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Abstract

Moringa oleifera is a famous tree species often known as horseradish tree or drumstick tree, belongs to the family Moringaceae. It is an evergreen and mineral rich plant that grows quickly, used in herbal medicine, agriculture, and the livestock sector. So far, only one draft genome assembly is available publicly for *M. oleifera*. Sparse availability of the genomic resources limits its use in genetic and genomic studies. So, we sequenced and de-novo assembled a draft genome of *M. oleifera* from Pakistan. The sequencing was performed using Illumina HiSeq platform with paired-end libraries. The draft assembled genome was 205,248,313 bp in size, and comprised of 13,872 scaffolds with N50 value of 17,279 bp. Annotation of the assembled genome revealed 26,215 protein coding genes. The draft de novo assembled genome is close to the genome size predicted by k-mers distribution and covers 83.09% and 84.68% of completeness and plant orthologous groups in BUSCO and CEGMA, respectively. This genome assembly would be an invaluable resource in understanding the genetic potential of this species, as well as in functional, comparative and evolutionary genomics within this species and in *Moringa* genus.

Under development