

**Five hundred and Sixty** biomass willow genotypes, primarily Salix viminalis and their hybrids, were selected based upon their genome sequence relatedness and planted at four main environmentally contrasting trial sites across the UK (map).

**Trials** (76 x 149 m) have 4 replicate blocks, each with 70 subblocks of 9 plots, including one control genotype plot per subblock, enabling adjustment for spatial variation.

An additional site at AFBI, Northern Ireland was planted with 144 genotypes for G x E comparison.

In total >70,000 cuttings were planted and will be managed as Short Rotation Coppice (SRC).

**Phenotyping** is ongoing for biomass traits of interest: establishment, pests, pathogens

with cutting production, planting & ongoing site management to:

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## and yield.

Site management and weather data will be collated.

**Genomic selection** will model phenotype and genotype sequence data to:

- **Predict parental selection for** complex traits, e.g. biomass yield, in contrasting environments i.e. drought, flood, cool, warm, exposed, short day length, high disease pressures.
- **Bring new, superior varieties** to market faster.



Lower breeding costs. 

**Micropropagation techniques** are being developed to ensure new willow varieties can be rapidly upscaled, as faster breeding schemes will provide less planting material in the early phase of variety introduction.