

1. [The fate of duplicated genes in a polyploid plant genome](#)

ผู้แต่ง: Roulin, A., Auer, P. L., Libault, M., Schlueter, J., Farmer, A., May, G., Stacey, G., Doerge, R. W. and Jackson, S. A.

วารสาร: The Plant Journal, Volume 73, Issue 1, pages 143–153, January 2013

Summary: Polyploidy is generally not tolerated in animals, but is widespread in plant genomes and may result in extensive genetic redundancy. The fate of duplicated genes is poorly understood, both functionally and evolutionarily. Soybean (*Glycine max* L.) has undergone two separate polyploidy events (13 and 59 million years ago) that have resulted in 75% of its genes being present in multiple copies. It therefore constitutes a good model to study the impact of whole-genome duplication on gene expression. Using RNA-seq, we tested the functional fate of a set of approximately 18 000 duplicated genes. Across seven tissues tested, approximately 50% of paralogs were differentially expressed and thus had undergone expression sub-functionalization. Based on gene ontology and expression data, our analysis also revealed that only a small proportion of the duplicated genes have been neo-functionalized or non-functionalized. In addition, duplicated genes were often found in collinear blocks, and several blocks of duplicated genes were co-regulated, suggesting some type of epigenetic or positional regulation. We also found that transcription factors and ribosomal protein genes were differentially expressed in many tissues, suggesting that the main consequence of polyploidy in soybean may be at the regulatory level.

2. [The molecular and enzymatic basis of bitter/non-bitter flavor of citrus fruit: evolution of branch-forming rhamnosyltransferases under domestication](#)

ผู้แต่ง: Frydman, A., Liberman, R., Huhman, D. V., Carmeli-Weissberg, M., Sapir-Mir, M., Ophir, R., W. Sumner, L. and Eyal, Y.

วารสาร: The Plant Journal, Volume 73, Issue 1, pages 166–178, January 2013

Summary: Domestication and breeding of citrus species/varieties for flavor and other characteristics, based on the ancestral species pummelo, mandarin and citron, has been an ongoing process for thousands of years. Bitterness, a desirable flavor characteristic in the fruit of some citrus species (pummelo and grapefruit) and undesirable in others (oranges and mandarins), has been under positive or negative selection during the breeding process of new species/varieties. Bitterness in citrus fruit is determined by the composition of branched-chain flavanone glycosides, the predominant flavonoids in citrus. The flavor-determining biosynthetic step is catalyzed by two branch-forming rhamnosyltransferases that utilize flavanone-7-O-glucose as substrate. The 1,2-rhamnosyltransferase (encoded by *Cm1,2RhaT*) leads to the bitter flavanone-7-O-neohesperidosides whereas the 1,6-rhamnosyltransferase leads to the tasteless flavanone-7-O-rutinosides. Here, we describe the functional characterization of *Cs1,6RhaT*, a 1,6-rhamnosyltransferase-encoding gene directing biosynthesis of the tasteless flavanone rutinosides common to the non-bitter citrus species. *Cs1,6RhaT* was found to be a substrate-promiscuous enzyme catalyzing branched-chain rhamnosylation of flavonoids glucosylated at positions 3 or 7. *In vivo* substrates include flavanones, flavones, flavonols and anthocyanins. *Cs1,6RhaT* enzyme levels were shown to peak in young fruit and leaves, and gradually subside during development. Phylogenetic analysis of *Cm1,2RhaT* and *Cs1,6RhaT* demonstrated that they both belong to the branch-forming glycosyltransferase cluster, but are distantly related and probably originated separately before speciation of the citrus genome. Genomic data from citrus, supported by a study of *Cs1,6RhaT* protein levels in various citrus species, suggest that inheritance, expression levels and mutations of branch-forming rhamnosyltransferases underlie the development of bitter or non-bitter species/varieties under domestication.

[3. The late steps of plant nonsense-mediated mRNA decay](#)

ผู้แต่ง: Mérai, Z., Benkovics, A. H., Nyikó, T., Debreczeny, M., Hiripi, L., Kerényi, Z., Kondorosi, É. and Silhavy, D.

