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Regulatory Divergence between Parental Alleles Determines Gene Expression Patterns in Hybrids

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Abstract

Both hybridization and allopolyploidization generate novel phenotypes by conciliating divergent genomes and regulatory networks in the same cellular context. To understand the rewiring of gene expression in hybrids, the total expression of 21,025 genes and the allele-specific expression of over 11,000 genes were quantified in interspecific hybrids and their parental species, Coffea canephora and Coffea eugenioides using RNA-seq technology. Between parental species, cis- and trans-regulatory divergences affected around 32% and 35% of analyzed genes, respectively, with nearly 17% of them showing both. The relative importance of trans-regulatory divergences between both species could be related to their low genetic divergence and perennial habit. In hybrids, among divergently expressed genes between parental species and hybrids, 77% was expressed like one parent (expression level dominance), including 65% like C. eugenioides. Gene expression was shown to result from the expression of both alleles affected by intertwined parental trans-regulatory factors. A strong impact of C. eugenioides trans-regulatory factors on the upregulation of C. canephora alleles was revealed. The gene expression patterns appeared determined by complex combinations of cis- and trans-regulatory divergences. In particular, the observed biased expression level dominance seemed to be derived from the asymmetric effects of trans-regulatory parental factors on regulation of alleles. More generally, this study illustrates the effects of divergent trans-regulatory parental factors on the gene expression pattern in hybrids. The characteristics of the transcriptional response to hybridization appear to be determined by the compatibility of gene regulatory networks and therefore depend on genetic divergences between the parental species and their evolutionary history.

Key words: hybridization, cis- and trans-regulation, allele-specific expression, allopolyploidy.

Introduction

Hybridization and allopolyploidization, both prominent events in plant evolution, generate novel hybrid phenotypes (Hegarty and Hiscock 2009). Changes in gene expression have been observed in hybrids that reconcile divergent genomes and regulatory networks in the same cellular context (Landry et al. 2007). Elucidating the regulatory changes at the origin of the variability of gene expression in hybrids is a key to understanding gene-expression novelty and its role in adaptive evolution (Wolf et al. 2010; Buggs et al. 2014). In recent years, several genome-wide studies have investigated gene regulatory divergences and/or inheritance of gene expression in hybrids and allopolyploids (Chagué et al. 2010; McManus et al. 2010; He et al. 2012; Qi et al. 2012; Shi et al. 2012; Bell et al. 2013; Yoo et al. 2013; Cox et al. 2014). In these studies, cis and trans effects have been identified in gene expression differences between parental alleles or homoeologs (McManus et al. 2010; He et al. 2012; Shi et al. 2012; Bell et al. 2013; Xu et al. 2014). In addition, nonadditive gene expression variations in hybrids or allopolyploids relative to parental expression level have been shown. In particular, dominance expression was observed for numerous genes, the expression level in the hybrid or in the allopolyploid being similar to that exhibited by one of the parent, up or down regulated
Relative to the other parent. Furthermore, for most of these studies, the genome-wide expression level dominance was skewed toward one parent (termed as biased expression level dominance; Grover et al. 2012). This phenomenon appears to be common and was reported in various organisms (flies, yeast, plants) (McManus et al. 2010; Qi et al. 2012; Bell et al. 2013; Yoo et al. 2013; Cox et al. 2014). Although overall patterns in gene expression changes in hybrids were described, the relationships between inheritance of gene expression and gene regulatory divergences have not been completely explored and the genetic bases of the variations in allelic expression are poorly understood. To understand the rewiring of gene expression in hybrids, we investigated interspecific hybrids between two Coffea species, Coffea canephora (C) and Coffea eugenioides (E). The two species are perennial woody trees and display considerable variation in morphology, size, and ecological adaptation. Nevertheless, they are closely related, display low sequence divergence (i.e., 1.3% average difference for genes) with very high gene synteny (Cenci et al. 2012), and are characterized by similar genome sizes, 710 Mbp for C and 660 Mbp for E (Noirot et al. 2003). In addition, they hybridize readily (Louarn 1976), and are parental species of the cultivated natural allotetraploid Coffea arabica (Lashermes et al. 1999). To understand the relationships between the inheritance of gene expression and allele-specific expression (ASE), using RNA-seq technology, we analyzed inheritance of gene expression, cis- and trans-regulatory divergences, and variations in ASE in the hybrids.

