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Population genetic analysis of *Deschampsia antarctica* from two regions of Maritime Antarctica

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Deschampsia antarctica Desv., one of the only two vascular plants native to Antarctica, was studied in two 430-kilometer distant regions of Maritime Antarctica, namely from Admiral bay of King George Island (the South Shetland Isl.) ($n = 6$) and from surroundings of the Argentine Isl. ($n = 9$). Sequencing of ribosomal DNA (rDNA) region including the first internal transcribed spacer (ITS1), the 5.8S rRNA gene, and ITS2 revealed significant identity (96.3%) of the sequences in the studied plants. The largest divergence was found between ITS1 (6.5%), and the lowest — between the 5.8S rRNA gene (1.8%) regions. Identity between all but one of the studied rDNA sequences and four rDNA sequences of *D. antarctica* from Argentina and the Falkland Isl. available from GenBank ranged from 97% to 98%. The unweighted pair-group method with arithmetic mean (UPGMA) analysis based on 28 polymorphic amplicons out of 289 random amplified polymorphic DNA (RAPD) markers produced with 30 primers allowed grouping the objects into two clusters according to geographical distribution. These two groups differed by the level of genetic variation: percentage of polymorphic amplicons for plants from the Argentine Isl. was 3.4%, and for plants from King George Isl. — 6.2%; Shannon's diversity index values were 0.015 and 0.024, respectively. Differentiation of these *D. antarctica* groups from two geographical regions suggests the limited gene flow between them. The different levels of genetic polymorphism in the two groups might be due to the differences in time of colonization or environmental conditions.

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