Reap the genome harvest

Kellye Eversole provides an insight into her work at the helm of a large-scale, international consortium whose aim is to advance agricultural genomics by sequencing the bread wheat genome.

What first attracted you to the area of agricultural genomics, and what motivates you in your everyday work?

When I started Eversole Associates in 1991, I wanted to focus on projects that would increase sustainability and profitability in agriculture. To me, this is dependent upon advancements in agricultural science and technology, and upon bringing together industry, academia and governmental entities to ensure that the basic science supported is translated into useful applications for farmers.

The Human Genome Project was gaining ground at the time and, in 1994, I was asked by growers to help launch the Maize Genome Sequencing Project. This led to the establishment of the US National Plant Genome Initiative and has since resulted in draft sequences of many crop genomes. The idea that we could take very fundamental scientific knowledge and use it to improve the productivity, quality and sustainability of crops was – and still is – fascinating to me. I am passionate about agriculture and science and I feel fortunate that all of my projects have been at the nexus between these two areas.

As Executive Director of the International Wheat Genome Sequencing Consortium (IWGSC), could you define its ultimate goal?

The ultimate goal of the IWGSC is to develop a high-quality reference genome sequence-based platform that will provide breeders and scientists with the tools they need to accelerate and improve the development of wheat varieties for growers. Reference genome sequences hold the key to understanding how an organism works; the more accurate the sequence, the more efficient the pipeline for development of new varieties using a myriad of technologies.

Why is it important to sequence the genome of *Triticum aestivum*, more commonly known as bread wheat?

Wheat is grown on more land than any other crop, with at least 220 million hectares harvested annually. Wheat provides the largest proportion (44 per cent) of cereal consumed for food, and 32 per cent of the total cereals consumed for animal feed. The Food and Agriculture Organization of the UN estimates that wheat production will need to increase by more than 60 per cent by 2050 to meet the demands of 9.6 billion people.

We must therefore provide breeders and growers with the knowledge and tools they need to achieve these production increases in a sustainable manner. Ninety-five per cent of all wheat cultivated in the world is bread wheat, and that is why the Coordinating Committee of the Consortium (which includes public and private breeders) chose bread wheat as the target for the reference genome sequence of wheat.

Could you provide a brief synopsis of the IWGSC’s strategy?

Obtaining a high-quality sequence of bread wheat is challenging because the genome is very large (at 17 Gb, it is five times larger than the human genome), it contains three sets of chromosomes containing highly similar genes, and the vast majority of the sequence is comprised of repetitive DNA.

To reduce this complexity and maintain a commitment to delivering a high-quality sequence, the IWGSC adopted a ‘chromosome-based’ approach that includes three key milestones for all of the 21 bread wheat chromosomes: first, survey sequences, which provide a gene catalogue and information about their localisation along the chromosomes for slightly more than half of them; second, physical maps, which provide a substrate for sequencing and assembling pseudomolecules; and third, physical map-based reference sequences, which accurately order more than 90 per cent of the genomic information and link the sequence to genetic and phenotypic maps.

How are you progressing towards these key milestones?

The first milestone was reached last year with the publication of draft sequences for all 21 wheat chromosomes in the journal *Science*. Completion of the second milestone is well underway; we have physical maps for 16 chromosomes and draft maps for the last five. We are also making progress towards our final milestone; the reference sequence for one chromosome, 3B, was completed in France and published in *Science* last year. Reference sequencing of 13 other chromosomes is underway in 12 countries and will be completed over the next two years.

We are now focusing on securing the funding for reference sequencing of the remaining seven chromosomes, and have proposals for two of these pending before funding agencies.
Wheat for tomorrow’s world

The International Wheat Genome Sequencing Consortium is coordinating activities across the globe to achieve its goal of delivering a publicly available high-quality genome sequence of bread wheat.

WHEAT IS ONE of the most important crops on the planet: as the most widely grown cereal in the world, it forms a staple food for more than one third of the global population. It is of immense value, both as a source of nutrition and of income. As such, any threat to its production or profitability must be treated with the utmost seriousness.

In recent years scientists have been increasingly keen to sequence the wheat genome in order to improve resilience and productivity. Unfortunately, this has not been without its challenges because the wheat genome is both extremely complex and very large. However, as and when these difficulties are overcome, the resulting sequences will form an immensely useful basis for wheat research, guiding the development of new, improved varieties suitable for the grand challenges that lie ahead, such as climate change and rapid population growth.

A GLOBAL SEQUENCING EFFORT

The International Wheat Genome Sequencing Consortium (IWGSC) was founded in 2005. A decade later, the IWGSC has expanded from its original group of public and private breeders, wheat growers and plant scientists to bring together over 1,100 members spread across 55 countries, with projects currently running in 21 of these. The Consortium’s diverse members are united by a clear shared goal: to produce and make publicly available a high-quality genome sequence of bread wheat.

