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GENOMIC RESOURCES NOTE

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Abstract

This article documents the public availability of (i) raw transcriptome sequence data, assembled contigs and BLAST hits of the Antarctic plant *Colobanthus quitensis* grown in two different climatic conditions, (ii) the draft genome sequence data (raw reads, assembled contigs and unassembled reads) and RAD-tag read data of the marbled flounder *Pseudopleuronectes yokohamae*, (iii) transcriptome resources from four white campion (*Silene latifolia*) individuals from two morphologically divergent populations and (iv) nuclear DNA markers from 454 sequencing of reduced representation libraries (RRL) based on amplified fragment length polymorphism (AFLP) PCR products of four species of ants in the genus *Tetramorium*.

Table 1 contains information on the focal species, data type and resource developed, as well as access details for the data. The authors responsible for each genomic resource are listed in the final column. Full descriptions of how each resource was developed and tested are uploaded as Supporting Information with the online version of this manuscript.

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Table 1 Information on the focal species, data type and resource developed, as well as access details for the data. The authors responsible for each genomic resource are listed in the final column.

Species (no. of individuals)	Data type	Resources	Authors
Colobanthus quitensis (60 [10 per transcriptome])	Transcriptome sequencing, assembly and BLAST hits	Sequence files: NCBI SRA accession SRX814890 Transcriptome Assembly: DDBJ/EMBL/GenBank accession GCIB00000000 Blast hits: Dryad doi:10.5061/dryad.jp1mk	Laura Bertini, Silvia Proietti, Carla Caruso
Pseudopleuronectes yokohamae (1 draft genome; 6 RAD-seq)	Draft genome sequence data and RAD-tag reads	Raw reads for genome sequencing: DDBJ Read Archive DRA002624 Assembly contigs: DDBJ/EMBL/GenBank accession numbers BBOV01000001 –BBOV01525502 and Dryad doi:10.5061/dryad.11n64 Unassembled reads: DDBJ Read Archive DRA002629 Raw RAD-tag reads: DDBJ Read Archive DRA002628	Yuki Minegishi, Minoru Ikeda
Silene latifolia (4)	Transcriptome sequencing, assembly and SNP discovery	Sequence files: NCBI SRA PRJNA232801 Reference transcriptome: Dryad doi:10.5061/dryad.d0 h71 Sequence alignment files: PRJNA232801 SNP file: Dryad doi:10.5061/dryad.d0 h71 Script files: Dryad doi:10.5061/dryad.d0 h71	Peter D. Fields, Laura A. Weingartner, Lynda F. Delph
Tetramorium alpestre (1), *Tetramorium caespitum* (1), *Tetramorium impurum* (1) and *Tetramorium insolens* (1)	RRL amplicon sequencing, primer pairs	Sequence data: NCBI SRA PRJNA274653 Fasta and Alignment files: Dryad doi:10.5061/dryad.fk558 Scripts and pipeline protocol: Dryad doi:10.5061/dryad.fk558 Distance table: Dryad doi:10.5061/dryad.fk558 Primer pairs: Table 3 in Genomic Resources Note (Supporting Information)	Herbert C. Wagner, Francesco Cicconardi, Gregor A. Wachter, Heike Ritthammer, Florian M. Steiner, Birgit C. Schlick-Steiner, Wolfgang Arthofer

Supporting Information

Additional Supporting Information may be found in the online version of this article:

Appendix S1 Transcriptome sequencing of the Antarctic *Colobanthus quitensis* (Kunth) Bartl (Caryophillaceae).

Appendix S2 Transcriptome resources for two highly divergent *Silene latifolia* populations.

Appendix S3 Development of the draft genome sequence of the marbled flounder *Pseudopleuronectes yokohamae* as a reference for population genomic analyses using IonTorrent PGM.

Appendix S4 A reduced representation libraries approach for nuclear marker development via 454 sequencing applied on *Tetramorium* (Hymenoptera: Formicidae).