

Transgressive expression of genes at the transcript level among ILs

Interspecific crosses combining divergent genomes can sometimes result in improved performance. Transcriptomic studies of wild and resynthesized hybrids show extensive gene expression alterations in the hybrids compared to their parents (Hegarty et al., 2008). The IL population allows us to study the combination of divergent genomes across many genetically distinct lines. Many of the changes we see are “transgressive”, falling outside the range seen in either parent. A total of 2,286 genes, more than one fourth of unique DE genes between the ILs and cv. M82, showed transgressive expression patterns, i.e. genes were differentially expressed for the IL but not for *S. pennellii* compared to cv. M82 (Supplemental Dataset 22). These genes were distributed across all ILs but the extent of transgressive gene expression varied among the ILs. ILs with high number of differentially expressed genes, such as IL6.2.2, IL4.3, and IL8.1, also showed higher number of transgressively expressed genes (Figure S12A in this document). While synthetic allotetraploids generated from interspecific crosses show large scale down regulation of gene expression (likely due to silencing of duplicate gene copies (Wang et al., 2006) and the affected genes fall in the categories of cell defense, ageing and hormonal regulation, the transgressive genes in this IL population generated by interspecific crossing show mostly upregulation of gene expression with genes falling in the broad categories of photosynthesis, energy metabolism, microtubule movement, and extrinsic membrane components (See following table on GO-enrichment). In order to estimate the relative effect of the introgression on transgressive gene expression, we quantified the ratio of the number of genes with transgressive expression to

the number of genes with *S. pennellii* like expression (transgressive_to_*S. pennellii*-like) for each IL (Figure S12B in this document). A few ILs, such as IL1.4.18, IL4.3, IL7.3, IL8.1, IL11.1, and IL12.1.1, showed a transgressive_by_*S. pennellii* value greater than 0.5, suggesting a higher effect of the corresponding introgression on gene expression in M82 background. Most of the transgressively expressed genes for each IL were located in *trans*, beyond the introgression region (Figure S12A in this document). These may result from novel combinations of regulatory factors (Riddle and Birchler, 2003), recombination of alleles present at different loci in the parent species through complementary gene action (Rieseberg et al., 1999), more abundant production of small interfering (si) RNAs in progeny of interspecific crosses than in either parent with concomitant suppression of the corresponding target genes, and hypermethylation of the corresponding genomic DNA (Shivaprasad et al., 2012).

References:

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Table: GO-enrichment results for genes showing transgressive expression

Enriched GO-categories for the genes showing transgressive expression	
GO:0010287	plastoglobule
GO:0009535	chloroplast thylakoid membrane
GO:0009523	photosystem II
GO:0016168	chlorophyll binding
GO:0009765	photosynthesis, light harvesting
GO:0009522	photosystem I
GO:0015979	photosynthesis
GO:0009941	chloroplast envelope
GO:0018298	protein-chromophore linkage
GO:0030095	chloroplast photosystem II
GO:0009543	chloroplast thylakoid lumen
GO:0009654	photosystem II oxygen evolving complex
GO:0019253	reductive pentose-phosphate cycle
GO:0016717	oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water
GO:0009538	photosystem I reaction center
GO:0009570	chloroplast stroma
GO:0019898	extrinsic component of membrane
GO:0042651	thylakoid membrane
GO:0007018	microtubule-based movement

Enriched GOslim-categories for the genes showing transgressive expression	
GO:0015979	photosynthesis
GO:0009579	thylakoid
GO:0009536	plastid
GO:0006091	generation of precursor metabolites and energy
GO:0005576	extracellular region
GO:0003774	motor activity
GO:0003824	catalytic activity
GO:0003674	molecular_function