Materials and Methods

Plant Materials

Interspecific hybrids were generated between C, widespread species in West and Central Africa (0–1,500 m asl.), and E, endemic species in East Africa at much higher altitudes (1,000–2,200 m asl.). The hybrids were produced by crossing C, used as the female parent, with E (C × E) and reciprocally using E as the female parent (E × C) following the standard hybridization technique (Couturon et al. 1998). All the plants belong to the core collection of the Colombian National Center of Coffee Research (CENICAFE: www.cenicafe.org ). For this study, we selected 17 plants including three plants of C. canephora species, four plants of C. eugenioides species, six plants of the F1 interspecific hybrids C × E, and four plants of the reciprocal F1 crosses E × C. All plant materials were grown in common garden growing conditions at Naranjal experimental station (Chinchina, Colombia). Special care was taken to sample, young and just fully expanded leaves on each plant and to frozen the material immediately in liquid nitrogen.

RNA Extraction and RNA Sequencing

Total RNA was extracted using the Qiagen RNeasy kit (Qiagen, Stanford, CA) according to the manufacturer’s instructions. The quality and concentration of extracted RNAs were determined using the Agilent DNA 1000 (Agilent, Santa Clara, CA). The messenger RNA (mRNA) libraries were constructed with the Illumina “RNA-seq sample prep” kit (Illumina, San Diego, CA) and sequenced separately on a HiSeq 2000 (Illumina) at the MGX platform (Montpellier Genomix, France). After quality filtering (Phred score higher than 28 and removal of reads less than 50 bp), a total of 375 million single-end reads (~72 nt) were retained (ranging from 12 to 31 million reads per library), including 80 million, 73 million, 135 million, and 87 million for the C. canephora, C. eugenioides, C × E hybrid, and E × C hybrid libraries, respectively.

RNA-seq Data Processing

The data concerning the parents and the reciprocal interspecific hybrids were treated using the same method. Owing to the low genetic divergence between parental species, the 72-nt reads of each library were mapped to a C. canephora coding DNA sequence reference (25574 CDS) as transcriptome reference (Denoeud et al. 2014) using Burrows Wheeler Aligner MEM (BWA MEM) (Li and Durbin 2010) with the default parameters. The RSeqC v2.4 software package was used to check the quality of RNA-seq data from BAM files (.bam) (Wang et al. 2012). Gene coverage profiles that were slightly biased toward the 3’ extremity of the genes were observed uniformly in all the samples used in the study. As previously (Combes et al. 2013) described, the gene expression estimates for the E parent were assumed to be slightly underestimated, due to a slight technical bias caused by the nature of the transcriptome reference. The aligned sequences of each library were then analyzed to find SNPs (single nucleotide polymorphism) with the GATK toolkit (http://www.broadinstitute.org/gatk/) using the Unified-Genotyper module with default parameters to obtain a list of SNPs and allelic data, and the depth-of-coverage module to obtain information on depth coverage. To avoid artifacts due to reads from pseudogenes or repeat sequences, only the CDS identified as single copy was used for subsequent analyses. A species-specific database of 82,916 SNPs, representing 14,206 CDS, was produced by retaining only divergent polymorphic nucleotide sites at which accessions of both parents were homozygous for differences.

