Whole-genome sequencing of trees to ascertain long-term adaptive traits

Forest trees occur over wide geographical ranges coupled with different environmental conditions. These two factors strongly influence the local adaptation of a tree species. As forest trees are long-lived and dominant components of terrestrial ecosystems, studies that describe their adaptation potential over the years are considered highly significant. Several reports have been published for candidate gene identification towards the expression of interesting phenotypic traits. Nevertheless, whole-genome approach for identifying adaptive traits in trees is highly limited. A recent study conducted in the tree Populus trichocarpa has described the long-term adaptive trait association using whole-genome analyzes.

A group of researchers from West Virginia University, The Joint Genome Institute, California, Oak Ridge National Laboratory, Tennessee and Virginia Tech's College in USA and Aberystwyth University, situated in UK were involved in the present investigation. *Populus trichocarpa* Torr & Gray, commonly known as 'Black cottonwood' is a dominant riparian tree and it serves as a model tree for genome-level insights in forest trees. Their findings were published in the journal 'Nature Genetics'. Plant materials in form of stem cuttings from 1,100 wild black cottonwood populations in California, Oregon, Washington and British Columbia were collected and grown in research plots in four distinct environments from California to British Columbia. From this collection, a total of 544 individuals were subjected to complete genome sequencing.

Inflorescence of *P. trichocarpa*

Leaves of *P. trichocarpa*

"Basically, most of our knowledge of what genes are important for environmental adaptation of trees has been learned by guessing built on studies in the model plant, Arabidopsis, a member of the mustard family" said Amy Brunner, a co-author and Associate Professor in Virginia Tech's College of Natural Resources and Environment. He said that the main aim of the study is to understand how trees adapt to different climates and to use that information to advance tree breeding for different environments. "Our approach is

particularly powerful because we are mining standing natural variation resulting from tens of thousands of years of evolution and selection" explained Stephen DiFazio, team Head and Associate Professor of biology at West Virginia University.

"With this approach there is no need to have a preconceived notion of what genes are important", Brunner added. "Instead, existing natural variation in physical traits can be associated with genetic variation in all the genes in a tree. This work advances the first step -- the need to know which genetic variations are important to adaptation. Then you have to know why that variation is important". "The challenge is that we have identified all these genes but don't yet have a good idea of their function", Brunner continued.

A notable exception is that this study identified two related genes in trees that Brunner and others had previously characterized from *Populus.* The FT1 gene was known to regulate the transition to flowering and FT2 is important for controlling fall growth cessation and bud set. Besides, the study has identified more than 17 million SNPs (Single Nucleotide Polymorphism). These polymorphisms revealed significant spatial and geographic structure, even at fine spatial scales.

A plantation of *P. trichocarpa*

"The population genomics data not only supported that genetic variation in FT2 is associated with variation in time of fall bud set, but added an interesting twist in that it indicated an additional function for FT1 in release of winter dormancy," said Brunner. "Trees must time entry and exit from winter dormancy appropriately for their climate to maximize growth but avoid damage by fall and spring frosts, so it is very interesting that these two genes may have a crucial role in the timing of both dormancy transitions," she continued.

Further, the collaboration of scientists with computational skills, others with population genetics and large-scale genomics knowledge, and those with in-depth understanding of gene function and interaction from the molecular to the whole-tree level is a major step forward in accomplishing the target. "We need to do more in the actual tree system rather than relying solely on extrapolating from model herbaceous plants" Brunner concluded.

A complete detail related to Forest Biology of the species can be accessed at:
http://owic.oregonstate.edu/black-cottonwood-populus-trichocarpa