

PERMANENT GENETIC RESOURCES NOTE

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¹Molecular Ecology Resources Editorial Office, 6270 University Blvd, Vancouver, BC, V6T 1Z4, Canada, ²Graduate School of Science, Kyoto University, Kyoto 606-8502, Japan, ³Estación Biológica de Doñana, Consejo Superior de Investigaciones Científicas (CSIC), Avda. Américo Vespucio s/n, 41092 Seville, Spain, ⁴Departamento de Biología Experimental, Universidad de Jaén, Campus Las Lagunillas, s/n, E-23071 Jaén, Spain, ⁵Instituto Nacional de Pesquisas da Amazônia (INPA), Laboratório de Ecofisiologia e Evolução Molecular, Manaus, AM, CEP 69060-001, Brazil, ⁶Departamento de Matemática Aplicada, Facultad de Matemáticas, Universidad de Santiago de Compostela, 15782 Santiago de Compostela, Spain, ⁷Department of Biology, University of Padova, via Ugo Bassi 58/B, I-35121 Padova, Italy, ⁸Department of Ecology and Evolutionary Biology, Yale University, 21 Sachem Street, New Haven, CT 06511, USA, ⁹Departamento de Fisiología y Zoología, Universidad de Sevilla, Avda. Reina Mercedes, 6, 41012 Sevilla, Spain, ¹⁰Departamento de Biología Animal, Facultad de Ciencias, Universidad de Granada, Campus Fuente Nueva s/n, 18071 Granada, Spain, ¹¹CNRS USR 2936, Station d'Ecologie Expérimentale du CNRS à Moulis, 09200 Moulis, France, ¹²Grupo de Biodiversidad y Recursos Genéticos, Instituto de Genética, Universidad Nacional de Colombia, Bogotá, Colombia, ¹³Michael Smith Laboratories, University of British Columbia, 321-2185 East Mall, Vancouver, BC, V6T 1Z4, Canada, ¹⁴Department of Entomology and W.M. Keck Centre for Behavioral Biology, North Carolina State University, Campus Box 7613, Raleigh, NC 27695-7613, USA, ¹⁵210 Universidade Estadual de Campinas (UNICAMP), Centro de Biologia Molecular e Engenharia Genética (CBMEG), Campinas, SP, CP 6109, CEP 13083-970, Brazil, ¹⁶CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Campus Agrário de Vairão, 4485-661 Vairão, Portugal, ¹⁷Departamento de Zoologia e Antropologia, Faculdade de Ciências da Universidade do Porto, Rua do Campo Alegre, s/n, 4169-007 Porto, Portugal, ¹⁸USDA-ARS, Department of Plant Pathology, North Carolina State University, Raleigh, NC 27695, USA, ¹⁹Departamento de Biodiversidad y Biología Evolutiva, Museo Nacional de Ciencias Naturales, CSIC, José Gutiérrez Abascal 2, 28006 Madrid, Spain, ²⁰Universidade Federal do Amazonas (UFAM), Laboratório de Evolução e Genética Animal Manaus, AM, CEP 69077-000, Brazil, ²¹Departamento de Genética e Evolução, Universidade Federal de São Carlos, Via Washington Luiz, Km 235, PO Box 676, CEP 13565-905, São Carlos, SP, Brazil, ²²Laboratorio de Genética y Biotecnología Acuicola, Centro de Biotecnología, Universidad de Concepción, Concepción, Chile, ²³Infectious and Tropical Diseases Department, London School of Hygiene and Tropical Medicine, Keppel Street, London WC1E 7HT, UK, ²⁴Departamento de Bioquímica y Biología Molecular IV, Universidad Complutense de Madrid (UCM), Facultad de Veterinaria, 28040 Madrid, Spain, ²⁵Laboratorio de Diversidad

Correspondence: Molecular Ecology Resources Primer Development Consortium, E-mail: editorial.office@molecol.com

