Micropropagation of diverse willow genotypes to enable rapid GS-based breeding

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Accelerating Willow Breeding and Deployment

Introduction

Short rotation coppice (SRC) willow is an important source of renewable carbon for bioenergy and biofuels. Genomic selection tools for accelerated breeding of SRC willow and improving selection for complex traits such as yield are being developed at Rothamsted, allowing improved varieties to be brought to market faster. A limitation of faster breeding schemes is the reduced availability of planting material (woody cuttings) in the early phases. Implementation of micropropagation could save around 4−5 years by significantly reducing the time required to generate the number of plants needed to carry out multisite yield tests.

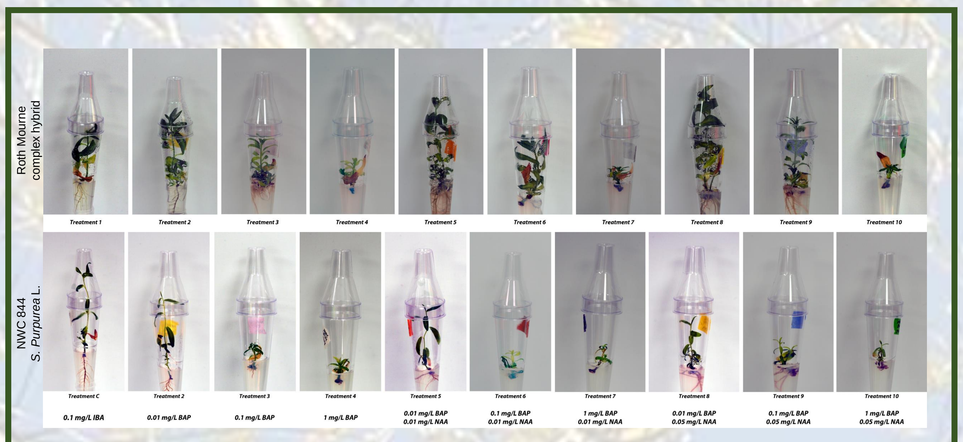
Sterilization

Establishment

Micropropagation

Methods

We are assessing micropropagation responses through nodal segment culture in a diverse range of willow genotypes, building on efficient tissue-culture propagation methods established previously in our laboratory (Palomo-Ríos *et al*, 2015). Various factors affecting multiplication rate and growth *in vitro* are being assessed in 30 diverse willow genotypes. Micropropagation traits measured include rooting and shooting responses, shoot length, and number of nodes.