Differential Expression Analysis

Mapped reads of each sample were analyzed with the “DESeq” package (Anders and Huber 2010) in R software version 3.0 (R Foundation for Statistical Computing, Vienna, Austria). To remove the negative effect of background expression noise on differential expression estimation, we restricted analysis to genes with minimum cumulated read counts (depending on the number of replicates) of 30, 40, and 60 for the C. canephora samples, the C. eugenioides, and C × E and C × C hybrid samples, respectively, in at least one parental
and hybrid group. For genes whose allele was not detected in interspecific hybrids, we changed the number of mapped reads from 0 to 1 in order to calculate ratios and perform statistical analyses (Marioni et al. 2008). Data were first normalized on the total number of counts with the DESeq package (using “per condition” and “maximum” as arguments), taking the variance and the mean of the biological replicates into account. Next, pairwise comparisons were performed of the total level of gene expression of the parental species, and those of the hybrids with each of the parental species (negative binomial test). The distribution of P values was checked for a false discovery rate using the Benjamini and Hochberg method at α = 0.05.

Inheritance Classifications

Expression inheritance was determined for differentially expressed genes in hybrids. Log-transformed and DESeq-normalized expression values of each parent were subtracted from those of the hybrid to examine changes in expression. As described by McManus et al. (2010), genes whose total expression in hybrids deviated more than 1.25-fold from that of either parent were considered to have nonconserved inheritance. Based on the magnitude and the direction of the changes, the genes were classified as displaying additivity (with E expression lower or higher than C expression), E or C expression level dominance (lower or higher than either parent: down and up), and transgressivity (lower or higher than both parent: down and up).

ASE and Assignment of cis- and trans-Regulatory Divergence

Using the species-specific SNP database, the reads of hybrids with SNPs were sorted into C or E allele-specific bins using Custom Perl Scripts. Genes with more than 5% of reads exhibiting ambiguous assignment (not consistent with the species-specific SNP database) due to the potential presence of paralogs were discarded (around 1.5% of genes). To examine the possibility of biased ASE, genes with low coverage (cumulative numbers of C-specific reads and E-specific reads was ≤80) were filtered out. ASE of replicates of each hybrid and parental expression of replicates of parents were then treated and normalized using the DESeq package. The count data were normalized on the total number of counts taking the variance and the mean of the biological replicates was taken into account. Relative allelic expression (RAE) corresponding to allele-specific read counts (Chyb or Ehyb) among the total read counts (Chyb + Ehyb) was determined and expressed as the percentage of the Chyb allele (%Chyb) in the total gene expression of the hybrid.

At the transcription level, gene expression is governed by interactions between cis- and trans-regulatory factors. In hybrids, both parental alleles are in the same cellular context and exposed to a common set of trans-regulatory factors; allelic expression can therefore be altered due to cis- and/or trans-regulatory divergence between parental species. ASE in the hybrids compared with allelic expression in their parents makes it possible to distinguish between cis- and trans-regulatory divergences. Several tests were performed (Wittkopp et al. 2004; Shi et al. 2012), first to compare the ratio of expression of the two parental alleles in the hybrids with the relative expression of the same alleles in their parents (two-sided prop.test in R, H0: C/E = CHyb/Ehyb, P value adjusted for multiple testing; Benjamini–Hochberg method) and then to compare the RAE with the balance parental expression (two-sided prop.test in R, H0: Chyb/Ehyb = 1, P value adjusted for multiple testing; Benjamini–Hochberg method). Based on these tests, genes were categorized as conserved, or as belonging to cis-regulatory, trans-regulatory, or cis- + trans-regulatory divergence categories. A similar and balanced allelic expression between parents and hybrids indicated conserved regulation, whereas a conserved unbalanced allelic expression between parents and hybrids was the signature of parental cis-regulatory divergences, and a balanced allelic expression only in hybrids revealed parental trans-regulatory divergences. For the remaining genes, parental expression divergences were the result of a combination of cis and trans effects. Compensating and enhancing cis and trans interactions were identified by comparing the directions of cis and trans effects. A compensating cis + trans interaction was inferred if the cis and trans effects of one gene were in the opposite direction (Chyb/Ehyb > 1 and C/E < Chyb/Ehyb or Chyb/Ehyb < 1 and C/E > Chyb/Ehyb). If the cis and trans effects of one gene acted in the same direction (Chyb/Ehyb > 1 and C/E > Chyb/Ehyb or Chyb/Ehyb < 1 and C/E < Chyb/Ehyb), then the interaction was categorized as enhancing cis + trans interaction.