วารสาร: The Plant Journal, Volume 73, Issue 1, pages 50–62, January 2013

Summary: Nonsense-mediated mRNA decay (NMD) is a eukaryotic quality control system that identifies and degrades mRNAs containing premature termination codons (PTCs). If translation terminates at a PTC, the UPF1 NMD factor binds the terminating ribosome and recruits UPF2 and UPF3 to form a functional NMD complex, which triggers the rapid decay of the PTC-containing transcript. Although NMD deficiency is seedling lethal in plants, the mechanism of plant NMD remains poorly understood. To understand how the formation of the NMD complex leads to transcript decay we functionally mapped the UPF1 and SMG7 plant NMD factors, the putative key players of NMD target degradation. Our data indicate that the cysteine–histidine-rich (CH) and helicase domains of UPF1 are only essential for the early steps of NMD, whereas the heavily phosphorylated N- and C-terminal regions play a redundant but essential role in the target transcript degradation steps of NMD. We also show that both the N- and the C-terminal regions of SMG7 are essential for NMD. The N terminus contains a phosphoserine-binding domain that is required for the early steps of NMD, whereas the C terminus is required to trigger the degradation of NMD target transcripts. Moreover, SMG7 is a P-body component that can also remobilize UPF1 from the cytoplasm into processing bodies (P bodies). We propose that the N- and C-terminal phosphorylated regions of UPF1 recruit SMG7 to the functional NMD complex, and then SMG7 transports the PTC-containing transcripts into P bodies for degradation.

[4. New allelic variants found in key rice salt-tolerance genes: an association study](#)

ผู้แต่ง: Negrão, S., Cecília Almadanim, M., Pires, I. S., Abreu, I. A., Maroco, J., Courtois, B., Gregorio, G. B., McNally, K. L. and Margarida Oliveira, M.

วารสาร: Plant Biotechnology Journal, Volume 11, Issue 1, pages 87–100, January 2013

Summary: Salt stress is a complex physiological trait affecting plants by limiting growth and productivity. Rice, one of the most important food crops, is rated as salt-sensitive. High-throughput screening methods are required to exploit novel sources of genetic variation in rice and further improve salinity tolerance in breeding programmes. To search for genotypic differences related to salt stress, we genotyped 392 rice accessions by EcoTILLING. We targeted five key salt-related genes involved in mechanisms such as Na^+/K^+ ratio equilibrium, signalling cascade and stress protection, and we found 40 new allelic variants in coding sequences. By performing association analyses using both general and mixed linear models, we identified 11 significant SNPs related to salinity. We further evaluated the putative consequences of these SNPs at the protein level using bioinformatic tools. Amongst the five nonsynonymous SNPs significantly associated with salt-stress traits, we found a T67K mutation that may cause the destabilization of one transmembrane domain in OsHKT1;5, and a P140A alteration that significantly increases the probability of OsHKT1;5 phosphorylation. The K24E mutation can putatively affect Salt interaction with other proteins thus impacting its function. Our results have uncovered allelic variants affecting salinity tolerance that may be important in breeding.

[5. Transgenic rice with inducible ethylene production exhibits broad-spectrum disease resistance to the fungal pathogens *Magnaporthe oryzae* and *Rhizoctonia solani*](#)

ผู้แต่ง: Helliwell, E. E., Wang, Q. and Yang, Y.

วารสาร: Plant Biotechnology Journal, Volume 11, Issue 1, pages 33–42, January 2013

Summary: Rice blast (*Magnaporthe oryzae*) and sheath blight (*Rhizoctonia solani*) are the two most devastating diseases of rice (*Oryza sativa*), and have severe impacts on crop yield and grain quality. Recent evidence suggests that ethylene (ET) may play a more prominent role than salicylic acid and jasmonic acid in mediating rice disease resistance. In this study, we attempt to genetically manipulate endogenous ET levels in rice for enhancing resistance to rice blast and sheath blight diseases. Transgenic lines with inducible production of ET were generated by expressing the rice ACS2 (1-aminocyclopropane-1-carboxylic acid synthase, a key enzyme of ET biosynthesis) transgene under control of a strong pathogen-inducible promoter. In comparison with the wild-type plant, the OsACS2-overexpression lines showed significantly increased levels of the OsACS2 transcripts, endogenous ET and defence gene expression, especially in response to pathogen infection. More importantly, the transgenic lines exhibited increased resistance to a field isolate of *R. solani*, as well as different races of *M. oryzae*. Assessment of the growth rate, generational time and seed production revealed little or no differences between wild type and transgenic lines. These results suggest that pathogen-inducible production of ET in transgenic rice can enhance resistance to necrotrophic and hemibiotrophic fungal pathogens without negatively impacting crop productivity.

