A willow breeding programme for the UK, part of the Biomass for Energy Genetic Improvement Network (BEGIN).

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The primary objective of the programme is the improvement of the willow crop for renewable energy. This is increasing in importance as the UK Government seeks to incorporate into law it's aspirations for a 60% reduction in CO_2 emissions (over 1990 levels) by 2050.

Suitable willow cultivars are available for growing in the UK but great potential for improvement remains. We bred two new varieties before joining Svalöf Weibull AB, Sweden, and Murray Carter, UK, to form the European Willow Breeding Partnership, which bred 8 more varieties. During Institute re-structuring in 2003 the partnership was dissolved, but UK willow breeding continued through "BEGIN", funded by the Department of Environment, Food and Rural Affairs (Defra).

Yield improvement is the main target, followed by durable resistance to diseases and insects. More recently, wood quality is also being investigated. Advantage is taken of the wide genetic diversity present in the National Willow Collection held at Rothamsted, which has *ca*. 1,300 accessions, including 100 pure species. Five promising improved genotypes have already been identified from BEGIN's efforts.

The main disease of SRC willow is rust caused by the *Melampsora* fungus. New lines are tested against rust pathotypes and willows with new sources of resistance are being used in the crossing programme. The pathogenicity of new isolates is continually tested and any potentially new pathotypes tested against willow varieties and elite lines. Pest studies have concentrated on the blue and brassy willow beetles *Phratora vulgatissima* and *P. vitellinae*, which are the main insect pest. Subtle but important differences in host preference were detected and found to be determined by a combination of specific leaf volatiles and secondary metabolites in the leaves. Crosses have been made to breed for insect resistance.

The programme is underpinned with molecular genetics and genomics research. A dense willow genetic map has been constructed from a uniquely large (*ca*. 1000 progeny) genetic mapping population grown at on two contrasting sites. Six robust quantitative trait loci (QTLs) for biomass yield and three QTLs for rust resistance have been identified. More recently, the willow genetic map has been aligned with the poplar genome and the macro-syntenic relatedness of willow and poplar has been demonstrated. Dissection of the QTL to determine the underlying genes is underway and markers for use in marker-assisted selections are being developed.

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