

DEVELOPMENTS IN FOREST GENOMICS IN BRITAIN

Professor John MacKay, from the University of Oxford, shows how the most rapidly advancing field in the life sciences is advancing forestry research

The word ‘genomics’ has become part of our daily news, most often relating to human health, but scientific developments and novel technologies in genomics are also poised to bring positive benefits to forestry. The potential for application is diverse and significant progress has already been made. New research is now starting in Britain, which aims to accelerate selective breeding in Sitka spruce by applying a method developed in humans and domestic animals called ‘Genomic Selection’ to forest trees. Here, we take a brief look at the progress and practical applications in this rapidly evolving area of forest science.

From sequencing

The entire genome has now been sequenced in several forest tree species and the genomes of other tree species are imminent. Poplar has a relatively small genome and, for this reason, was the first tree species to be sequenced in 2006. This was a costly exercise and, consequently, very few others were sequenced until 2013 when faster and more cost effective technologies became available. Over a dozen tree species now have whole genome sequence data available and these include conifers such as spruce and pine, and hardwoods like birch, oak, eucalyptus and ash. However, with these new technologies many of the tree genome sequences remain in a draft state, meaning that the information is in large fragments which cannot yet be assembled into a whole genome. While the assembly of entire genomes still poses definite challenges, other methods have been developed, such as ‘transcriptome sequencing’, which are very efficient at

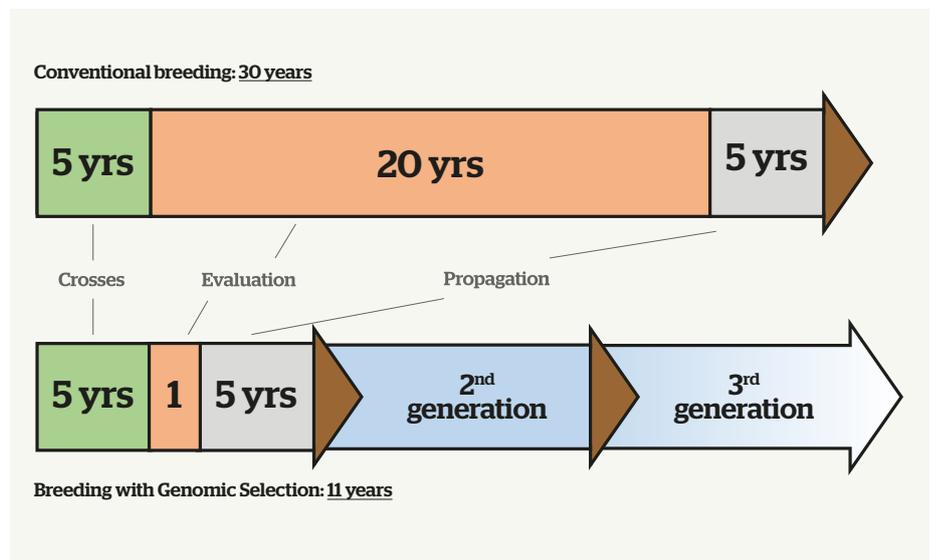
uncovering the sequences of each gene individually. With transcriptome sequencing, scientists are able to gather large-scale information on protein coding DNA sequences and this is useful for investigating many aspects of genome function, diversity and evolution. Data on forest tree genomes and genes are becoming widely accessible in public databases¹. These databases may include DNA sequences, gene expression, and information on genetic diversity – variations in DNA sequence that make each individual unique and account for differences between species.

To consequence

– *Insights into the evolution of forest trees*
Together, genome and transcriptome sequencing have increased our understanding of the evolution of forest



trees. For example, a phenomenon known as Whole Genome Duplication has influenced the number and types of genes in a genome and has ultimately influenced the potential for evolutionary adaptation and innovation. Tree genomes also contain an abundance of DNA fragments called retrotransposons which move





Each individual seed within a cone has a unique genome due to small variations in its DNA makeup. These differences result in some trees being able to grow faster or cope better with threats. The ability to select the trees that harbour useful variation enables breeding of elite trees

throughout the genome and play a part in shaping its overall structure. The genomes of broadleaf trees bear clear traces of multiple Whole Genome Duplications. Conifers, however, have the most ancient and largest numbers of retrotransposons, which have accumulated to hundreds of thousands of copies and stretched conifer genomes to be among the largest studied to date.

Understanding how trees respond to changing conditions

Genomic methods like transcriptome sequencing allow us to monitor when specific genes are being switched on and off. This novel approach to the study of tree biology is known as ‘gene expression’ and can inform which genes are active in certain conditions; something that cannot be learned from the gene sequence alone. Insights into gene expression are useful for discovering how trees develop and respond to specific conditions, e.g. thousands of genes may change their expression following a drought and orchestrate the physiological responses that allow a tree to manage the lack of water.

From understanding to prediction

The ability to know in advance how particular species or individuals will perform under given conditions is one of forestry’s perennial challenges and is central to tree breeding. Until now, tree breeders have selected superior individuals by establishing expensive field trials and assessing the field performance of individual trees. Those selected are then used to set up cross-pollinations, seed orchards or mass propagation programs. This ‘selective breeding’ is effective for increasing yields in many tree species but it takes 30 years or more to select and propagate new varieties.

