Alfalfa Genome Sequencing

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In the past twenty years, reference genome assembly has greatly promoted plant functional genomics research and molecular breeding. Alfalfa (*Medicago sativa*) is one of the most widely planted forages. Because of autotetraploidy and heterozygosity, alfalfa genome assembly has always been retarded. Although the whole genome sequencing program of the related diploid model *M. truncatula* started as early as 2003, it was not published until 2011 and there were still many gaps. Up to now, the reference genome of *M. truncatula* has undergone several updates with improved sequencing technologies and assembling strategy. For the cultivated alfalfa with a more complex genome, the reference genome assembly has made a breakthrough in the past three years. Our team released the high-quality reference genome of the cultivar Zhongmu No. 1 in 2020, and the other two Chinese research teams released the genome assembly of the cultivars XinJiangDaYe and Zhongmu No. 4 in 2020 and 2022 respectively. We *de novo* assembled the haploid genome of Zhongmu No. 1 with eight putative chromosomes of 816 Mb in total, and the contig N50 reached 3.92 Mb. We also sequenced the whole genomes of 137 alfalfa global core germplasms and 25 subspecies *caerulea* accessions and conducted population analysis and Genome-Wide Association Studies (GWAS) with public agronomic phenotypic data, by which we identified that *MsFTa2*, a *Flowering Locus T* homolog, is probably associated with fall dormancy, salt resistance, frost damage, and internode length. Our research provides abundant genomic resources for alfalfa genetic research and agronomic improvement. We look forwards to constructing the gapless reference genome and further pan-genome of alfalfa in the future.