Up- and Downregulation of Hybrid Alleles

For genes whose ASE was available, the expression regulation of both alleles was evaluated. For each allele, the variation in expression in the parents and in the hybrid was plotted on a graph (Chyb/C on the x axis and Ehyb/E on the y axis). Because for each allele, the genome-specific cis-regulator factors are similar between the parental and hybrid cellular contexts, this graph provides information about changes in allelic expression due to trans-regulatory factors of the other genome. The position of each gene depends on the up- and downregulation of both alleles and on the origin of trans-regulatory effects. Although negative values of the log2 transformed allele-specific ratio (Chyb/C or Ehyb/E) indicate downregulation of alleles in hybrids, positive values indicate upregulation.

Analysis of Functional Enrichment of Gene Ontology (GO)

Computational mapping and plant GO-slim annotation were performed using BLAST2GO PRO software (Conesa et al. 2005; Conesa and Gotz 2008) with default parameters for
Global Pattern of Gene Expression in Hybrids Biased Toward Coffea eugenioides

We characterized changes in gene expression in ten hybrids resulting from distinct hybridization events between accessions of C and E (3 and 4, respectively), and subdivided them into two groups according to the crossing direction (C × E and E × C). To assess the reproducibility of the results, we examined the two groups separately throughout the study. In all comparisons of the total level of gene expression of the hybrids with those of each parental species, we

Results and Discussion

Differential Gene Expression among Parental Species

Before studying gene expression patterns in hybrids, we first characterized pre-existing differential gene expression between the two parental species; 33% of the 21,052 genes we examined were significantly differentially expressed between parental species. Although in E, the gene expression was slightly underestimated due to the use of the C transcriptome as mapping reference (Combes et al. 2013), 59% of differentially expressed genes were more highly expressed in E than in C (fig. 1). In addition, after setting a threshold (log2 fold change ±1.25) so as to consider only markedly differentially expressed genes, the percentage of differentially expressed genes between parents was reduced to 23%, but 60% of differentially expressed genes was still more highly expressed in E than in C. Thus, the estimate of the level of expression divergence between low genetic divergent Coffea species is slightly higher than those between intraspecific Cirsium parents (Bell et al. 2013) and considerably lower than those between divergent Drosophila interspecific parents (McManus et al. 2010). In the GO term enrichments of differentially expressed genes, the processes of “regulation” and “response to stimulus” were over represented, whereas the “metabolic process” and “binding” function were under represented (supplementary table S1, Supplementary Material online). GO term enrichments of the most expressed genes in each parental species were also identified, whereas enrichments of GO terms linked with binding function, metabolic process, “regulation of metabolic process” and “development” process (supplementary table S2, Supplementary Material online) were observed in C. GO terms associated with response to stimulus appeared over represented in E (supplementary table S3, Supplementary Material online). These data suggest that the expression profiles of the parental species are quite similar for basic cellular functions, but differ for genes involved in the regulation of metabolic processes and in the response to stimulus. However, more differences between both species may exist, indeed subtle changes (less than log2 fold change ±1.25) for some parental genes that could considerably affect the phenotype were not considered in the analysis. Nevertheless, the observed transcriptomic divergences for genes involved in the regulation of metabolic processes and in response to stimulus are not surprising for Coffea species which result from a recent and rapid speciation (Cros et al. 1998; Anthony et al. 2010). Under different environmental pressure conditions, each species could have rapidly evolved by regulating gene expression leading to morphological variations and ecological adaptations as observed for species resulting from rapid adaptive radiation (Barrier et al. 2001; Kapralov et al. 2013). The role of gene expression variation in rapid evolution has already been suggested for Senecio aethnensis and Senecio chrysanthemifolius, two closely related species that recently diverged and are adapted to different altitude environments. In these species, regulatory differences in genes involved in environmental adaptation appear to determine their phenotypic differences (Chapman et al. 2013; Muir et al. 2013). In addition, variations in gene expression inducing changes in cellular function with relatively little change in genomic sequence are part of evolutionary processes (Whitehead and Crawford 2006; Ames and Lovell 2011).

