The Application Of Genomics To
Sitka Spruce Tree Improvement

Genomics has considerable potential to accelerate Sitka spruce tree improvement Ireland. Niall Farrelly, Ronan Cashell, Brian Tobin and Shui Zang outline new research into research in the area of forest genetics.

GenESIS Research Project

The GenESIS research is a new four year project funded by DAFM and features researchers from Teagasc, UCD, Trinity College Dublin, NUI Galway, National Botanic Gardens assisted by Coillte and hopes to document the genetics of Sitka spruce forests in Ireland and develop genotyping tools to assist tree-breeding efforts. The new research involves the development of a new genotyping platform that will be utilised for assessing differences in the genetic makeup of trees, used to assess diversity in Sitka spruce populations, for DNA fingerprinting, and also for genomic selection which has the potential to accelerating tree breeding efforts.

Tree Breeding

Tree breeding strategies aim to select the best trees to use as parents to produce future generations of forests suitably adapted to their environment. In some cases what looks like a good tree could often be a result of a favourable growing environment (good soils, shelter, etc.) rather than its genetic composition (Figure 1). To determine whether a set of desirable characteristics of an individual are a result of its genetic makeup (genotype) or as a result of its interaction with the environment – genetic testing is required. This is especially necessary for tree breeding- to determine the levels of genetic gain that can be expected by using selected individuals. This can be achieved by testing the progeny of selected individuals (plus trees). Seed can be collected from the plus trees and grown in a nursery and the resultant seedlings can be tested to determine if these desirable characteristics are under genetic control (i.e. inherited). Progeny testing often involves laying down multiple experiments to test the seedlings from selected parents (families) under field conditions and evaluating if these families perform better than an unimproved seed lot.

Progeny testing

Progeny tests can be used to evaluate faster growth rates by assessing height and diameter growth or other characteristics of interest such as frost damage, stem form or pest damage. Parent trees are cloned, grafted and placed into a seed orchard to produce improved seed which is available to produce improved seedlings to create new forests with increased vigour (Figure 3). More detailed assessments of stem straightness and wood properties can only be performed as the trees mature and generally assessments can be made to determine if timber from selected trees show a loss in density as a result of increased vigour. More recently, tree-breeding efforts have focused on selecting individuals that may be more suited to growing the forests of the future through being more adapted to future climates. This can be achieved by evaluating the offspring of selected parents and their performance in particular conditions or their resistance to specific pests or diseases. Tree breeding can be a long term process before results can be seen in the forest. For example the Irish Sitka Spruce Tree Improvement programme has been selecting trees with desirable traits since the late 1970's (Fenessey et al. 2012) and testing the progeny of 458 plus trees in a series of experimental trials planted between 1981 and 1993. Initial selections of 86 improved genotypes occurred after 6 years growth. The parents of selected families were screened for timber density to ensure that there was no loss in timber quality associated with vigour and a smaller breeding population was selected (Thompson, 2103). The research will confirm the long term performance of 86 selected families and the current breeding population (55 families) and assess if there is potential to select families or populations which may have additional timber quality or resilience traits which were not previously evaluated.

Figure 1: A superior stand of Sitka spruce in the Slieve Bloom Mountains. The performance of these trees may be a result of favourable site conditions rather than as a result of superior genetics.

Figure 2: A selected Sitka spruce tree (plus tree) showing good vigour, stem properties and straightness, seed is collected and the progeny are tested to determine if genetics or environment are responsible for the good phenotype.

Figure 3: An improved Sitka spruce seed orchard in Ballintemple, owned and managed by Coillte Teoranta.
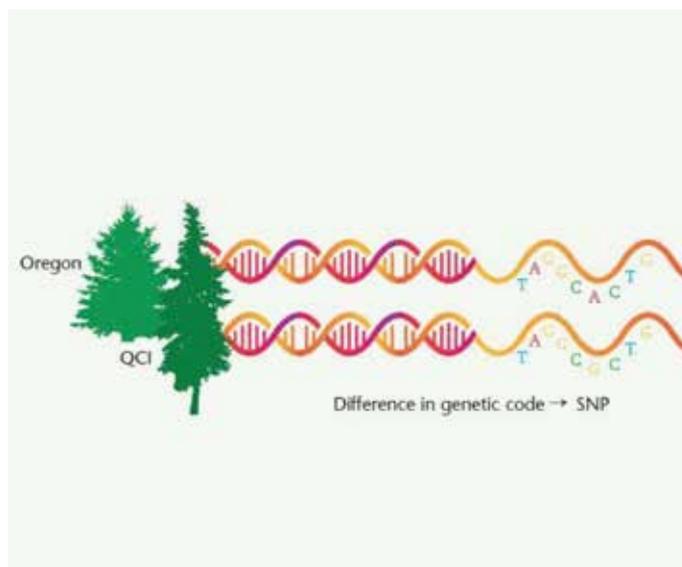
Figure 5: Differences in the genetic code of Sitka spruce may be used to assess levels of genetic diversity in Sitka spruce populations which may contain valuable traits that can be used to breed trees that are taller, stiffer, straighter, more resistant to insect pests and more adapted to future climates