The fact that this sequence must be made freely available is core to the IWGSC mission: “Such fundamental knowledge should be available to everyone,” underscores Kellye Eversole, IWGSC Executive Director. “This precompetitive information, once available, will enable wheat seed companies and public sector organisations to make positive developments, such as improving yield, resilience and nutritional quality.”

It is also the hope of the Consortium’s members that the successful sequencing of the wheat genome will significantly reduce the amount of time required to breed new varieties. At present, without genomic tools, the average timeframe for developing a new variety is 12 years – a lag that does not allow for rapid responses to novel threats, nor does it encourage the widespread development and adoption of new varieties.

THREE MILESTONES

To accomplish its aims, the IWGSC has adopted a chromosome-based strategy around three milestones: the production of survey sequences of all 21 bread wheat chromosomes, the development of physical maps to serve as a substrate for sequencing and, finally, the completion of each chromosome’s reference sequence.

The IWGSC members have opted for a chromosome-by-chromosome approach that is based on physical maps, as opposed to a ‘whole genome shotgun’ strategy in which sequences are produced by sequencing randomly generated fragments of DNA from the entire genome and then assembled using specifically designed algorithms. “For complex, large genomes such as wheat, the physical map-based approach is the only strategy that can be used with today’s technology to efficiently deliver a high-quality, ordered sequence comparable to the gold standard reference sequence of rice,” Eversole explains.

The insights generated by this approach will be of significant use to wheat breeders looking to develop new and improved wheat varieties as they will enable the identification and functional analyses of regulatory features and chromosomal organisation, while also providing access to the complete gene catalogue as well as maps of genetic markers and intra- and inter-species variation.

DISSEMINATING WHEAT GENOME KNOWLEDGE

Achieving its first milestone last year, the IWGSC published draft sequences for all 21 wheat chromosomes in the journal Science. This sequencing provided unparalleled insights into the structure, organisation and evolution of the bread wheat genome, laying a foundation for the future identification and isolation of genes of agronomic interest. In addition to this, significant progress has been made towards achieving the second milestone; physical
The International Wheat Genome Sequencing Consortium (IWGSC) now requires just €11.5 million more to complete its work and place the data in the publicly accessible IWGSC repository.

Steps are also being taken towards the third and final milestone. Reference sequencing for 13 chromosomes are expected to be produced in the upcoming two years, and the reference sequence for the 3B wheat chromosome was produced and published last year (also in Science). As the largest wheat chromosome (more than two times the size of the entire rice genome), this achievement established a benchmark for subsequent sequencing, achieving a high-quality reference sequence in which 94 per cent of the chromosome was ordered. “While some gaps remain, it is of higher quality than most of the crop sequences produced to date, and proved that wheat could be sequenced efficiently and for a reasonable cost using such a strategy,” expands Eversole. “New sequencing technologies can now be used to reduce the cost even further while using the same physical map-based approach.”

COORDINATED CROP SEQUENCING

The IWGSC has had to overcome its share of difficulties to make such progress since its foundation 10 years ago. For example, as a large-scale, international and highly multidisciplinary consortium, finding ways to work effectively in close collaboration has been key.

Although this has presented difficulties at times, Eversole believes that, ultimately, it has produced ample benefits: “If we are to meet the demands for wheat production in the future sustainably and profitably, we have to make certain that breeders, both in academia and industry and across all countries, can rapidly exploit the tools and resources we have developed,” she elaborates. “Bringing them into the sequencing project has enabled this.”

Furthermore, the IWGSC’s international, collaborative approach to constructing physical maps and sequences has facilitated skill- and resource-building amongst its members while also enabling cost-sharing and paving the way for more rapid application and impact on a global scale.

The greatest challenge facing the IWGSC is, however, financial. Having raised approximately €50 million over the past decade, the IWGSC now requires just €11.5 million more to complete its work and place the data in the publicly accessible IWGSC repository. Providing that funding can be secured, the researchers predict this can be achieved as early as 2017-18.

FURTHER READING


INTERNATIONAL WHEAT GENOME SEQUENCING CONSORTIUM (IWGSC)

OBJECTIVE

To provide a high-quality genome sequence of bread wheat that serves as a foundation for the accelerated development of improved varieties and that empowers all aspects of basic and applied wheat science.

LEADERSHIP TEAM

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KELLY EVERSOLE has been a science and technology consultant since 1991 and a leader in agricultural genomics since 1994. After working in the US Senate on agricultural, environmental, trade and budget issues for 10 years, and serving two years as the head of a federal study commission, she established Eversole Associates. Currently, she is leading the international effort to sequence the genome of bread wheat, the most widely grown crop in the world, as Executive Director and Chairman of the Board of the IWGSC. She is also leading a new Phytobiomes Initiative (www.phytobiomes.org).