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observed fewer differentially expressed genes relative to the E parent than relative to the C parent. Moreover, for each pairwise comparison between hybrids and one of the parents, most differentially expressed genes were more highly expressed in the hybrids than in the parental species, providing evidence for changes in the regulation of gene expression (mainly upregulation) after the genome merger that resulted from hybridization (fig. 2).

Inheritance of Gene Expression in Hybrids and Expression Level Dominance of *Coffea eugenioides*

Changes in gene expression in hybrids were also evidenced by classifying gene expression inheritance patterns. Indeed, in both groups of hybrids, among divergently expressed genes between parental species and hybrids (around 27%), we observed all the different forms of altered gene expression (additivity, up and down dominance, and up and down transgressivity) (fig. 3). Although around 13% and 10% of genes were binned in additivity and transgressivity categories, respectively, the majority of categories contained expression level dominance (the remaining 77%) and the E expression level dominance “up” accounted for almost half the genes. Although we applied different methods of gene classification, the distribution of genes in categories was close to that previously reported for hybrids and allopolyploids (McManus et al. 2010; Qi et al. 2012; Bell et al. 2013; Yoo et al. 2013).

Furthermore, the expression level dominance where the total expression of homeologs for a given gene in an allopolyploid is statistically equivalent to the expression level of that gene in only one of the parents has been described many times before (Grover et al. 2012), but the molecular mechanisms of this phenomenon are still poorly understood.

**Contribution of cis and trans Effects to Gene Expression Divergence**

For genes with species-specific SNPs, RAE was determined and expressed as the percentage of the Chyb allele (%Chyb) in the total gene expression of the hybrid (supplementary Methods, Supplementary Material online). In all the genes we analyzed, both alleles were always expressed in both groups of hybrids and 70% contributed equally to the transcriptome of hybrids, that is, the average percentage of the Chyb allele was around 50%. For genes showing unbalanced RAE, the Chyb allele was no more frequently expressed than the Ehyb allele. For *C. arabica*, the genome-wide analysis of the relative homoeologous gene expression has also revealed that neither of the two subgenomes was preferentially expressed (Combes et al. 2013).