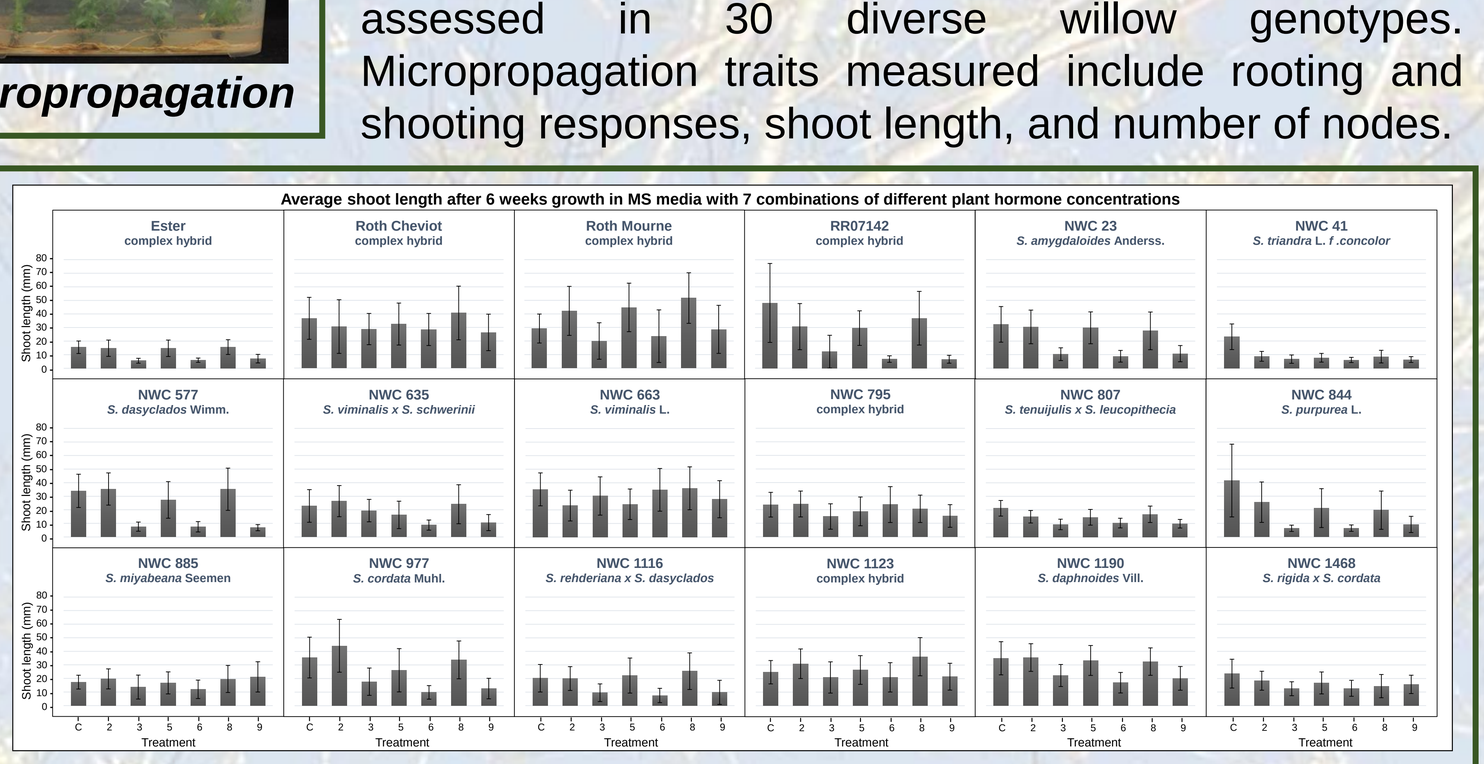
Plant hormone combinations

Vessel type

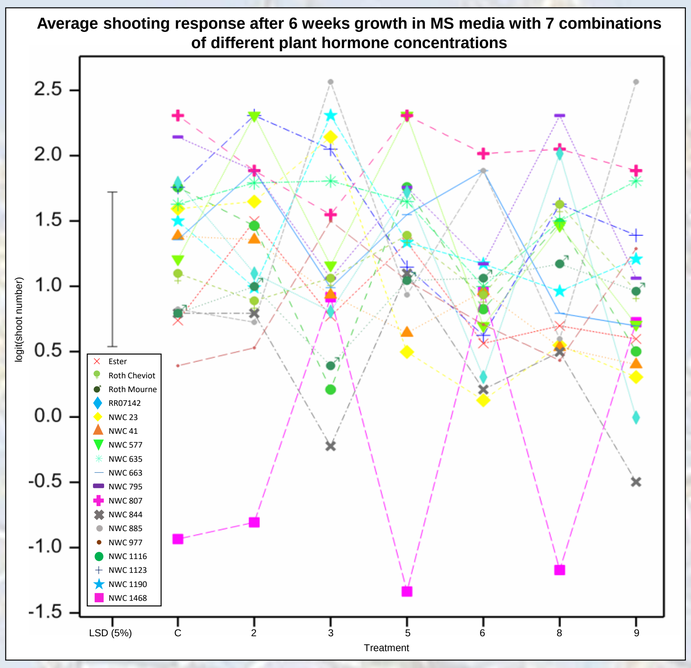
Media formulation

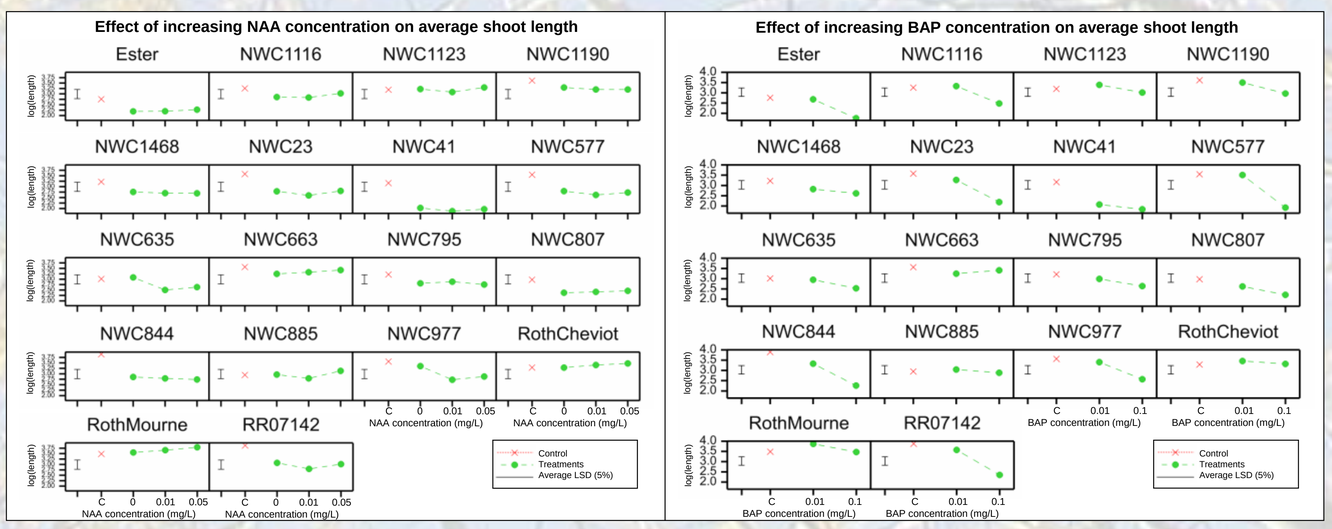
Temporary Immersion Systems

Rapid upscaling to woody cuttings



Preliminary results with 18 genotypes showed that different concentrations of cytokinin 6-Benzylaminopurine (BAP) and auxin 1-Naphthaleneacetic acid (NAA) in the media had significant effects on shoot length and rooting response. For most genotypes, an increase in BAP concentration had a negative effect on shoot length. However, in other genotypes, no significant response to BAP was observed.





Conclusions

Overall, our results indicate that the optimal micropropagation conditions vary significantly for different genetic backgrounds. This was observed in previous studies and would be expected in a genus as diverse as *Salix*. Despite this, we have found the standard micropropagation conditions to be sufficient to micropropagate the majority of willow genotypes tested.

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