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# Plant and Animal Whole Genome Sequencing

With advancements in next-generation sequencing technology, whole genome re-sequencing (WGS) has become a more rapid and effective method to unravel, at the genomic level, the underlying mechanisms of species origin, development, growth and evolution. Using WGS, the complete genome data from one or more variants can be aligned to known genomic sequences for the species. Applications of WGS include detection of genetic differences between variants, transposon fingerprinting for assessing germplasm diversity and lineages, and mapping loci associated with specific traits.

**Why Novogene?**

**Extensive experience with over 3000 projects**

**Industry-leading data quality guarantee**

**In house pipeline to meet different analysis requirement**

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## Sample requirements

| Sample Type | Amount | Volume | Concentration | Purity |
|---|---|---|---|---|
| Genomic DNA | ≥ 0.2 μg | ≥ 20 μL | ≥ 10 ng/μL | OD260/280: 1.8 –2.0 |
| Genomic DNA (PCR-free library) | ≥ 1.5 μg | ≥ 20 μL | ≥ 20 ng/μL | |
| HMW Genomic DNA | ≥ 8 μg | ≥ 20 μL | ≥ 80 ng/μL | |

## Sequencing parameters

| Library type | Sample type | Platform | Sequencing strategy | Data quality |
|---|---|---|---|---|
| Illumina library | Genomic DNA | Illumina NovaSeq 6000 | PE 150 | Q30 ≥ 85% |
| | Genomic DNA (PCR-free library) | | | |
| PacBio sequel II DNA CLR library | HMW Genomic DNA | PacBio Sequel II | 10 – 30K insert library | |
| PacBio sequel II DNA HiFi library | | | | |

## Publications using Novogene's expertise

**Science,** 2020.
Horizontal gene transfer of Fhb7 from fungus underlies Fusarium head blight resistance in wheat

**Nature Communications,** 2018.
Genome re-sequencing reveals the evolutionary history of peach fruit edibility

**BMC Genet,** 2019.
Characterization of the extra copy of TPOX locus with tri-allelic pattern.

**Nature Genetics,** 2018.
Resequencing a core collection of upland cotton identifies genomic variation and loci influencing fiber quality and yield

**Cell Research,** 2017.
The genetics of tiger pelage color variations

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Case study

# Genome assembly provides insights into the genome evolution and flowering regulation of orchardgrass.

Huang et al., 2020. Plant Biotechnology Journal. DOI: 10.1111/pbi.13205.

**Research objective:**
To assemble a reference genome for orchardgrass *(Dactylis glomerate L.)* to facilitate the discovery of genes that control important agronomic traits of this forage grass that is used to cultivate livestock worldwide.

**Sample collection:**
Diploid orchardgrass accession 2006-1, originally collected from Wuxi, Chongqing, China, was acquired from Sichuan Agriculture University where it is maintained.

**Sequencing strategy:**
PE150 on Illumina NovaSeq 6000 and PacBio Sequel long-read sequencing.

**Data amount:**
212Gb of raw data.

## Results

Of the assembled genome sequences, 68.56% were transposable elements (TEs). A strong correlation was found between the proportion of TEs and genome size, suggesting this high proportion was responsible for the large genome size of orchardgrass (1.84Gb).

The amplification of these TEs was estimated to have occurred between 0 an 1 million years ago, when the global climate was harsh and cold. TEs are activated by stress, so these environmental conditions may have resulted in the reorganisation of plant genomes for survival. The amplification also coincided with the divergence time of grass species (fig. 1), suggesting that TEs are involved in grass speciation.

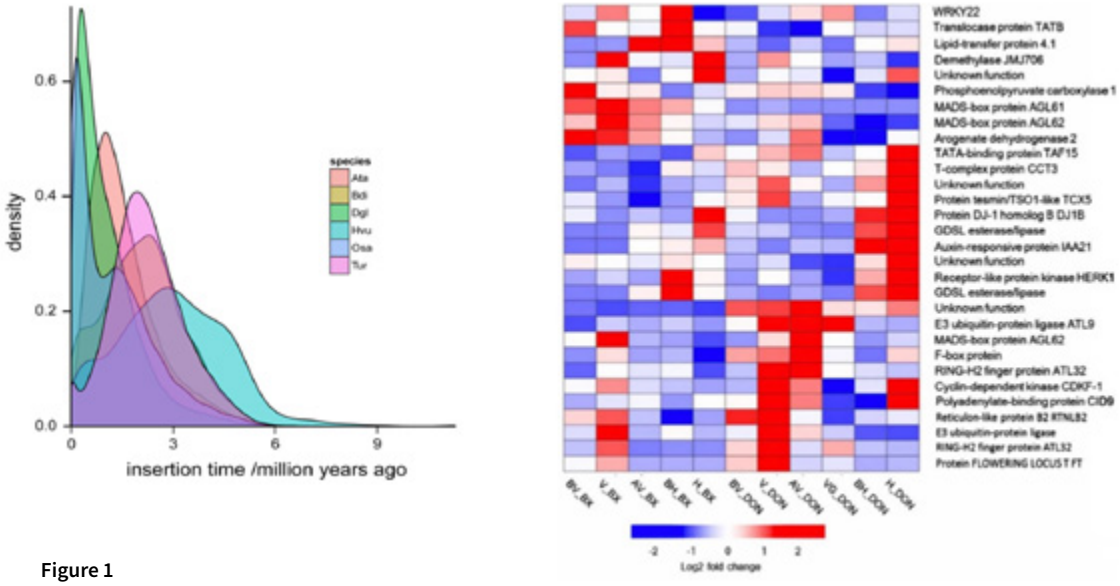


**Figure 1**
Insertion times of TEs in 6 species. Orchardgrass is denoted as Dgl.

MADs-BOX genes have been shown previously to be a highly conserved gene family responsible for flowering time and flower organ development. The MADs-BOX genes in orchardgrass were found to be highly expanded, likely contributing to the high variability in flowering time and strong adaptability of orchardgrass to environmental changes.

An investigation into the differential expression of these genes in early- and late-flowering highlighted gene DG6G02970.1, a gene similar to MADs-BOX AGL61 which is responsible for pollen tube guidance and the initiation of endosperm development, suggesting that DG6G02970.1 might participate in flowering regulation in orchardgrass.

A further 38 differentially expressed genes were identified between the two stages and found to be involved in processes such as photosynthesis, chlorophyll catabolism and hormone signal transduction, and gene ontology indicated enrichment of genes involved in carbohydrate metabolism. The need for high levels of carbohydrate to transition from vegetative growth to flowering has been previously demonstrated in other species, suggesting the same for orchardgrass.

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