In hybrids, gene expression differences between parental alleles can result from cis- and/or trans-regulatory changes. To elucidate the genetic basis of gene expression divergence, we compared the ASE in parental and hybrid samples to identify cis- and trans-regulatory divergences (fig. 4A). The RAE in hybrids, in which parental alleles and regulatory networks interact in the same cellular environment, provides readout of relative cis-regulatory divergences. Allelic expression divergences not explained by cis-regulatory divergences between the parental species are inferred to be caused by...
trans-regulatory divergences (Cowles et al. 2002; Wittkopp et al. 2004). In our experimental conditions, half the genes showed no expression divergence between parental species and no allelic expression changes in hybrids. In the remaining genes, divergence in allelic expression was classified in three categories with no clear majority among the three: on average, 15.5% in the cis-regulatory category alone, 18.5% in the trans-regulatory category alone, and 17.5% in the cis + trans-regulatory categories (fig. 4B), in the two groups of hybrids. The absolute magnitude of parental gene expression divergence in each regulatory divergence category was evaluated. Trans effects appeared to play a larger role than cis effects in parental gene expression divergence in both groups of hybrids (fig. 4C). The data indicate that divergent evolution between diploid species may have impacted the regulatory sequences of genes (cis-regulatory factors) and abundance, as well as the activity of upstream regulators throughout the genome (trans-regulatory factors). In addition, the data also provided evidence for the compatibility of diverged parental regulatory networks and of intertwined regulation of alleles. Indeed for all genes showing trans-regulatory expression divergence (combined with cis-regulatory or not), ASE was controlled by trans-regulatory factors from both parental genomes that are able to cause up- or downregulation of one or both alleles. Intertwined regulation of parental species has been already reported in gene expression in C. arabica (Combes et al. 2013). In several studies considering intra- or interspecific hybrids of variable organisms (flies, yeast, plants), cis-regulatory divergences predominated and explained more of the expression differences between species than within species (Emerson and Li 2010; Shi et al. 2012). With the exception of the study of McManus et al. (2010), trans-regulatory divergences contributed preferentially to the expression differences within species (Emerson et al. 2010; Bell et al. 2013; Xu et al. 2014). Others observations, such as the relative proportion of genes with evidence of cis- and/or trans-regulatory divergences,
were more variable among studies. For Coolon et al. (2014) who studied expression differences within and between species of Drosophila, the proportion of genes with cis-regulatory divergences increases with divergence time but also depends on the mode of regulatory evolution of the species. In the study of Drosophila melanogaster and Drosophila sechellia hybrids, McManus et al. (2010) interpreted the higher proportion of trans-regulatory divergences than expected for an interspecific hybrid as an effect of particular demographic and ecological history of D. sechellia (McManus et al. 2010). In the case of Coffea species, gene expression differences result notably from cis-regulatory divergences but also from a larger part than expected of trans-regulatory divergences associated or not with cis-regulatory divergences. This finding could be related to the recent speciation and the low genetic divergence between parental species. In addition, the perennial habit of Coffea species and the long generation time (i.e., 10–20 years) of coffee trees in natural conditions associated with a slow molecular evolution rate could be considered (Cenci et al. 2013).

The GO term enrichments of genes belonging to cis- or trans-regulatory divergences categories have revealed that GO terms related to “cellular metabolic process” were over represented among genes displaying cis-regulatory changes.
A Clear Relationship between Regulation of Allelic Expression and Expression Inheritance in Hybrids

In hybrids, trans-regulatory factors from both parental origins could bind cis-regulatory regions of alleles differently and have different effects on expression between alleles. Analysis of the expression variation of alleles from both genomes between the parental and the hybrid contexts reveals the roles of trans-regulatory factors, and hence should elucidate the evolution of the parental species (Shi et al. 2012). To further analyze regulation of alleles in the differentially expressed genes in the hybrids compared with the parental species, we assessed variation in ASE in the two groups of hybrids. For each gene, we estimated variations in ASE in either the C genome (C-ASE) with the RAE C_{hyb}/C or the E genome (E-ASE) with the RAE E_{hyb}/E between the parental and hybrid contexts (fig. 5 and supplementary fig. S2, Supplementary Material online, for C x E and E x C hybrids, respectively). Given that the genome-specific cis-regulatory factors are similar in the parents and the hybrids, trans-regulatory effects on the variation in ASE were revealed as well as their genome origin. The RAE of the C genome (C_{hyb}/C) was plotted against the RAE of the E genome (E_{hyb}/E) on a logarithmic scale. Log2 positive values of the RAE C_{hyb} > C or E_{hyb} > E indicate upregulation of the alleles by the trans-regulatory factors of the homologous genome, while negative values of this ratio indicate downregulation of the alleles. The gene position relative to both axes reveals the single or combined genome origin of the trans-regulatory factors acting on that gene. Although alleles of both C and E genomes displayed both upregulated and downregulated allelic expression, the effects of trans-regulatory factors on both genomes appeared to be genome dependent. The E_{hyb} alleles were up- and downregulated by C trans-regulatory factors, whereas C_{hyb} alleles were mainly upregulated by E trans-regulatory factors. What is more, the E trans-regulatory factors had a greater impact on C-ASE than the C trans-regulator factors on E-ASE; the magnitude of variation in the expression of the C_{hyb} allele was higher than that of the E_{hyb} allele. These results suggest asymmetric effects of the activation of alleles of one genome by trans-regulatory factors of the other.