Molecular, Departamento de Biología Marina, Universidad de Católica del Norte, Coquimbo, Chile,²⁶Laboratory of Plant Ecology, University of Leuven, Kasteelpark Arenberg 31, 3001 Heverlee, Belgium,²⁷Division of EcoScience, Ewha Womans University, Science B Building (rm 554), 11-1 Daehyon-Dong, Sodaemun-Ku, Seoul, 120-750, Korea,²⁸Instituto Murciano de Investigación y Desarrollo Agrario y Alimentario (IMIDA), C/Mayor, 1, La Alberca, 30150 Murcia, Spain,²⁹Inland Fisheries Research Institute, National Fisheries Research & Development Institute, Gapyeong, Gyeonggi-do, 444-815, Korea,³⁰Department of General Zoology, A. Mickiewicz University, Umultowska 89, 61-614, Poznań, Poland,³¹College of Animal Science and Technology, Northwest A & F University, 712100 Yangling, Shanxi, China,³²College of Fisheries, Huazhong Agricultural University, 430070 Wuhan, Hubei, China,³³Departamento de Genética, Facultad de Veterinaria, Universidad de Santiago de Compostela, Campus de Lugo, 27002 Lugo, Spain,³⁴Natural Resources and Environmental Studies Institute, University of Northern British Columbia, 3333 University Way, Prince George, BC, V2N 4Z9, Canada,³⁵National Livestock Resources Research Institute, P.O. Box 96, Tororo, Uganda,³⁶Trypanosomiasis Research Centre, Kenya Agricultural Research Institute, P.O. Box 362-00902, Kikuyu, Kenya,³⁷Southern Insect Management Research Unit, USDA-ARS, Stoneville, MS 38776, USA,³⁸CNRS UMR 7625, Université Pierre et Marie Curie, Case 237, 7 Quai St Bernard, 75005 Paris, France,³⁹FRS-FNRS, University of Liège, 22 Quai VanBeneden, 4020 Liège, Belgium,⁴⁰Department of Evolutionary Ecology, Estación Biológica de Doñana, CSIC, Avda. Americo Vespucio, s/n, 41092 Sevilla, Spain,⁴¹CCMAR, FCMA, Universidade do Algarve, Gambelas, 8005-139 Faro, Portugal,⁴²Institute of Evolutionary Biology and Environmental Studies (IEU), University of Zürich, Winterthurerstrasse 190, 8057 Zürich, Switzerland,⁴³Graduate School Advanced Technology and Science, The University of Tokushima, 2-1 Minami-josanjima, Tokushima 770-8506, Japan,⁴⁴Environmental Symbiosis Studies, Graduate School of Integrated Arts and Sciences, The University of Tokushima, 1-1 Minami-josanjima, Tokushima 770-8502, Japan,⁴⁵Department of Biology, Kim Il-sung University, Taesong District, Pyongyang, Korea

Abstract

This article documents the addition of 238 microsatellite marker loci to the Molecular Ecology Resources Database. Loci were developed for the following species: *Alytes dickhilleni*, *Arapaima gigas*, *Austropotamobius italicus*, *Blumeria graminis* f. *sp. tritici*, *Cobitis lutheri*, *Dendroctonus ponderosae*, *Glossina morsitans morsitans*, *Haplophilus subterraneus*, *Kirengeshoma palmata*, *Lysimachia japonica*, *Macrolophus pygmaeus*, *Microtus cabrerai*, *Mytilus galloprovincialis*, *Pallisentis* (Neosentis) *celatus*, *Pulmonaria officinalis*, *Salminus franciscanus*, *Thais chocolata* and *Zootoca vivipara*. These loci were cross-tested on the following species: *Acanthina monodon*, *Alytes cisternasii*, *Alytes maurus*, *Alytes muletensis*, *Alytes obstetricans almogavarii*, *Alytes obstetricans boscai*, *Alytes obstetricans obstetricans*, *Alytes obstetricans pertinax*, *Cambarellus montezumae*, *Cambarellus zempoalensis*, *Chorus giganteus*, *Cobitis tetralineata*, *Glossina fuscipes fuscipes*, *Glossina pallidipes*, *Lysimachia japonica* var. *japonica*, *Lysimachia japonica* var. *minutissima*, *Orconectes virilis*, *Pacifastacus leniusculus*, *Procambarus clarkii*, *Salminus brasiliensis* and *Salminus hilarii*.

This article documents the addition of 238 microsatellite marker loci to the Molecular Ecology Resources Database. Table 1 contains information on the focal species, the number of loci developed, any other species the loci were tested in and the accession numbers for the loci in both the Molecular Ecology Resources Database and

GenBank. The authors responsible for each set of loci are listed in the final column. A full description of the development protocol for the loci presented here can be found on the Molecular Ecology Resources Database (<http://tomato.biol.trinity.edu/>).

Table 1 Information on the focal species, the number of loci developed, any other species the loci were tested in and the accession numbers for the loci in both the Molecular Ecology Resources Database and GenBank. The authors responsible for each set of loci are listed in the final column

Species	No. primers developed	Other species tested	MER database no.	GenBank accession no.	Authors
<i>Alytes dickhilleni</i>	13	<i>A. obstetricans pertinax</i> , <i>A. obstetricans obstetricans</i> , <i>A. obstetricans boscai</i> , <i>A. obstetricans almogavarii</i> , <i>A. muletensis</i> , <i>A. maurus</i> , <i>A. misticernasi</i>	45209–45221	HQ693828–HQ693840	Carvalho, B. M.; Lopes, S.; Van de Vliet, M. S.; Dias, G.; Benítez, M.; Beltrán, J. F.; Tejedo, M.; Ferrand, N.; Gonçalves, H.