One way to accelerate tree breeding is to use information gleaned directly from the DNA sequence, rather than relying on the field performance alone to predict genetic value and thus select superior breeding individuals. The first approach to achieving this was to try and identify the small variations in the large genomes that help one tree to perform better than another. To date, like searching for a needle in the haystack, this has met with limited success. However, after nearly

two decades of research – which has seen much cheaper sequencing technology introduced as well as new approaches to prediction – it is proving to be fit for purpose and holds real promise for accelerating tree breeding at least for well-defined family structures². The new approach to prediction, called ‘genomic selection’, was initially introduced in the commercial breeding of domestic animals where it is now used routinely. Along the way, other methods have been developed that improve our understanding of the genetic basis of economic traits like growth, wood yield, wood density, and resistance to insects, among others. DNA-based techniques such as fingerprinting have also been developed to manage genetic diversity or track genotypes and illegally logged wood.

Development of genomic selection for Sitka spruce

In July, a new research project – Sitka Spruced – was launched to develop genomic selection in Sitka spruce in Britain³. Like the research I have talked about, it is a collaboration between the

University of Oxford, University of Edinburgh (The Roslin Institute), and Forest Research.

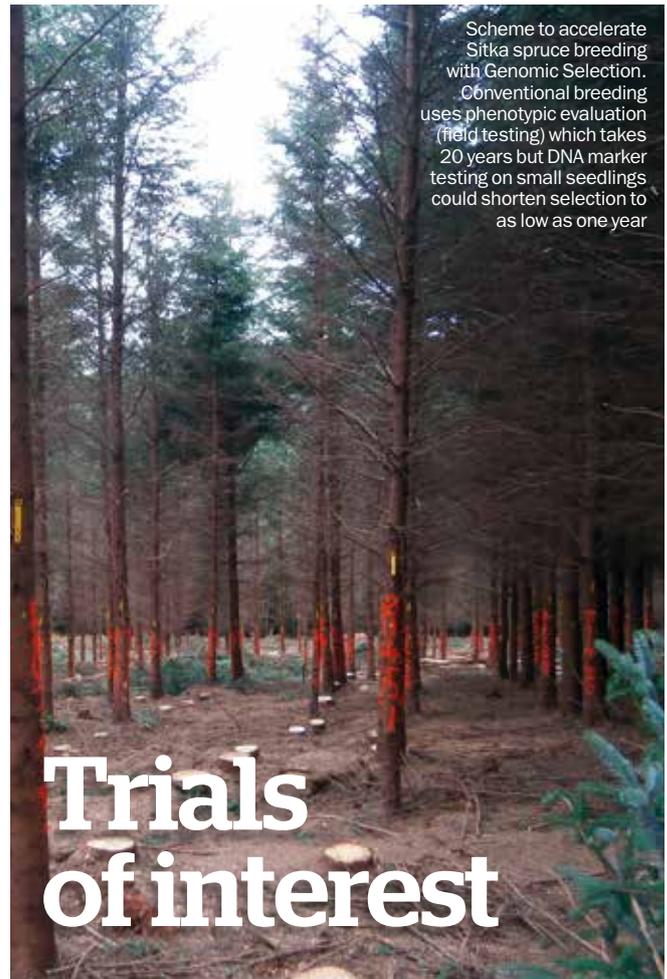
The project is funded by the Biotechnology and Biological Sciences Research Council and a group of forest and wood processing industries, and aims to set up novel capacity to increase the rates of genetic gain in the breeding programme and build on recent progress in spruce^{4,5}. It will develop a large-scale genotyping capacity, a genetic map for

Sitka spruce and a training set for predictive genomics model development. We will use this platform to investigate genomic prediction accuracy, models for both yield and wood quality traits, and resistance to damaging insects.

Professor John MacKay, Wood Professor of Forest Science, Department of Plant Sciences, University of Oxford, with Professor John Woolliams, The University of Edinburgh

References

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Scheme to accelerate Sitka spruce breeding with Genomic Selection. Conventional breeding uses phenotypic evaluation (field testing) which takes 20 years but DNA marker testing on small seedlings could shorten selection to as low as one year

As key project partners, scientists Dr Steve Lee and Dr Joan Cottrell explain the importance of Forest Research's work to the science of genomics in forest trees

Genomics works by forming an association between a suite of molecular markers and the traits of interest as observed in the forest. Once established, further selection can be based on those markers alone and at a very early age, well before the full expression of the trait itself. Forest Research's (FR) role is to bring key experiments to the development of this new research into Sitka spruce by providing the most appropriate trials to facilitate this work.

FR's expertise in trial management, selective harvesting and sampling, and wood quality assessment is key to the success of this project. FR holds a pivotal position that bridges the development of new areas of forest science, and its application and impact on the forestry sector. Through these links FR was able to secure

the necessary 10% industry contribution required as a prerequisite of the funding bid. The Impact Advisory Board, which represents seed merchants, nurseries, forestry management companies, a breeding co-operative, and a sawmill, will ensure good two-way communications between the project and core elements within the industry.

Genomics is well established in some areas of animal breeding, such as poultry and cattle where it is already being successfully applied by private industry to improve yields and efficiency. The new Sitka Spruced project is strengthened by the involvement of an experienced animal breeder from The University of Edinburgh.

Dr Steve Lee is a Science Group and Programme Leader and Dr Joan Cottrell is a Science Group Leader at Forest Research

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