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***De novo* genome assembly of *Sanionia uncinata* (Amblystegiaceae: Hypnales), a pleurocarpous moss dominant in Antarctica**

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Mosses in Antarctica grow mostly in coastal areas and are expected to have developed various unique physiological/molecular mechanisms to survive in extreme environments. *Sanionia uncinata* (Hedw.) Loeske (Amblystegiaceae: Hypnales) is a dominant moss species in the maritime Antarctic and considered as a good target to investigate genes associated with abiotic stress tolerance of mosses. It has several distinct characteristics when compared to *Physcomitrella patens*, the first model moss species. First, *S. uncinata* is a pleurocarpous moss. Second, it belongs to the order Hypnales which contains the largest number of species in the moss phylogeny. Third, it is an alpine species that lives in cold regions unlike *P. patens* mostly found in temperate regions. Here, we report the draft genome sequence of an Antarctic *S. uncinata*, obtained using third-generation PacBio sequencing technology. About 1 million reads were attained from four Sequel sequencing runs and merged together into a single dataset of 21 Gb. The *de novo* assembly produced 673 contigs comprised of 621 Mb with an N50 contig length of 2.2 Mb and the longest contig length of 10.3 Mb, and a total of 28,651 coding genes were inferred. When the completeness of the genome was assessed by BUSCO analysis with the Eukaryota odb9, *S. uncinata* draft genome showed 91.1% complete, 0.3% fragmented, and 8.6% missing BUSCO. Our dataset can be used as a comparative genome for evolution and speciation studies for bryophytes, as well as for the analysis of molecular adaptation of plants to harsh environment.

Keywords: Antarctica, genome, Hypnales, *Sanionia uncinata*