



**W190**

## **Contribution Of Subgenomes To The Transcriptome and Their Intertwined Regulation In The Allopolyploid *Coffea arabica* L. Grown In Contrasted Temperatures**

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Polyploidy occurs throughout the evolutionary history of many plants, giving rise to novel phenotypes and leading to ecological diversification and colonization of new niches. *Coffea arabica* a recent allopolyploid between two low divergent diploid species, *Coffea eugenioides* and *Coffea canephora*, can be grown in regions with marked variations in thermal amplitude while the parental species are less adapted to temperature variations. To assess the contribution of subgenomes to the *C. arabica* transcriptome and its variation in relation to the adaptation to variable culture conditions, the transcriptome of leaves of *C. arabica* plants grown in two contrasted thermal regimes were examined using RNA sequencing (RNA-seq) approach. Then the relative homoeologous gene expression was compared to the relative expression between the modern-day diploid progenitor species. Whatever the growing conditions, 65% of the studied genes showed equivalent level of homoeologous gene expression, and for a large majority (92%), the relative homoeologous gene expression between both growing conditions varied less than 10 %. In *C. arabica* growing conditions do not disrupt the relative homoeologous gene expression and the overall gene expression appears to be regulated by intertwined mechanisms. Unlike others allopolyploids analyzed previously, *C. arabica* showed no preferentially expressed subgenome illustrating the interest of considering the age of the allopolyploidization event and the evolutionary divergence of progenitor species when studying allopolyploidy.