Table 1 Continued

Species	No. primers developed	Other species tested	MER database no.	GenBank accession no.	Authors
<i>Arapaima gigas</i>	10	n/a	45253–45262	HM013750–HM013759	Santos, Carlos Henrique dos Anjos; Climaco, Gisele Torres; Sousa, Carolina Fernandes da Silva; Paula-Silva, Maria Nazaré; Sousa, Adna Cristina Barbosa; Farias, Izeni Pires; Campos, Tatiana; Almeida-Val, Vera Maria Fonseca
<i>Austropotamobius italicus</i>	12	<i>Pacifastacus leniusculus</i> , <i>Cambarellus zempoalensis</i> , <i>C. montezumae</i> , <i>Orconectes virilis</i> , <i>Procambarus clarkii</i>	45393–45404	HQ593123–HQ593134	Pedraza-Lara, C.; Gonzalez, E. G.; Bloor, P.; Doadrio, I.
<i>Blumeria graminis</i> f. sp. <i>tritici</i>	9	n/a	45222, 45223, 45225–45231 (see also 45224)	HQ631364, HQ631366–HQ631373	Parks, Ryan; Booth, Warren; Cowger, Christina
<i>Cobitis lutheri</i>	11	<i>C. tetralineata</i>	45281–45291	HQ158597–HQ158607	Kwan, Ye-Seul; Lee, Wan-Ok; Won, Yong-Jin
<i>Dendroctonus ponderosae</i>	50	n/a	45343–45392	GO486077, GT317345, GT320845, GT322895, GT324623, GT324841, GT325939, GT328703, GT331212, GT339861, GT344705, GT345241, GT350467, GT350767, GT356832, GT357891, GT363660, GT369500, GT373329, GT381367, GT383057, GT393905, GT401041, GT403944, GT404280, GT408450, GT413070, GT413201, GT415941, GT416554, GT419741, GT421807, GT429515, GT430043, GT433817, GT436798, GT451465, GT457678, GT458184, GT461671, GT464982, GT465588, GT473994, GT474165, GT485805, GT486724, GT489170, GT490424, GT490498, GT490735, GT491361	Samarasekera, N Gayathri; Keeling, Christopher I.; Bohlmann, Jörg; Murray, Brent W.
<i>Glossina morsitans morsitans</i>	14	<i>G. fuscipes fuscipes</i> , <i>G. pallidipes</i>	45232–45252	See paper for details	Hyseni, Chaz; Beadell, Jon S.; Gomez Ocampo, Zaneli; Ouma, Johnson O.; Okedi, Loyce M.; Gaunt, Michael W.; Caccone, Adalgisa
<i>Haplophilus subterraneus</i>	11	n/a	45198–45208	HQ670723–HQ670733	Congiu, L.; Boscarì, E.; Bino, G.; Barbisan, F.; Leśniewska, M.; Fusco, G.

