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 databases. 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...
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 structures. 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.

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 structures. 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 Britain. Like the research I have talked about, it is a collaboration between the
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 Spruce project is strengthened by the involvement of an experienced animal breeder from The University of Edinburgh.