FINAL REPORT

GRDC
GRAINS RESEARCH & DEVELOPMENT CORPORATION

DAW00233

Sequencing the Barley Chromosome 7H

PROJECT DETAILS

PROJECT CODE:	DAW00233
PROJECT TITLE:	SEQUENCING THE BARLEY CHROMOSOME 7H
START DATE:	01.12.2013
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Summary

This project completed sequencing 8,521 clones with an average length of 122,000 base pairs covering chromosome 7H. A gold standard chromosome sequence was assembled with a total length of 664 million base pairs. A draft gene map was generated with approx. 13,000 candidate genes. Key Australian barley varieties were sequenced with 100 billion base pairs for each variety. Genomic features of North American, European and Australian barleys were identified. Molecular map and gene-specific diagnostic markers were developed. The gold standard barley genome sequences enable breeders to significantly reduce the time taken to develop new high performance barley varieties tailored to local environments.

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Conclusions

Triticeae crops, including bread wheat, durum wheat, barley and rye, have some of the most complex genetic histories among the world's cultivated species. Barley is the first crop to be sequenced in such detail. This project enabled the Australian barley community to access a large amount of sequence information generated in the International Genome Sequence Consortium with more than $25 million investment from partners. The 'gold standard' barley genome sequence will provide the base for advancing barley crop improvement in terms of malting quality, grain and biomass yield, resilience to biotic and abiotic stresses, and non-food applications, as well as nutrient use efficiency.

The availability of an entire genome sequence will provide a fundamental resource for isolating genes based on genomic positional information and as such, enhance the research community's ability to investigate and understand the molecular processes underlying phenotypes such as biomass, quality, yield and disease resistance. It will enable plant breeders to significantly reduce the time taken to develop new high performance barley varieties tailored to local environments, which will improve industry productivity and profitability. Barley pre breeding and breeding will enter the next chapter with much higher precision and efficiency.

Recommendations

1. A large amount data were generated in this project, including reference genome sequences, whole genome shotgun sequences, transcriptomic sequences, exome capturing sequences and genotype by sequencing. The partnerships in the International Barley Genome Sequencing Consortium also enable access to a large amount of sequence data from other countries. Dedicated resources are required to maximise the value of these data, which include capable personnel and infrastructures.

2. The reference genome sequence provides an efficient tool to identify key genes controlling economic important traits. The advance in genome editing technology, e.g. CRISPR-cas9, makes it possible to manipulate key genes for improvement of productivity and sustainability. Investment is required to characterise the key genes for important traits.

3. Sequencing technology has made fast progress in the past few years. It is possible to conduct a large scale genome re-sequencing project to explore genetic variation. The European Union is making large investments in re-sequencing barley germplasm. Similar investment should be considered in Australia and a partnership built with the European countries to

share the resources.

Outcomes

A gold standard chromosome sequence was assembled with a total length of 664 million base pairs in this project, which enabled the Australian pre breeding and breeding community to access the whole reference barley genome sequence from six other countries with a total investment of more than $20 million. The reference genome sequences are already being used in a number of ways, such as addressing the issue of blue aleurone in acid barley, and to provide a variety fingerprinting service for the barley industry. Using the reference genome sequence as a template, the genomes of key barley varieties Hindmarsh(Þ), La Trobe(Þ), Commander(Þ) and Baudin(Þ) were mapped. This will lay a solid foundation for development of new barley varieties. Furthermore, genomic features of the Australian, European and Canadian malting barleys were mapped to provide technical solutions to match up the malting quality improvement in these countries.

Barley breeders and pre breeders now have access to the genomic sequence to dissect the quantitative trait loci (QTL) and genes for yield, adaptation, quality, biotic and abiotic stress tolerance and to develop diagnostic molecular markers and genomic breeding tools.The speed for development of molecular markers and identification of functional genes for agronomic traits is multiple times faster. The gold standard genome sequence also provides greater precision and more detailed data, which will provide barley breeders and researchers with confidence to manipulate the genes and enable them to reduce the time taken to develop new high performance barley varieties tailored to local environments.