6. [Plant functional diversity and carbon storage – an empirical test in semi-arid forest ecosystems](#)

ผู้แต่ง: Conti, G., Díaz, S.

วารสาร: Journal of Ecology, Volume 101, Issue 1, pages 18–28, January 2013

Summary:

1. Carbon storage in vegetation and soil underpins climate regulation through carbon sequestration. Because plant species differ in their ability to capture, store and release carbon, the collective functional characteristics of plant communities (functional diversity) should be a major driver of carbon accumulation in terrestrial ecosystems.
2. Three major components of plant functional diversity could be put forward as drivers of carbon storage in ecosystems: the most abundant functional trait values, the variety of functional trait values and the abundance of particular species that could have additional effects not incorporated in the first two components.
3. We tested for associations between these components and carbon storage across 16 sites in the Chaco forest of Argentina under the same climate and on highly similar parental material. The sites differed in their plant functional diversity caused by different long-term land-use regimes.
4. We measured six plant functional traits in 27 species and weighted them by the species abundance at each site to calculate the community-weighted mean (CWM) and the functional divergence (FDvar) of each single trait and of multiple traits (FDiv). We also measured plant and soil carbon storage. Using a stepwise multiple regression analysis, we assessed which of the functional diversity components best explained carbon storage.
5. Both CWM and FDvar of plant height and wood-specific gravity, but no leaf traits, were retained as predictors of carbon storage in multiple models. Relationships of FDvar of stem traits and FDiv with carbon storage were all negative. The abundance of five species improved the predictive power of some of the carbon storage models.
6. *Synthesis.* All three major components of plant functional diversity contributed to explain carbon storage. What matters the most to carbon storage in these ecosystems is the relative abundance of plants with tall, and to a lesser extent dense, stems with a narrow range of variation around these values. No consistent link was found between carbon storage and the leaf traits usually associated with plant resource use strategy. The negative association of trait divergence with carbon storage provided no evidence in support to niche complementarity promoting carbon storage in these forest ecosystems.

7. [Tree species diversity increases fine root productivity through increased soil volume filling](#)

ผู้แต่ง: Brassard, B. W., Chen, H. Y. H., Cavard, X., Laganière, J., Reich, P. B., Bergeron, Y., Paré, D., Yuan, Z.

วารสาร: Journal of Ecology, Volume 101, Issue 1, pages 210–219, January 2013

Summary:

1. Although fine roots (< 2 mm in diameter) account for a major share of the production of terrestrial ecosystems, diversity effects on fine root productivity and their mechanisms remain unclear.
2. We hypothesized that: (i) fine root productivity increases with tree species diversity, (ii) higher fine root productivity is a result of greater soil volume filling due to species-specific patterns of root placement and proliferation, and (iii) differences in fine root productivity and soil volume filling associated with tree species diversity are more pronounced in summer when plants are physiologically active and demand for water and nutrients is at its greatest.
3. We investigated the effects of tree species diversity on fine root productivity and soil volume filling of boreal forest stands that have grown naturally for 85 years on similar sites.
4. Annual fine root production was 19–83% higher in evenly mixed- than single-species-dominated stands, and increased with tree species evenness, but not tree species richness. Fine root biomass was higher in evenly mixed- than single-species-dominated stands in summer months, but not in spring or fall. Higher fine root productivity in evenly mixed- than single-species-dominated stands was realized by filling more soil volume horizontally and vertically in the forest floor in the mixtures of deep- and shallow-rooted species vs. the deeper mineral soil in the mixtures of deep-rooted species.
5. *Synthesis.* Our results provide some of the first direct evidence for below-ground species complementarity in heterogeneous natural forests, by demonstrating that tree species evenness increases fine root productivity by filling/exploiting the soil environment more completely in space and time, driven by differences in the inherent rooting traits of the component species and variations of root growth within species.

