

## **Exciting times for wheat genomics**

*Ed Flatman, Senior Wheat Breeder, RAGT Seeds*

It is one of the most exciting times ever for wheat breeding in Europe, but then you'd probably expect me to say that because I'm a wheat breeder and the wheat genome is my daily bread!

Farmers and the food chain want more from wheat - yield, quality and robust disease resistance, coupled with traits that may suit more erratic weather patterns as well as the increasingly specific requirements of end markets. Delivering the range of traits to suit takes foresight, industry collaboration and patience.

Detailed marker maps of wheat genes have earned us plant breeders a step change in the techniques and speed of progress in new variety development. Our team at Ickleton has been working with the wheat genome map for over a decade. 'The map' has redefined wheat breeding programmes by enabling us to locate the positions and interrelationships of important genes within wheat's genetic make-up.

What's more, we are only just scratching the surface of what modern breeding techniques can deliver. The genetic sequencing power at our disposal is increasing exponentially. We will soon be able to map as many genes in one afternoon as we could over several years less than a decade ago. So the opportunities we have today are truly immense.

And we have lots and lots of genes to 'play' with. With the full chromosome set of three wild relatives, the wheat genome is five times bigger than the human genome. To give an idea of the scale, currently our team is producing over seven million segregating lines of winter wheat each year.

Tracking genes with increasing precision is allowing us plant breeders to 'fix' trait combinations we don't want to lose as we make improvements in other areas like yield. It also means we are able to combine genes with complementary effects or to compensate for any negative effect a desirable gene for one trait may have on another. It offers great advantages too in selecting for characters that are difficult or time-consuming to identify. And it makes the introduction of new characters from wide crosses very much easier.

Take for example a variety like Relay, the candidate Group 4 wheat, it has the highest resistance rating of 9 for yellow rust in the HGCA Recommended List. Our understanding of the wheat genome has allowed us to breed the variety with an accompanying minor gene with a rating of 6, so if, or when, there is a rust mutation which bypasses the gene

responsible for the resistance rating of 9, there is still a valuable gene in place to prevent the variety breaking down completely in field situations.

Another example is breeding for high Hagberg Falling Number (HFN), the measure important to millers. By breeding for an accompanying good resistance to grain sprouting in the ear, in essence we breed in some degree of protection to the HFN which is deleteriously affected by the sprouting brought on by wet and humid weather when crops are ripe and awaiting harvest.

We're progressing with traits that matter like the genes for resistance to fusarium head blight, orange wheat blossom midge, eyespot, brown rust and yellow rust as well as disentangling the whole *Septoria tritici* story. We're also well advanced in establishing the various components of protein and starch functionality, and in pinpointing genes with a surprisingly large effect on yield so we can maximise both quantitative and qualitative genetic improvements.

We now have the sort of technological resources we could only dream of about 10 years ago. That's why we're so confident of being able to deliver greater and greater farm and end market value through our wheat seed in the years ahead.