With 870 million people still hungry (<http://faostat3.fao.org/home/index.html>), the publication of the most comprehensive analysis to date of two of the most elusive cereal genomes – wheat and barley – opens a realm of possibilities for optimizing the supply of these vital crops.

Bread wheat accounts for 20% of humankind’s caloric intake, while barley, being more tolerant than other cereals to harsh climates and nutrient-poor soils, is a major food source in least developed countries. Not to forget that most beer, whiskey, and malted products, come from barley grains. Feels good to know that researchers are closer to preserving the world’s supply of these mighty Triticeae cereals.

It wasn’t until recently that, due to their highly repetitive DNA composition, the size of Triticeae cereal genomes had severely compromised the assembly of whole-genome shotgun sequences. Fortunately, two independent groups set to integrate complementary and heterogeneous sequence-based genomic and/or genetic data sets to generate high-quality reference genomes for both, wheat and barley.

In addition to size, polyploidy was also a barrier for the analysis of the wheat genome. Bread wheat is a hexaploid genome (AABBDD) made of three related ancestral genomes (AA, BB, and DD), each having 7 chromosomes. In other words, wheat cells have six copies of seven different chromosomes or two sets of 21 chromosomes (2n=6x=42), each comprising 17 Gigabases (Gb). In contrast, human cells are diploid, packed in 23 chromosome pairs (2n=46), each pair comprising 3 Gb.

In the quest to decode the bread wheat genome, Mike Bevan and colleagues (Brenchley *et al*, 2012) used 454 pyrosequencing and compared it to sequences of diploid ancestral and progenitor genomes. This approach led them to identify ~95,000 genes, and assign two-thirds to the three component (A, B, D) genomes. They discovered significant loss of gene family members upon poliploidization and domestication, and expansion of gene classes with predicted roles in defence, nutritional content, energy metabolism and growth, which may be associated with crop productivity. Of note is that a public resource of shotgun sequences for each chromosomal arm is close to completion (Dolezel *et al*, 2007).

As for decoding the secrets of barley, the International Barley Genome Sequencing Consortium developed a physical map anchored to a high-resolution genetic map, over which they projected a deep whole-genome shotgun (WGS) assembly, cDNA and RNA-seq data to create the first in-depth genome-wide survey of the barley genome, a gene-centric reference gene-ome assembly (International Barley Genome Sequencing Consortium, 2012).

The barley genome is also a diploid of 5.1 Gb packed in seven chromosome pairs (2n=14). The Consortium observed that ~84% of the barley genome was comprised of repetitive DNA, the majority of which are long terminal repeat retrotransposons. The transcribed complement of the barley gene space was annotated by mapping 167 Gb of RNA-seq reads, as well as 28,592 full-length cDNAs to the WGS assembly. A high-confidence gene set of 26,159 was obtained by homology support of a transcribed gene cluster to at least one of the reference genomes of sorghum, rice, Brachypodium, and Arabidopsis.

Both reference genome sequences, coupled with the identification of extensive genetic variation, provide resources for accelerating gene discovery and crop improvement through breeding.