

NAU forest geneticist collaborates on first full-genome sequence analysis of aspen trees

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Although the North American quaking aspen tree is a time-honored local icon here in Flagstaff, it has the broadest distribution of any tree on the continent, growing from coast to coast across the U.S. and Canada. It's also a close relative of the Eurasian trembling aspen, which can be found in Europe, Asia and parts of Africa. The two species belong

to the genus *Populus*, and because of their prevalence across the northern hemisphere, a multidisciplinary international team of 26 scientists recently completed the first study to understand how genomic determinants affected the trees' adaptive evolution. The study is important because it provides a starting point for comparative and evolutionary genomics in the field of forest trees. Assistant professor of forest genetics **Amanda De La Torre**, who joined NAU's School of Forestry in 2018, collaborated on the



team and co-authored a paper in the *Proceedings of the National Academy of Sciences* describing the study, which produced the first aspen genome sequences. By selecting these species for the study, De La Torre and her collaborators from Ghent University, Umeå University, Swedish University of Agricultural Sciences, the Institute of Life Sciences, Uppsala University, Royal Botanic Gardens and Norwegian University of Life Sciences established the aspen genome as a basis for future studies. "We have demonstrated the power of the aspen genome resources for understanding how natural selection varies among genes differing in gene expression, and how effects of linked selection vary across the genome within and among species to help decipher the history of speciation in aspens and identify the genomic basis of local adaptation," said De La Torre. "By developing an extensive genomic resource for aspen, our goal is to enable functional, comparative and evolutionary genomic analyses in *Populus* and to extend the utility of the genus as a unique study system in plant and evolutionary biology."

Study data integrated into web resource for future analyses

The *Populus* genus has a number of novel features compared to many other model systems, including its ability to self-clone, great longevity the oldest living organism in the world is an 80,000-year-old aspen grove—and abundant genomic diversity. To facilitate future studies of the many novel aspects of *Populus* biology, the team integrated all data generated during the study into the *Populus* Genome Integrative Explorer web resource. "These data will serve researchers performing evolutionary and comparative analyses as well as functional genomics studies aimed at deciphering genes underlying complex phenotypes by, for instance, aiding with the design of CRISPR guided-RNAs (ribonucleic acids) for gene editing," said De La Torre.

SOURCE:- <https://news.nau.edu/analysis-of-aspen-trees/#.XIH3bigzPZ>