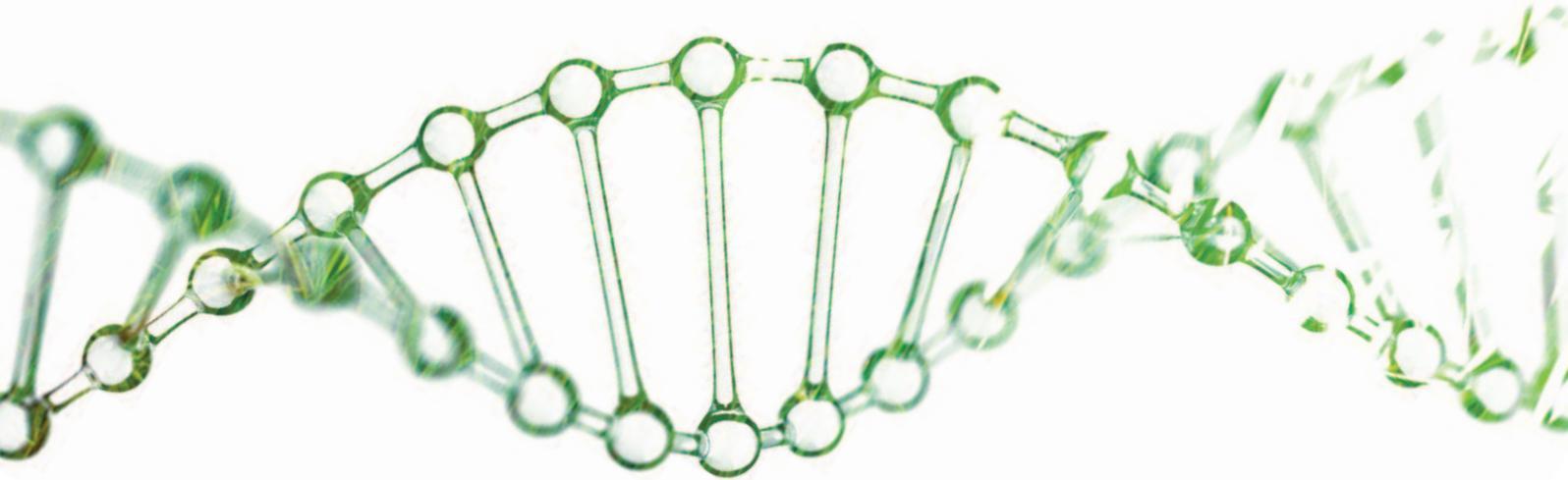


Turbocharging perennial ryegrass breeding



A **TEAGASC** project is addressing how we can make faster selection decisions and develop improved grass varieties that will meet the needs of the agri-food sector.

Breeding new varieties of perennial ryegrass

Teagasc has been breeding perennial ryegrass at Oak Park since the early 1960s and to date has successfully bred 27 varieties that have been commercialised by our partners. The release of a new variety is the culmination of 15 to 20 years of investment that consists of:

- plant breeding to construct an improved variety;
- independent variety testing to ensure value for cultivation and use, and distinctness, uniformity and stability; and,
- commercial seed production and release for use by farmers, typically in the form of varietal mixtures.

Teagasc is responsible for the plant breeding component, which consists of a multistep and cyclic process, known as recurrent selection, where the best plants (genotypes) are evaluated, selected and intercrossed to produce a new variety. The goal is to increase the frequency of favourable alleles and superior genotypes in the population over time.

A typical cycle of recurrent selection takes around five years and includes seed multiplication for establishing sward plots, multi-year field evaluation, and data analysis and selection. There is scope to increase the rate of genetic gain by reducing the length of time it takes to complete a single cycle of recurrent selection. This is a major goal of forage breeders worldwide and has led to the adoption of new and faster selection tools.

Using DNA-based selection tools

Genomic selection is a new breeding tool that uses information from a plant's DNA to predict its breeding value. In recent years there has been increased interest in its application to forage grass breeding, mainly driven by a reduction in the cost of DNA sequencing, but also from the demonstrable success of genomic selection in animal breeding. In genomics-assisted breeding, DNA evaluations are related to field measurements in a reference population and used to develop statistical models for genomic selection.