Barley growers will have access to and increase production of adapted barley varieties with a significant yield potential and stability increase over current elite varieties, which will improve industry productivity and profitability.

The genome sequence provides the base for advancing barley crop improvement for resilience to biotic and abiotic stresses, and non-food applications, as well as nutrient use efficiency. Improvements in any of these traits will have significant positive effects environmentally and thus will help meet future challenges caused by human population growth and climate change.

Achievements/Benefits

This project contributed to the International Barley Genome Sequence Consortium to complete a reference barley genome sequence, which will enable Australian barley breeders and researchers to leverage access to reference barley genome sequence.

This project has completed sequencing 8,521 clones covering chromosome 7H using next generation sequencing technology with an average length of 122,000 base pairs. The total length of the sequences was assembled to 976 million base pairs. A pseudomolecule of chromosome 7H was assembled with a total length of 664 million base pairs by integrating the high throughput sequencing with an optical map and chromosome conformation capture sequencing. A draft gene map of chromosome 7H was generated with approx. 6,000 high confidence genes and 7,000 other genes.
The Australian barley varieties Baudin(Þ), Buloke(Þ), Scope(Þ), Commander(Þ), Hindmarsh(Þ), Vlamingh(Þ), WI4304 and LaTrobe(Þ) were sequenced and 100 billion base pairs clean DNA sequence data was generated for each variety. The key genomic features of the North American, European and Australian malting barley varieties were identified through comparative mapping. New molecular markers and maps were developed. Based on the analysis results, candidate genes and gene-specific (diagnostic) markers for malting quality (malt extract, alpha-amylase, beta-glucanase, diastatic power) were developed and validated in the Australian barley populations.

The project constructed an integrated database, BarVarDB. The database contains the Morex reference genome sequence, whole genome shotgun sequences of the barley varieties Baudin, Buloke, Commander, Hindmarsh, LaTrobe, Vlamingh, WI4304, Morex, Barke, Bowman and other wild species, MTP BAC sequences of seven chromosomes, more than 10,000 molecular markers and 500 QTL.

The project conducted extensive RNA transcriptomic sequencing from the Australian, Canadian and European barley malts. Genomic features of the Australian, European and Canadian malting barleys were mapped to provide technical solutions to match up the malting quality improvement in these countries.

The International Barley Genome Sequencing Consortium has completed sequencing of 87,075 bacterial artificial chromosome (BAC) clones. A non-redundant sequence was assembled to seven pseudomolecules with a total length of 4.79 billion base pairs. The first version of barley reference genome sequence is ready for delivery to barley breeders and pre

breeders.

The project gave one presentation to the Plant and Animal Genome - Asia and to the 17th Australian Barley Technical Symposium, two presentations to the Barley Breeder Conference, to the Grain Industry Association of Western Australia (GIWA)-Barley Council and to the International Barley Genome Sequencing Consortium. The project published eight scientific papers including one in Nature. Sequence information was also provided to the Australian Winter Cereal Molecular Marker Program (AWCMMP) and Wheat Genome Sequencing Program. Two media stories are pending on the publication of the main paper.

Other research

The outputs from this project have enhanced the ability in other research projects, for example, to identify the blue aleurone gene in the acid soil tolerance variety. The project also provided resources to AWCMMP to isolate the CCN gene and to the wheat genome sequence project.

Intellectual property summary

1. A Memorandum of Understanding (MOU) was signed with the International Barley Genome Sequencing Consortium to share and access the barley reference sequence data.
2. A MOU was signed to access the Morex BAC clones.
3. A contract was signed with BGI-Hong Kong to complete the BAC, DNA and RNA sequences.
4. A Material Transfer Agreement (MTA) will be signed with the breeding companies to provide new molecular markers.

Additional information

Attachment

Publications list.