

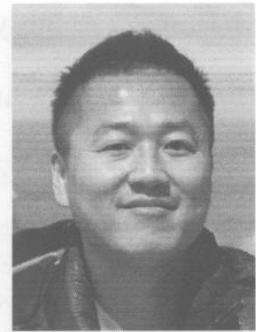
Genomic blueprint of a dominant Antarctic moss,

Sanionia uncinata

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Genomic information for the bryophytes are very limited, currently only one moss species *Physcomitrella patens* has sequenced, annotated genome available. Moreover, the Antarctic vegetation is dominated by the bryophytes, there is no report on the genome for the Antarctic bryophytes despite its ecological importance. *Sanionia uncinata* is the dominant moss species in the maritime Antarctic. It has been researched as an important marker for ecological studies and as an extremophile plant for studies on stress tolerance. We report the draft genome sequence of *S. uncinata* and compare its features with that of the model moss species *P. patens*. Our core data for contig assembly is composed of 88.5 million high-quality short reads data generated using Miseq platform, which covers 33x of the estimated genome length (615 Mb), and were assembled into 65,367 contigs (N50 = 17,341 bp, 463 Mb) in 14,419 scaffolds (N50 = 527,545 bp, 622 Mb). Gene prediction and genome-wide duplication analysis revealed that several gene families likely be involved in tolerance to low temperature stress contain significantly more gene copies within the *S. uncinata*. Furthermore, genes showing evidence of positive selection are significantly enriched in functional categories related to abiotic stresses. Some of these genes, and others within the same categories, are significantly upregulated under freezing condition relative to their expression in more favorable temperature condition. Our large-scale genomic and transcriptomic data pave the way for further genomic studies not only on *S. uncinata* but also other mosses and bryophytes.