Table 1 Continued

Species	No. primers developed	Other species tested	MER database no.	GenBank accession no.	Authors
<i>Kirengeshoma palmata</i>	8	n/a	45176–45183	AB571675–AB571678, AB571681, AB571682, AB598398, AB598399	Yamashiro, T.; Yamashiro, A.
<i>Lysimachia japonica</i>	10	<i>L. japonica</i> var. <i>japonica</i> , <i>L. japonica</i> var. <i>minutissima</i>	45162, 45163, 45331–45342	AB591815–AB591824	Shinohara, Wataru; Kakezawa, Akihiro; Kawaguchi, Eri; Agata, Kiyokazu
<i>Macrolophus pygmaeus</i>	10	n/a	45264–45273	HM208591–HM208599, HQ853699	Sanchez, Juan A.; La Spina, Michelangelo; Perera, Omaththage P.
<i>Microtus cabrerai</i>	12	n/a	45292–45303	AF268902, AF268903, EF666983, EF666984, EF666987, EF666990, EF666991, EU101013, EU101014, EU101016, EU101021, FR820649	Alasaad, Samer; Soriguer, Ramón C.; Wandeler, Peter; Jowers, Michael J.; Sánchez, Antonio
<i>Mytilus galloprovincialis</i>	15	n/a	45132–45146	AJ625605, AJ626093, AJ624322, AJ938131, AJ938131, EH663192, EH663098, EH663076, EH662757, FL498494.1, FL500528.1, FL498564.1, FL495095.1, FL501296.1, BV725482	Pardo, B.G.; Vera, M.; Pino-Querido, A.; Álvarez-Dios, J.A.; Martínez, P.
<i>Pallisentis (Neosentis) celatus</i>	11	n/a	45324–45336	HQ588802–HQ588812	Li, Yang; Liu, Xiaolin; Liu, Haixia; Wang, Weimin; Zhu, Changcheng
<i>Pulmonaria officinalis</i>	8	n/a	45304–45311	HQ452963–HQ452970	Meeus, S.; Honnay, O.; Vandepitte, K.; Jacquemyn, H.
<i>Salminus franciscanus</i>	10	<i>S. brasiliensis</i> , <i>S. hylarii</i>	45184–45197 (includes monomorphic loci)	HQ317313–HQ137316, HQ137320–HQ137326	Rossini, Bruno C.; Nunes, Aline G.; Freitas, Patrícia D.; Galetti Jr, Pedro M.
<i>Thais chocolata</i>	12	<i>Acanthina monodon</i> , <i>Chorus giganteus</i>	45312–45323	HQ700360–HQ700371	Gallardo-Escárate, CristianValenzuela-Bustamante, Myriam; Haye Pilar
<i>Zootoca vivipara</i>	12	n/a	45164–45175	HQ337631–HQ337642	Stevens, Virginie M.; Richard, Murielle; Bleay, Colin; Clobert, Jean

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Microsatellite isolation in a population of the geophilomorph centipede *Haplophilus subterraneus* with high frequency of morphological anomalies

Congiu L.^{*1}, Boscari E.², Bino G.³, Barbisan F.⁴, Leśniewska M.⁵, Fusco G.⁶

^{1, 2, 3, 4, 6} Department of Biology, University of Padova, Italy

⁵ Department of General Zoology, A. Mickiewicz University, Poznań, Poland

*leonardo.congiu@unipd.it

Abstract

This study reports the first isolation and characterization of microsatellites from the major arthropod clade Chilopoda. The species of interest is the geophilomorph centipede *Haplophilus subterraneus*, for which a high incidence of morphological anomalies has been recorded in several European populations. With the aim of investigating the causes of malformations in the context of the phylogeographic history of the species, we set up a panel of microsatellites to be used in population genetics studies.

Main text

An exotic population of the geophilomorph centipede *Haplophilus subterraneus* (also cited as *Stigmatogaster subterranea*), living in a city park of Poznań (West Poland), exhibits a high proportion (26%) of individuals with morphological anomalies of several kinds. The study of these anomalies, in particular those affecting trunk segmentation, provided precious information about normal developmental dynamics in these animals during late embryogenesis, with implications for the process of segmentation in arthropods at large (Leśniewska *et al.* 2009a).

However, the causes of the anomalies are still to be identified. The high incidence and the extreme diversity of the morphological defects would suggest the presence of some environmental physico-chemical factors responsible for the recorded high level of developmental instability. However, further observations allowed to exclude this hypothesis: (a) physico-chemical parameters of the soil, including heavy metal content and radioactivity, are within standard values; (b) no comparable frequency of morphological anomalies of any kind was found in any of the other nine species of centipedes living in the same site, including other four geophilomorph species; (c) preliminary data show that segmental anomalies of the same kind occur with comparable high frequency also in other European populations of *H. subterraneus*, both within and outside its natural range (Leśniewska *et al.* 2009b).

Specifically targeted investigations are thus necessary to identify the causes of the high level of developmental instability in the populations of this species. With this aim, we have planned a study for evaluating the genetic structure of the European populations of *H. subterraneus* in its relation to the incidence of anomalies, and for reconstructing the phylogeography of the same population, as a basis for the comparative analysis of developmental instability.

The absence of microsatellite markers for the species made necessary the isolation here reported, which also represent the first microsatellite isolation of the whole clade Chilopoda.

Genomic DNA was extracted from 4-5 trunk segments using a salting-out protocol (Patwary *et al.* 1994). As for sample conservation, only animals stored in 100% ethanol immediately after collection yielded DNA of acceptable quality. Lower concentrations of ethanol resulted in highly degraded DNA.

