Genomic Selection for Improved Growth in Sitka Spruce

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# Background - Sitka spruce in Ireland

- Sikta (*Picea sitchensis* (Bong). Carr) comprises 51% of all Irish forests (DAFM, 2017)
- Potential for breeding program investigated c. 1980 – 2007, examining juvenile height and width
- Recent revitalisation of the breeding program supported by genomic characterisation

Table 4: Summary of Sitka spruce progeny tests.

| Test series | Number of locations | Number of<br>plus-trees | First<br>assessment | Second<br>assessment |
|-------------|---------------------|-------------------------|---------------------|----------------------|
|             |                     |                         |                     |                      |
| 2           | 3                   | 32                      | 1986                | 1995                 |
| 3           | 3                   | 29                      | 1990                | 1999                 |
| 4           | 4                   | 54                      | 1993                | 2002                 |
| 5           | 4                   | 40                      | 1993                | 2002                 |
| 6           | 4                   | 42                      | 1993                | 2002                 |
| 7           | 1                   | 17                      | 1994                | 2003                 |
| 8           | 3                   | 45                      | 1994                | 2003                 |
| 9           | 3                   | 44                      | 1994                | 2003                 |
| 10          | 3                   | 44                      | 1994                | 2003                 |
| 11          | 3                   | 43                      | 1998                | 2007                 |
| 12          | 3                   | 46                      | 1998                | 2007                 |
| 13          | 2                   | 36                      | 1998                | 2007                 |
| Total       |                     | 505                     |                     |                      |

Thompson, 2013

### Data Availability – Genomic Selection

Genomic Selection requires genotypic and phenotypic data:

- Phenotypic Data EBVs for a genotype predicted from measurements on its half-sib progeny (similar to msGBLUP)
- Genotypic data Genotyping-by-Sequencing resulting in a large amount of data, but prone towards loci with many missing data (i.e., Chen et al., 2013)

#### Methodology – Model Evaluation

Six models evaluated on ~78,000 SNPs at 15% missing data threshold for additive genetic effect on phenotypes:

- G-BLUP & RKHS Using the Genetic Relationship Matrix (GRM) to predict for phenotypic effects
- rrBLUP, BayesA, BayesCπ & Bayesian Lasso, Using all markers as predictors
  - rrBLUP uses ML, Bayesian methods use MCMC
  - Bayesian methods differ in assumptions about marker effects

#### Results & Conclusions

| Model             | Predictive Accuracy -<br>Height | Predictive Accuracy –<br>Width (DBH) |
|-------------------|---------------------------------|--------------------------------------|
| G-BLUP            | 0.2806                          | 0.1963                               |
| RKHS              | 0.2725                          | 0.1806                               |
| rrBLUP            | 0.2712                          | 0.1932                               |
| BayesA            | 0.2427                          | 0.1636                               |
| BayesCπ           | 0.2702                          | 0.1853                               |
| Bayesian<br>Lasso | 0.2522                          | 0.1646                               |

Model Accuracy similar, though with clearly better models for both traits. Accuracy lower than for other similar GS models in other species

Potential for GS in Sitka spruce could be expanded to other traits i.e., resistance and drought tolerance. Potential for increasing production with land already is use

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