

Identification and characterization of constitutive Fraser fir (*Abies fraseri*) promoter and terminator elements to facilitate *in planta* functional genomic analyses

James R. Dudit¹, Estefania Elorriaga¹, Angela Chiang¹, Robert Thomas¹, Ross W. Whetten¹, Macaire M. S. Yuen¹, and Justin G. A. Whitehill¹

¹Department of Forestry and Environmental Resources, North Carolina State University, Raleigh, USA, 27695

Fraser fir (*Abies fraseri*) is the most economically important Christmas tree species commercially grown throughout North America accounting for ~40% of all species sold. However, Fraser fir is vulnerable to multiple biotic and abiotic threats including *Phytophthora* spp. and the cascading impacts associated with accelerated climate change. Due to long breeding cycles and an absence of resistant germplasm, the evaluation of native transcriptional elements is critical for the development of a plant transformation pipeline to circumvent traditional breeding limitations. The common use of the 35S promoter and NosT in angiosperms has proven less effective in many gymnosperms with significant gene silencing. The use of native promoter and terminator elements expressing resistance genes from related *Abies* spp. or CRISPR-Cas for genetic modification will allow for faster breeding response times in the context of cisgenic plant transformations for wider public approval. The promoters and terminators of highly constitutively expressed genes were identified in an in-house draft genome, selecting 2kb and 200bp for the 5'UTR promoter and 3'UTR terminator, respectively. 12 promoters and 7 terminators were amplified from Fraser fir genomic DNA and cloned into Gateway compatible vectors for combinatorial testing using the markers RUBY, PAP1, and/or GUS. *Agrobacterium*-mediated transformation of *Abies* somatic embryos is ongoing with a high-efficiency transformation protocol currently being established. Genes identified as being highly expressed across needle and bark tissue types are estimated to have core cellular functions including apoptosis control and DNA damage repair which may allow for high expression of cis- and/or transgenes for pathogen resistance, drought resistance, or ornamental modification. These promoters will be the first identified and assayed from an *Abies* spp. and the terminators will be the first of any gymnosperm to our knowledge. The results from this work will also indicate the utility of the draft genome and transcriptome for sequence identification. This work will be valuable as it will facilitate evaluation of a wider range of genetic elements for gene expression studies in Fraser fir and other related gymnosperms. Further work will be pursued to identify and characterize inducible and tissue-specific gene elements for fine-tuned expression.