In Silico and *in Vitro* Analysis of the Isoprenoid Pathway in Coffee

I. TISKI[1,2], L. F. P. PEREIRA[3], L. G. E. VIEIRA[2], E. K. TAKAHASHI[4], L. P. FERREIRA[2], P. MARRACCINI[2,5], D. POT[2,5], T. LEROY[6], M. T. BENASSI[7], R. C. E. DIAS[7]

[1]Biotechnology Graduation Program – UEL, Londrina, PR, Brazil
[2]IAPAR, CP 481, 86001-970, Londrina, PR, Brazil
[3]EMBRAPA-Café/IAPAR, Londrina, PR, Brazil
[4]Águas Claras Biotecnologia Ltda, Santana do Paraíso, MG, Brazil,
[5]CIRAD/IAPAR, Londrina, PR, Brazil
[6]CIRAD TA 80/03 Avenue d'Agropolis, 34398 Montpellier Cedex 5 France
[7]UEL, Londrina, PR, Brazil

SUMMARY

The most important lipids in coffee, the diterpenes khaweol and cafestol, are originated from the isoprenoid pathway. Despite their diversity in functions and structures, all isoprenoids derive from the common-five carbon building unit isopentenyl diphosphate (IPP) and its isomer dimethylallyl diphosphate (DMAPP). In higher plants, there are two independent pathways located in the cytosol (mevalonic acid or MVA pathway) and in the plastids (methylerythritol phosphate – MEP – or non mevalonic pathway). Throughout the data mining of the Brazilian Coffee Genome Project we studied the genes that code for the enzymes 3-hydroxy-3-methyglutaryl-CoA reductase (HMGR) and mevalonate diphosphate decarboxylase (MPDC) for the MVA pathway and 1-deoxy-D-xylulose 5-phosphate reductoisomerase (DXR) and isopentenyl diphosphate/dimethylallyl diphosphate synthase (IDS) for the MEP pathway.