosidase gene are expressed in the endosperm but are silent in the perisperm. On the other hand, the two endo- β -mannanase genes, *manA* and *manB*, are only expressed during bean germination. Other examples of coffee genes expressed only in defined tissues like in leaves or perisperm, or on the contrary expressed in all coffee (*C. arabica* and *canephora*) tissues tested, will be shown.

For some of the cDNAs presented in this study, corresponding genes and promoters were cloned and tested in tobacco plants to check their specificity. These promoters could represent useful molecular tools to study tissue-specific gene expression in coffee plants.