Using these statistical models we can generate breeding values for progeny of the reference population based solely on its DNA. The huge advantage genomic selection offers grass breeding is that it allows the breeding values of plants to be computed in one year using information from the DNA alone. This compares very favourably to traditional field-based genotypic selection, which takes around five years per selection cycle. This means we can complete five cycles of genomic selection in the same time it takes to complete a single cycle of field-based selection. It also enables us to increase selection intensity, as there are fewer constraints on the number of genotypes that can be evaluated in the glasshouse using DNA techniques as opposed to multi-year field evaluations. The result of reducing the length of the breeding cycle and increasing selection intensity is greater genetic gain.

Implementing genomic selection

Teagasc, Oak Park has initiated a project to evaluate the potential of implementing genomic selection in a tetraploid perennial ryegrass breeding population. A reference population of half-sib families (each family consists of plants with a common maternal parent) with features favourable for genomic selection was established. Families were evaluated in a replicated field trial over multiple years for forage yield under both simulated-grazing and conservation management. At the same time, we performed DNA evaluations on the parental plants by partially re-sequencing the genomes of each maternal plant. The data sets were combined, and we built statistical models and tested how well we could predict forage yield with genomic data. In particular, we were interested in predicting annual and seasonal forage yield weighted according to values from the Teagasc Pasture Profit Index (PPI). Our ability to predict breeding values for forage yield using genomics was encouraging, and assuming no degradation in predictive ability over generations indicated that we could more than double the rate of genetic gain by incorporating genomic selection into the Teagasc breeding programme. Our ability to complete a cycle of DNA-based selection in a fifth of the time it takes to complete a cycle of field-based selection ensures that we can overcome any loss in predictive accuracy when selecting using genomics. Based on these findings, we are now selecting tetraploid perennial ryegrass varieties using genomic selection in the commercial breeding programme. We will continue this over a number of years (Figure 1), and at each stage evaluate the new populations for improvement, and any promising populations will be

submitted for independent variety testing with a view to commercialisation.

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Future of grass breeding

Forage grass breeders will take advantage of all available tools and technologies at their disposal to increase genetic gain and produce varieties to meet the demands of industry. Genomic selection is just one such tool that we see being fully integrated into routine breeding activities. In such a scenario, field evaluations will be used to continually update and improve statistical models, and to add new traits as breeding goals evolve.

In future we also see forage breeders exploiting advances in high-throughput and speciality phenotyping, together with strategies to exploit hybrid-based breeding. Investment in plant breeding results in social, economic, and environmental benefits, and continued investment in forage grass breeding in Ireland will ensure the best genetics are available to meet the specific needs of Irish grassland farmers.

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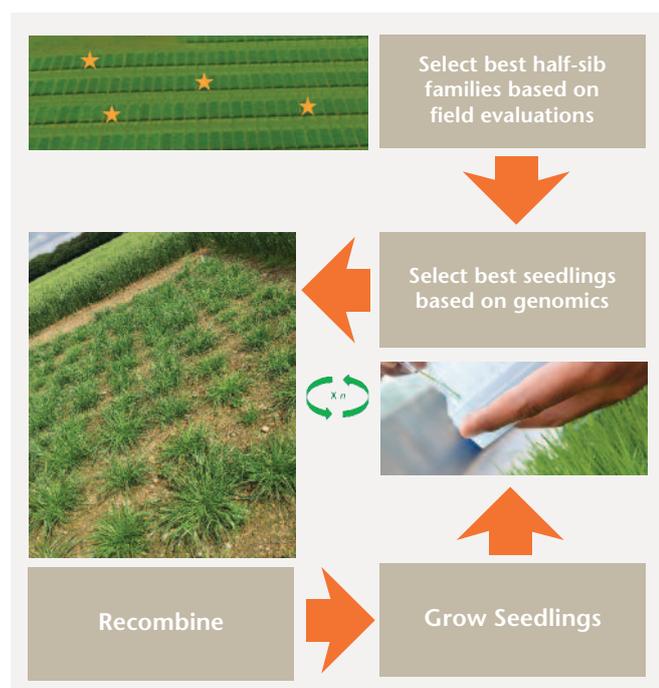


FIGURE 1: Implementing genomic selection at Teagasc in a tetraploid breeding population. Using rapid cycles of selection with genomics, it is anticipated that we can more than double the rate of genetic gain for complex traits like forage yield.

