Plant & Animal Genomes XVIII Conference

January 9-13, 2010
Town & Country Convention Center
San Diego, CA

W157 : Coffee Genomics

Gene Expression Divergences Between The Allopolyploid Coffea arabica And Its Diploids Relatives Appear Environment-Dependant

Amélie Bardil[1] , **Marie-Christine Combes**[2] , **Philippe Lashermes**[2] , **Benoit Bertrand**[1]

[1] CIRAD - Centre de Coopération Internationale en Recherche Agronomique pour le Développement, UMR RPB (CIRAD, IRD, Université Montpellier II), BP 64501, 34394 Montpellier Cedex 5, FRANCE
[2] IRD - Institut de Recherche pour le Développement, UMR RPB (CIRAD, IRD, Université Montpellier II), BP 64501, 34394 Montpellier Cedex 5, FRANCE

Polyploidy is widespread among many major crops. In coffee, the main cultivated species, Coffea arabica, is an allotetraploid containing two diploid subgenomes which originated from two different diploid species, C. canephora and C. eugenioides. Here we showed that the gene expression changes between the natural but recent coffee allopolyploid species in its two diploid relatives is environment-specific.
Using spotted 70-mer oligo-gene microarrays targeting 15522 unigenes, leaf gene expression patterns from plants growing in two temperature conditions were compared between the two parental species and C. arabica. At the lowest temperature, we observed a massive dominance and transgressive expression in C. arabica when compared to its two relatives since 47 to 49 % of unigenes were differentially expressed with the proportions of up- or down-regulation approximately equal (23-24%). Surprisingly at the warmest temperature, we observed a strong disequilibrium. The divergence between C. arabica and C. eugenioides was rather identical to that observed at the lowest temperature since we observed over 40% of the unigenes differentially expressed, but on the other hand the divergence between C. arabica and C. canephora were only 9%.
These data show that numerous genes in C. arabica are non-additively expressed and that divergences in gene expression pattern between allo and diploid genomes are function of the environment conditions. These results reinforce the hypothesis of a better functional plasticity of the allopolyploids in comparison to their related diploids species and consequently the evolutionary advantage of this genome architecture.

Return to the Intl-PAG home page.
For further assistance, e-mail help18@intl-pag.org