## **Genetically modified Poplars influence tree microbiome**

The interactions of human gut bacteria and their influence on our health are well understood and found to be tightly linked with host genotype. Similarly, how the variation in the plant genotype affects the associated bacteria and, in turn, plant health and productivity remains unknown, particularly in case of field-grown plants. In a recent study, researchers examined the response of co-existing microbial population while altering the genome of tree species. Such studies are essential to comprehend the effects of engineering the plant metabolic pathway and possibly to exploit the eukaryote–prokaryote associations in sustainable crop production, and the production of secondary metabolites.

Hybrid poplars are the thoroughbreds of the tree world. They are highly recognized for their fast growth, as sometimes a height increment of 5-8' per year is common. In particular, cottonless (male tree) hybrid can be harvested for firewood in five to seven years, making it a sustainable forest genetic resource. Due to great demand, extensive research works are being carried out in biotechnological aspects of the genus. Recently, scientists have developed genetically modified poplars and studied their influence on microbiome living in the plant endosphere.



In general, interactions between a plant and its microbiome are highly complex and dynamic, involving plant metabolic pathways. Even small changes in the host genome (ecotypes, cultivars, genetically modified genotypes, etc.) may influence the plant microbiome and may even feed back to modulate the behaviour and the productivity of the host plant. In the present investigation, the researchers examined the host genotype-

dependent effects of field-grown poplar (*Populus tremula*  $\times$  *P. alba*) trees modified in their lignin biosynthesis, on the bacterial rhizosphere and endosphere microbiome, namely the microbiota present in the roots, stems, and leaves. Un-modified trees served as control. The poplars used for this study formed part of field tests set up by Flanders Institute for Biotechnology (FIB), Belgium under the leadership of Prof. Wout Boerjan.

From the observations, the research team (comprising researchers from FIB, Universities in Belgium and Sweden) inferred that modifying the composition of poplar wood also transforms the function and structure of the microbial population of plant tiisue. Prof. Boerjan explained, "The wood in trees is formed by the cell walls, important components that come into close contact with microorganisms. When you make a relevant alteration to the structure of the wood, even if it is the result of silencing just one gene, this leads to an alteration in the composition of bacteria, moulds, viruses and other microorganisms. This is comparable to a change in the composition of our gut flora as a consequence of continued exposure to another type of food." Further, the important point should be noted is that these changes only occur within the plant tissue, called the endosphere. No changes could be observed in respect to the soil bacteria that live outside the plant close to the roots of the tree, known as rhizosphere bacteria.

Also through this project the researchers were able to reduce the levels of lignin, a component of wood in the poplars through genetic modification i.e., by down-regulating the synthesis of an enzyme known as 'cinnamoyl-CoA reductase'. Because of a reduced lignin content, the plant metabolic pathway modifies, thereby effecting the conversion of two other important components of wood (the cellulose and hemicelluloses) to sugars, and then, by way of fermentation, into bio-ethanol. Hence the authors argue that these interactions need to be taken into consideration to understand the full consequences of plant metabolic pathway engineering and its relation with the environment and the intended genetic improvement.

## Source:

http://www.sciencedaily.com/releases/2016/01/160113101119.htm