

# Welcome to the Wild Emmer Wheat Genome (accession Zavitan)

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wheat breeding.

Wheat (*Triticum* spp.) is one of the founder crops that drove the Neolithic transition from hunter-gatherer to sedentary agrarian societies in the Fertile Crescent over 10,000 years ago. Identifying the suite of genetic modifications underlying wheat's domestication and improvement requires knowledge of the genome of its allotetraploid progenitor, wild emmer (*T. turgidum* ssp. *dicoccoides*). An international consortium has generated a high quality reference sequence of the wild emmer wheat (WEW) accession 'Zavitan'. The WEW reference genome was constructed using a whole genome shotgun (WGS) approach to produce sequence scaffolds using the DenovoMagic2 software (NRGene Ltd.). These scaffolds were then validated using genetic data and combined with 3-dimensional (3D) chromosome-conformation-capture-sequencing (HiC) data, thus enabled construction of chromosome-scale assemblies (pseudomolecules) as well as analyses of WEW gene content. In total, the genome assembly pipeline used 2.1 Tb of raw sequence data, resulting in a total assembly size of 10.5 Gb comprised of 14 pseudomolecule sequences representing the 14 chromosomes of WEW (10.1 Gb) as well as one group of unassigned scaffolds (0.4 Gb). We are convinced that the availability of improved genomics resources such as the WEW assembly will underpin and accelerate global efforts in gene discovery, functional characterization, and ultimately



Intranet of Wild Emmer Wheat Genome Data: [Here](#)

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