8. [Epigenetic variation creates potential for evolution of plant phenotypic plasticity](#)

ผู้แต่ง: Zhang, Y.-Y., Fischer, M., Colot, V. and Bossdorf, O.

วารสาร: New Phytologist, Volume 197, Issue 1, pages 314–322, January 2013

Summary:

- Heritable variation in plant phenotypes, and thus potential for evolutionary change, can in principle not only be caused by variation in DNA sequence, but also by underlying epigenetic variation. However, the potential scope of such phenotypic effects and their evolutionary significance are largely unexplored.
- Here, we conducted a glasshouse experiment in which we tested the response of a large number of epigenetic recombinant inbred lines (epiRILs) of *Arabidopsis thaliana* – lines that are nearly isogenic but highly variable at the level of DNA methylation – to drought and increased nutrient conditions.
- We found significant heritable variation among epiRILs both in the means of several ecologically important plant traits and in their plasticities to drought and nutrients. Significant selection gradients, that is, fitness correlations, of several mean traits and plasticities suggest that selection could act on this epigenetically based phenotypic variation.
- Our study provides evidence that variation in DNA methylation can cause substantial heritable variation of ecologically important plant traits, including root allocation, drought tolerance and nutrient plasticity, and that rapid evolution based on epigenetic variation alone should thus be possible.

9. [Association genetics of chemical wood properties in black poplar \(*Populus nigra*\)](#)

ผู้แต่ง: Guerra, F. P., Wegrzyn, J. L., Sykes, R., Davis, M. F., Stanton, B. J. and Neale, D. B.

วารสาร: New Phytologist, Volume 197, Issue 1, pages 162–176, January 2013

Summary:

- Black poplar (*Populus nigra*) is a potential feedstock for cellulosic ethanol production, although breeding for this specific end use is required. Our goal was to identify associations between single nucleotide polymorphism (SNP) markers within candidate genes encoding cellulose and lignin biosynthetic enzymes, with chemical wood property phenotypic traits, toward the aim of developing genomics-based breeding technologies for bioethanol production.
- Pyrolysis molecular beam mass spectrometry was used to determine contents of five- and six-carbon sugars, lignin, and syringyl : guaiacyl ratio. The association population included 599 clones from 17 half-sib families, which were successfully genotyped using 433 SNPs from 39 candidate genes. Statistical analyses were performed to estimate genetic parameters, linkage disequilibrium (LD), and single marker and haplotype-based associations.
- A moderate to high heritability was observed for all traits. The LD, across all candidate genes, showed a rapid decay with physical distance. Analysis of single marker–phenotype associations identified six significant marker–trait pairs, whereas nearly 280 haplotypes were associated with phenotypic traits, in both an individual and multiple trait-specific manner.
- The rapid decay of LD within candidate genes in this population and the genetic associations identified suggest a close relationship between the associated SNPs and the causative polymorphisms underlying the genetic variation of lignocellulosic traits in black poplar.

10. [Abscisic acid accumulation modulates auxin transport in the root tip to enhance proton secretion for maintaining root growth under moderate water stress](#)

ผู้แต่ง: Xu, W., Jia, L., Shi, W., Liang, J., Zhou, F., Li, Q. and Zhang, J.

วารสาร: New Phytologist, Volume 197, Issue 1, pages 139–150, January 2013

Summary:

- Maintenance of root growth is essential for plant adaptation to soil drying. Here, we tested the hypothesis that auxin transport is involved in mediating ABA's modulation by activating proton secretion in the root tip to maintain root growth under moderate water stress.
- Rice and Arabidopsis plants were raised under a hydroponic system and subjected to moderate water stress (-0.47 MPa) with polyethylene glycol (PEG). ABA accumulation, auxin transport and plasma membrane H^+ -ATPase activity at the root tip were monitored in addition to the primary root elongation and root hair density.
- We found that moderate water stress increases ABA accumulation and auxin transport in the root apex. Additionally, ABA modulation is involved in the regulation of auxin transport in the root tip. The transported auxin activates the plasma membrane H^+ -ATPase to release more protons along the root tip in its adaption to moderate water stress. The proton secretion in the root tip is essential in maintaining or promoting primary root elongation and root hair development under moderate water stress.
- These results suggest that ABA accumulation modulates auxin transport in the root tip, which enhances proton secretion for maintaining root growth under moderate water stress.