ANALYSIS OF PINACEAE GENE FAMILY EVOLUTION SUGGESTS ACCELERATED GENE TURNOVER IN PINE TREES

***Claudio Casola**, Weixi Zhu, and Tomasz E. Koralewski*

Department of Ecosystem Science and Management, Texas A&M University, College Station, TX, USA

Gene duplications and losses are major determinants of evolutionary change. We investigated patterns of gene duplications and gene losses in four Pinaceae species: loblolly pine, sugar pine, Norway spruce and Douglas-fir. After clustering orthologous groups in gene families using OrthoFinder, we applied the likelihood framework implemented in the CAFE software to estimate gene turnover rates and patterns in 16,118 gene families (~24,000-28,000 genes per species). We found that gene turnover is at least twice as high in the two pines (~110 gene gains and/or losses per million years) compared to Norway spruce and Douglas-fir, a result that was robust to changes in the model of gene family evolution implemented in CAFE. Additionally, we identified 1,192 gene families with significant expansion or contraction, and a high proportion of gene duplications vs. gene losses in Douglas-fir. Overall, our results indicate that no less than 1/5 of all gene families experienced gains or losses during the evolution of these Pinaceae. However, we observed that 31-48% of genes have a length <75% of the longest gene in the same gene family, supporting previous findings of extensive occurrence of pseudogenes in conifers. Following removal of putative pseudogenes from the 1,192 gene families with high gene turnover rates, we identified several genetic pathways in the four Pinaceae with significant expansions or contractions in multiple gene families, suggesting selection across gene families involved in these biological processes.

Contact Information: Claudio Casola, Department of Ecosystem Science and Management, Texas A&M University, College Station, TX 77843. Phone: 979-845-8803, Email: ccasola@tamu.edu