Long term performance of selected families

To confirm the long term performance of selected families in the Sitka spruce breeding programme new measurements of height, diameter are being conducted in the existing progeny trials, to assess if selected families continue to show good performance and continue to show a gain in height and diameter at breast height (dbh) compared to control seed lots (see Figure 4). It will also ascertain if the performance of certain families is less than expected. The re-assessment of existing progeny trials will be useful to assess new timber quality traits on trees nearing maturity (see section on timber quality below) which were not previously available to be evaluated in the Irish tree breeding programme. The project has recruited three post graduate students who are conducting Phd studies into specific areas of genetic diversity, timber quality and genomic selection.

*Long term gain in dbh and height of selected families*
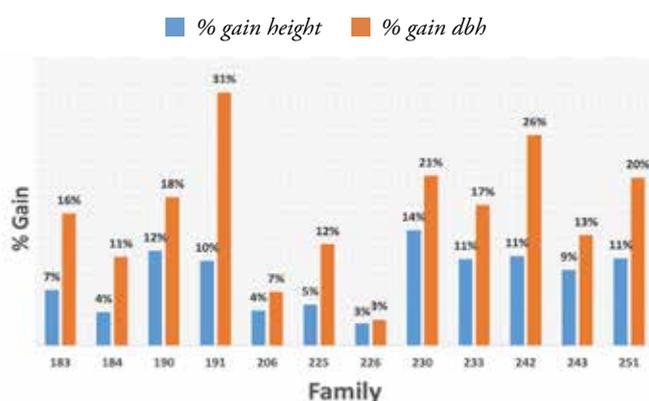
Figure 4: Long term performance of selected Sitka spruce families in the Coolgreaney 6/88 experiment, showing height and diameter (dbh) gain over the control seed lot.

Assessment of genetic diversity

To assess the extent of genetic diversity within the breeding populations GenESIS will assess levels of genetic diversity in the breeding population to compare with the native range of Sitka spruce. Higher levels of genetic diversity may be desirable in breeding populations, as the additive nature of traits such as height and pest resistance means that a more genetically diverse breeding population is more likely to achieve greater gains in height or

stronger pest resistance. To assess genetic diversity in Sitka spruce the research will first study the genetic diversity in the natural range of Sitka spruce over a 3,000 km range from Alaska to California. To achieve this cambium samples (bark samples) have been taken for DNA isolation from the JFK conservation collection in Co. Wexford representing Sitka spruce's indigenous range. An assay will be developed which allows the DNA to be compared for all the trees in the collection to determine the degree of relatedness among genotypes, ultimately it will assess if trees from different geographic regions differ substantially in their genetic composition (Figure 5). Effectively the assay will be used to identify where differences in the genetic code occur by targeting specific locations of the Sitka spruce genome. The research will assess the genetic diversity in the current breeding population and the background levels of genetic diversity in the natural range of Sitka spruce. Another valuable tool is genetic fingerprinting which may allow the identification of unknown origins or populations to known origins based on their DNA profile. Paternal testing to assess what parents are good seed producers to test for seed orchard efficiencies (Figure 3).

New Assessment of timber quality

More recently tree programs have expanded their objectives to include wood characteristics such as bending strength and enhanced mechanical properties. The GenESIS project is using non-destructive methods to assess timber quality of selected families and measurements have been conducted on a subset sample trees in the progeny trial at Coolgreaney. These measurements include acoustic velocity (Figure 5) and Pilodyn penetration depth. Acoustic velocity is a good predictor of modulus of elasticity (MOE) and Pilodyn is commonly used to estimate the density of standing trees. Relatively high correlation between acoustic velocity measurements and MOE, Pilodyn penetration depth and wood density have been reported. In addition, cores have been collected from the same trees and are being analysed by the WinDENDRO™ system which provides information on the development of ring width, density, and other mechanical properties. Results from non-destructive measurements and core measurements will then be compared to determine if vigour and timber quality are negatively correlated or if variability in mechanical properties within Sitka spruce populations could be included in future breeding populations without affecting other desirable traits.

Figure 6: The JFK Sitka spruce conservation collection contains trees whose origins cover a geographic distribution of 3,000 km. Cambium samples from over 1000 trees have been collected by the GenESIS project and will be used to assess genetic diversity in Sitka spruce.

