

Metabolomics Complexity in Forest Trees Expected from Intron-Exon Gene Structure

T.E. Koralewski¹, L.A. Zhivotovsky^{2,3}, and K.V. Krutovsky⁴

¹Graduate Student, ⁴Associate Professor, Department of Ecosystem Science and Management, Texas A&M University, College Station, TX 77843-2135, USA; ²Senior Scientist, N.I. Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow 119991, Russia;

³Professor, Morrison Institute for Population and Resource Studies, Stanford University, Stanford, CA 94305-5020, USA

Computer analysis has been used to infer exon-intron structure from completely sequenced plant and animal genomes. Through modeling of alternative splicing the metabolomics complexity has been predicted for different species including forest trees.