COMPARATIVE GENOMICS OF ENVIRONMENTAL STRESS RESPONSES IN NORTH AMERICAN HARDWOODS

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The increasing incidence of introduced exotic pests, diseases and invasive plants, combined with climate change and forest fragmentation, threaten the sustainability of our forest ecosystems. The eastern hardwood forests are complex biological systems, covering over 400 million acres of bottomland and riparian sites, major watersheds, mesic sites and upland xeric sites. These forests provide habitat and food for wildlife, stabilization of riparian zones, long-term carbon sequestration and other essential ecosystem services as well as wood and biomass products for human use. Currently, few genomic resources are available for use in studying the consortium of hardwood species that compose the eastern forests. An interdisciplinary team are working together to develop new genomic resources for important species that represent the major taxonomic groups of eastern hardwood trees, from the oldest to more recently evolved, including yellow poplar (*Liriodendron tulipifera*), sweetgum (*Liquidambar styraciflua*), honey locust (*Gleditsia triacanthos*), northern red oak (*Quercus rubra*), black walnut (*Juglans nigra*), sugar maple (*Acer saccharum*), blackgum (*Nyssa sylvatica*), and green ash (*Fraxinus pennsylvannica*). The project will produce sequence databases for expressed genes, genetic markers, genetic linkage maps, and reference populations This will provide lasting genomic and biological resources for the discovery and conservation of genes in hardwood trees for growth, adaptation and responses to environmental stresses such as drought, heat, insect pests and disease.