

## REVIEW

# Reference Genome Sequencing and Advances in Genomic Resources in Common Wheat–Chromosome 6B Project in Japan

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## Abstract

By successfully sequencing the entire genome of common wheat (*Triticum aestivum* L.) in 2018, the International Wheat Genome Sequencing Consortium (IWGSC) achieved its goal of publishing the first reference genome sequence of this important crop. During this period, various technological innovations have dramatically evolved genome sequencing technology; these advances have made it possible to rapidly decode large and complex genomes, including that of polyploid wheat. IWGSC completed reference genome sequence by exploiting these latest technologies via two primary approaches, “whole-genome sequencing” and “sequencing by chromosome.” As collaborators in the IWGSC project, a Japanese research team led by the National Agriculture and Food Research Organization was responsible for sequencing chromosome 6B, one of the 21 wheat chromosomes, and contributed to constructing the reference genome sequence. This article presents an outline of reference genome sequence construction and provides an overview of the common wheat genome information obtained. Moreover, it describes the methods used to sequence chromosome 6B, together with the associated analytical data and novel knowledge, including the structural analyses of *Nor-B2* and *Gli-B2* obtained during this work. Furthermore, it describes the recently undertaken sequencing of the genomes of diploid and tetraploid wheat and reviews the overall development of wheat genomic resources.

**Discipline:** Biotechnology

**Additional key words:** bacterial artificial chromosome library, next-generation sequencing, physical mapping, shotgun sequencing

## Introduction

Genome sequence data have become indispensable tools in promoting genetic improvements in crop varieties to achieve better quality, higher yield, adaptation to different environments, and tolerance to biotic stresses. In this regard, information on the rice (*Oryza sativa* L. subsp. *japonica* cv. Nipponbare) genome published in 2004 (IRGSP 2005) paved the way for genome-based breeding. Both basic and applied research on rice have undergone major advances as a consequence of developments in breeding technologies such as quantitative trait locus analysis, gene isolation, the

molecular marker design, and genetic resources development. Moreover, a range of related experimental and bioinformatics data have been released and stored, including primary databases for genome sequences and annotation data (Ouyang et al. 2007, Sakai et al. 2013), followed by secondary databases for omics data, including those of transcriptome studies (Kawahara et al. 2016, Sato et al. 2013). Databases for rice and other crop plants have been developed and can be mined for comparative analyses among plants (Rouard et al. 2011, Tello-Ruiz et al. 2016). This wide range of information plays an important role as a driving force for plant research, not only in rice breeding but also in basic

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