The potential of Genomic selection

Advances in genotyping have led to the emergence of genomic selection (GS), a method for maximising the gain in an additive trait achieved from selective breeding. GS uses models built by estimating the effect of alleles (a variant form of a gene) on the trait in question, and generally are made more accurate by including more instances of allelic variation. Genomic selection has to date been successfully employed in animal and plant breeding. While conifers, such as spruces, have traditionally been avoided for genomic analysis due to their large genomes in favour of species with much smaller genomes such as Eucalyptus, the advances which allow for GS also allow for the identification of alleles at densities necessary to carry out GS. GS works well where there is sufficient data on the performance of progeny and with the collection of additional data from progeny trials and opportunity exists to assess the potential to use GS to inform the potential gain that might be achievable from crossing parents whose progeny have good performance, this may result in more informed crossing decisions and improved gains in height or diameter growth of progeny. Genotype data has been derived from 215 genotypes of Sitka spruce covering tree in the current Sitka spruce breeding population (in Ballintemple Nursery in Co. Carlow) by way of Genotyping-by-sequencing (GBS) and tree from the original plus tree collection selected from 1972 to 1990. To complement the genotype data, a vast quantity of historical information together with data on the current performance of these genotypes has been compiled in order to assemble a comprehensive dataset of phenotype (trait) data. To assess the potential of genomics-assisted breeding we will associate the traits with GBS data to determine if differences in the DNA profile of genotypes can be linked to differences in a trees performance. The GBS analysis will be used to assess the potential of GS to identify genotypes that may show improvements in certain traits such as vigour, timber quality or aphid resistance and be suitable for future breeding work and could be used to prioritise a list of crosses in the breeding programme.

New Resilience Traits

Figure 8: Seedlings of Sitka spruce from British Columbia to California being grown in the glasshouse in Teagasc Ashtown. These seedlings will be subjected to screening for drought tolerance and insect resistance in future experiments under the GenESIS research project.
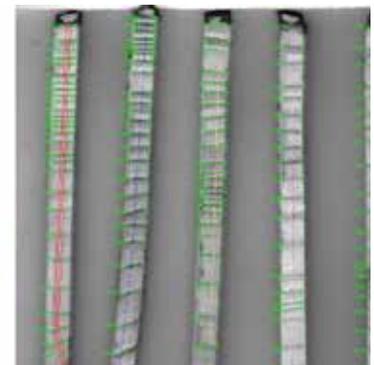
Figure 7: Testing timber quality of Sitka spruce families using a TreeSonic™ (left) which measures time of flight between two probes and has been linked to bending strength of timber (middle photo) and ring width analysis using the WinDENDROM™ system.

While performance and timber quality traits are very important, our forests are becoming increasingly challenged by the effects of climate change and pests and diseases, and there is a realisation among forest scientists that forest reproductive material needs to be adapted to future climatic conditions and be more resilient to biotic threats. Accumulation of traits that may prove useful in increasing resistance occurs naturally in trees as it does in virtually all other living organisms, but breeding without consideration for these traits risks their exclusion from breeding populations. Climate change necessitates that future forests are resilient so that they can continue to supply the ecosystem goods and services, including timber and carbon well into the future. Therefore the GenESIS research also aims to assess if Sitka spruce populations show differences in drought tolerance or resistance from insect pests. We have assembled a range of seed origins representing a portion of the natural distribution from British Columbia to California together with origins currently used in Irish forestry (Figure 8) and aim to screen these for drought tolerance in a controlled glass house experiment and conduct a controlled feeding experiment using pine weevil (Hylobius abeitus) in 2022 to assess if resilience traits exist in Sitka spruce populations and whether or not Irish breeding populations have this resistance. Ultimately the research hope to provide valuable information that will assist to improve Sitka spruce planting stock that will result in faster growing trees that utilise resources efficiently increasing carbon sequestration and storage. The increased use of wood and greater levels of recovery of harvested wood products will play a key role

GenESIS
Genomic Evaluations for Sustainable Improvement of Sitka spruce

to offset emissions from carbon intensive materials and maximise the contribution of forests to reducing our carbon footprint while ensuring the next generation of planting stock is sufficiently diverse and adapted to cope with the uncertainties of climate change.

Further Reading

- Fennessy J, Doody P, Thompson D. 2012. A review of tree improvement programmes in Ireland – historical developments, current situation and future perspective. Irish Forestry 69:184-203.
- Thompson, D. 2103. Development of improved Sitka spruce for Ireland. Irish Forestry 70; 104-118.
- Farrelly, N. Genetic Characterisation of Sitka spruce in Ireland. TResearch, Spring 2020, Teagasc, Oakpark, Co. Carlow. P34-35.

https://www.teagasc.ie/crops/forestry/research/genesis-project/

Acknowledgements