Researchers identify first 'coppicing response' gene in willow

January 8 2014

Willow trees in bud. Credit: Lawrence Weston

(Phys.org) —Scientists have, for the first time, discovered a gene that contributes to the 'coppicing response' of willows - the ability to make new growth when cut back to their base or stump.

Willows grow fast, produce high yields, need little fertilizer and easily re-grow after being coppiced, or cut back - qualities which make willow hugely important for commercial use as renewable and sustainable biomass for bioenergy.

'Coppicing response' - the rate and type of new growth following cut

back - is critical to these energy crops as it enables willows to be grown in three year harvesting cycles, affects vigour and yield, along with the ratio of bark to wood in the stem.

Despite its importance, the genetic regulation of coppicing response is little understood. Now, a team of plant scientists from the Sainsbury Laboratory, in collaboration with Rothamsted Research, have used knowledge and methodologies from the model plant species Arabidopsis to identify SxMAX4 as the first coppicing response gene known to date.

The study was funded by the BBSRC Crop Science Initiative, and is published today in the *Plant Biotechnology Journal*.

Although cultivated since the Roman times, and still used for baskets and cricket bats, willows have been subject to only minimal domestication. Luckily, the genus shows huge genetic diversity, from massive trees to small bushes, and scientists believe there is great potential for crop improvement through breeding.

But improving willows is challenging. Many target traits - including coppicing response - are complex, and a good understanding of the genetic basis of developmental processes is needed to improve willow varieties. However, due to their large size, perennial growth cycle and the effort required to assess characteristics in the field, studying development in willows is extremely difficult.

Gene function procedures routinely used in model organisms are not yet established in willows, but scientists are focusing on transferring knowledge from Arabidopsis - undoubtedly the best characterized and widely-studied model plant today - to species of commercial importance that are much harder to study, such as willow.

The latest findings demonstrate that great results can be achieved from

exploitation of the vast body of knowledge in this model, and by combining plant molecular biology with genetic mapping approaches, say the researchers.

"This has been a very exciting collaboration for me," said Professor Ottoline Leyser of the Sainsbury Laboratory. "I expected that our Arabidopsis work would be useful for understanding trees such as willow, but I did not anticipate quite how similar bud activation in these two species would be.

"The approach we have used to test willow genes in Arabidopsis could be widely useful for assessing functional genetic diversity in slow-growing species."

Dr Angela Karp, from Rothamsted Research, added: "It was really exciting to find that one of the MAX genes, SxMAX4, which affected branching in the Arabidopsis assay, was associated with differences in shoot re-sprouting in willow, and is located in exactly the area in the willow genome that is responsible for regulating this trait.

"This is the first time a gene has been shown to influence coppicing response and should enable the breeding of plants with desired stem numbers not only in willow but other coppiced trees."

More information: Salmon, J., Ward, S.P., Hanley, S.J., Leyser, O. and Karp, A. (2014) Functional screening of willow alleles in Arabidopsis combined with QTL mapping in willow (Salix) identifies SxMAX4 as a coppicing response gene. *Plant Biotechnol. J.,* DOI: 10.1111/pbi.12154

Provided by University of Cambridge