To refine this observation, the effects of C and E trans-regulatory factors on the C_{hyb} and E_{hyb} alleles in hybrids were analyzed. For genes in the cis-+ trans-regulatory categories and trans-regulatory divergence categories, C_{hyb} and E_{hyb} alleles were classified according to the magnitude of the variation in allele expression between the hybrid and the parents (fig. 6). More E_{hyb} alleles than C_{hyb} alleles displayed only slight changes in ASE between the hybrids and their parental species, whereas more C_{hyb} alleles than E_{hyb} alleles showed marked ASE changes. These observations confirm that the E trans-regulatory factors have greater effects than C trans-regulatory factors on ASE variation between parental species and hybrids, in agreement with the observed overall E expression level dominance. As in the study of He et al. (2012) where asymmetry of ASE in Arabidopsis hybrids has been explained by differences in the efficiency of epigenetic gene silencing (He et al. 2012), one can also imagine epigenetic causes of the asymmetric effects of the trans-regulatory factors of one genome on the activation of alleles of the other. Indeed, the more effective E trans-regulatory factors observed in both the C x E and E x C hybrids for genes showing trans-regulatory divergences could indicate divergent epigenetic states between the two parental species.

To elucidate the regulatory mechanisms at the root of the gene expression inheritance, the up- and downregulation of the expression of alleles and the expression inheritance of genes were interpreted jointly (fig. 5 for C x E and supplementary fig. S2, Supplementary Material online, for E x C hybrids). For the majority of genes classified in the E expression level dominance “up” category, the C_{hyb} alleles were upregulated by E trans-regulatory factors, whereas for genes in the E expression level dominance “down” category, the C_{hyb} alleles...
Variation in specific allelic expression (ASE) for genes differentially expressed between parents and the hybrid in the $C \times E$ hybrids. Each point represents a single gene, its position displays the combined up- and downregulation of both alleles ($C_{hyb}/C$ on the x-axis; $E_{hyb}/E$ on the y-axis, $C_{hyb}, E_{hyb}$ and $C$, $E$ corresponding to allelic and parental read counts, respectively), and its color code, the inheritance category of the gene. In this way, the combined regulation of alleles at the root of expression inheritance was elucidated for each gene analyzed (chi-square test, $P < 0.001$).

Effects of trans-regulatory factors of the $E$ and $C$ genome on up- and downregulation of $C_{hyb}$ and $E_{hyb}$ alleles in $C \times E$ and $E \times C$ hybrids. In line with the method of Shi et al. (2012), the genes subjected to either only trans- or only cis + trans effects were categorized according to differences in the absolute values of allelic expression between $C \times E$ and $E \times C$ hybrids and each parental species (on the x-axis, dark gray for $C_{hyb}/C$ and light gray for $E_{hyb}/E$). Although more $E_{hyb}$ alleles showed a low level of expression difference between the parents and the hybrid, more $C_{hyb}$ alleles displayed a high level of expression difference (chi-squared test, $P < 0.001$).
were downregulated. The same was observed for the C expression level dominance up and down categories, the Ehyb alleles being up- and downregulated by the C trans-regulatory factors. For the additivity and transgressivity categories, gene expression appeared to result from the combined effects of E and C trans-regulatory factors. Each category of expression inheritance of genes in hybrids depends on particular combinations of up- and downregulation of both alleles. In agreement with two previous studies that investigated both homoelogous and total gene expression in allopolyploids (Yoo et al. 2013; Cox et al. 2014), the present data confirmed that the biased expression level dominance toward one parent was mainly caused by up- or downregulation of the allele of the other parent. In addition, in this study, the observed biased expression level dominance was attributed to asymmetric effects of trans-regulators factors of parental genomes. Similarly, between Arabidopsis thaliana and Arabidopsis arenosa, Shi et al. (2012) observed higher effects of trans-regulatoty factors of A. arenosa on allelic expression in hybrids. Moreover, an overall expression dominance of A. arenosa genes over A. thaliana genes was previously reported in synthetic allopolyploids between A. arenosa and A. thaliana.
(Wang et al. 2006). For other studies in various biological organisms (Bell et al. 2013; Yoo et al. 2013; Cox et al. 2014), the phenomenon of expression level dominance would be also attributed to the unbalanced effects of parental trans-regulatory factors. Accordingly, we hypothesize that in hybrids, gene expression inheritance could depend on the effects of trans-regulatory factors of one genome on the other genome, and hence the regulatory divergence between parental species. Thus, the divergent evolutionary histories of parental species could partly explain the different patterns of gene expression inheritance in hybrids reported in previous studies (McManus et al. 2010; Shi et al. 2012; Bell et al. 2013).

**Particular RAE Distribution for Each Category of Expression Inheritance**

Next, we refined the description of regulatory mechanisms of differentially expressed genes in interspecific hybrids relative to their parental species in the two groups of hybrids. For each category of expression inheritance, the distribution of genes according to RAE and regulatory divergence were compared with the distribution of genes in the conserved genes category, and significant differences were revealed (fig. 7 for C x E and supplementary fig. S3, Supplementary Material online, for E x C hybrids). Whatever the category of expression inheritance, the distributions of RAE were always unbalanced and biased toward the parental allele corresponding to the parent more expressed for the considered category. In the transgressivity up category, in which the two parental species were not differentially expressed, the RAE was more balanced than in other categories. With regard to the distributions of regulatory divergence mechanisms, the proportion of genes classified in each category varied between the categories of expression inheritance. The data showed that both cis- and trans-regulatory divergences were associated with variable allelic expression and consequently involved in variations of gene expression in hybrids. These findings reveal the intertwined allelic expression regulation and the complex relationship between the cis- and trans-regulatory factors that modulate gene expression. In addition, trans-regulatory divergences between parental species can have different origins: Changes in chromatin structures but also in transcription factors, changes in effectors, and RNA interference (RNAi) (Groszmann et al. 2011; Chodavarapu et al. 2012; He et al. 2012; Shen et al. 2012; Donoghue et al. 2014; Greaves et al. 2014).

**Conclusions**

Our genome-wide analysis enabled us to characterize both the genetic divergence between parental species and new gene expression patterns in hybrids. Gene expression changes between C. canephora and C. eugenioides resulted from both cis- and trans-divergences. The importance of trans-regulatory divergences observed between these two species could be related to their low genetic divergence and perennial habit.

In *Coffea* hybrids, the pattern of gene expression inheritance was characterized by a genome-wide expression level dominance biased toward the *C. eugenioides* parent. Moreover, gene expression was shown to result from the expression of both alleles and was affected by intertwined parental trans-regulatory factors indicating compatibility of parental regulatory networks. Hence, gene expression inheritance appeared to be determined by a complex mix of cis-regulatory factors and asymmetric effects of divergent trans-regulatory parental factors on up- and downregulation of alleles. In particular, the phenomenon of biased expression level dominance was attributed to unbalanced effects of parental trans-regulatory factors. More generally in hybrids, the extent and relative rates of cis- and trans-divergence among the parental species would have a significant effect on the gene expression pattern. In addition, the more similar the parental genomes, the more likely it is that the transcription factors of one genome might be compatible with transcription factor binding sites on the other genome. It appears that in hybrids, the characteristics of the transcriptional response to genome merger depend on genetic divergences between the parental species and their evolutionary history.

**Supplementary Material**

Supplementary figures S1–S3, tables S1–S4, and Methods are available at *Genome Biology and Evolution* online (http://www.gbe.oxfordjournals.org/).

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**Literature Cited**


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