A partial genomic library was constructed after enrichment with a pool of biotin-labelled probes ((AC)₁₇ (AG)₁₇ (CAG)₁₁ (AAC)₁₂ (AAT)₁₂ (GATA)₉ and (CACC)₈), following the FIASCO procedure (Zane *et al.* 2002a) adapted as in Zane *et al.* (2002b). About 211 recombinant colonies were screened by PCR with universal M13 primers and those with an insert longer than approximately 400bp were selected for sequencing analyses. All the PCRs were performed on GeneAmp PCR System 9700 thermal-cyclers (Applied Biosystems). Out of 108 sequenced clones, 75 contained a microsatellite motif, and 19 also had adequate flanking regions for primer designing that was performed with the software OLIGOEXPLORER version 1.2 (www.genelink.com). A standard amplification with unlabelled primer was performed directly from genomic DNA of 3 individuals in 20 µl of reaction mixture containing: *Taq* buffer 1X (Resnova), MgCl₂ 1.5 mM, 0.6 µM of each primer, 200 µM dNTP's, 1 units of *Taq*, and about 50 ng of genomic DNA. Thermal cycler was set as follows: 94°C 30 sec, 50°C 30 sec, 72°C 30 sec, 30 cycles with an initial denaturing step of 5 min at 94°C and a final elongation of 5 min at 72°C. Amplification products were ran on 1.8% agarose gel to check amplification. A further selection was made on the basis of the efficiency of PCR amplification from genomic DNA. Finally, 12 loci (Tab. 1) were labelled with the appropriate dyes for fragment analysis with ABI PRISM 3100 or 3700 automated sequencer all yielding reliable and reproducible profiles (external service, BMR Genomics). PCR amplifications from genomic DNA were performed in 20 individuals from the Poznań population, and 11 out of the 12 tested loci resulted to be polymorphic, with a number of alleles ranging from 2 to 7. For all loci amplification conditions were the same as previously reported for unlabelled primers with the only exception that annealing temperature was optimized according to Table 1. Scoring was performed using PEAK SCANNER 1.0 software (Applied Biosystem). GENEPOP

73 3.4 (Raymond & Rousset 1995) was used to test for deviation from Hardy-Weimberg equilibrium
74 (HWE) and linkage disequilibrium (LD) with a statistical confidence interval (CI) of 99%;
75 Sequential Bonferroni correction for multiple comparison (Rice 1989) was applied. No locus pairs
76 were in significant LD and only locus H.sub13 was found to be significantly out of HWE.
77 MICROCHECKER (Van Oosterhout *et al.* 2004) analyses indicated the possible presence of null
78 alleles for locus H.sub13 (CI: 99%).
79 The relatively low number of alleles recorded in the Poznań population of *H. subterraneus* might be
80 the result of a founder effect, as the species has been probably accidentally introduced with garden
81 soil (Leśniewska *et al.* 2009b), but further comparative studies among populations inside and
82 outside the natural range of the species will be necessary to test this hypothesis.
83

Table 1. Characteristics of microsatellites loci in *Haplophilus subterraneus*. * = Significant deviation from HW equilibrium ($P < 0.01$) after sequential Bonferroni correction.

Fluorescent dyes used are reported for each labelled forward primer.

Locus	Primer sequences (5'-3')	Repeat motif	Annealing	GenBank accession number	No. alleles	Size range (bp)	Ho/He
H.sub16	F _(NED) GATAAATTGAGCATCAGCGAGTTT R CGTACGGGTTTACATCTTGTTTC	(CAA) ₆	54 °C	HQ670723	3	284-293	0.35/0.38
H.sub1	F _(FAM) GGATCTGCACTCAGATTTTCA R AACCTTCATTCTCCCTTTC	(TG) ₁₂	50 °C	HQ670724	3	159-181	0.25/0.46
H.sub47	F _(FAM) TTATGATGGACAGAAGTGTGA R ACGTGAAGTATAGAAGTGTGA	(GA) ₁₁	54 °C	HQ670725	3	322-338	0.45/0.59
H.sub48	F _(VIC) CGTGGTGACGTGAGAATTT R GTTGACAACCTCGATCGGT	(GA) ₁₆	53 °C	HQ670726	7	188-218	0.65/0.78
H.sub56	F _(NED) CGTCATTGTGGGAAGATCTAATTC R GTGGAATAACAGGGATGCTAT	(CT) ₉	54 °C	HQ670727	3	253-259	0.55/0.55
H.sub13	F _(NED) CTCGGGAAATCCAGACC R GGCTGTCGGCTGATTTT	(CA) ₃ CC(CA) ₅	58 °C	HQ670728	2	139-147	0.00/0.26*
H.sub36	F _(FAM) TAACACATCACAATTTTATCTACG R AAGGTTGTTTTGTGATACAA	(CT) ₈	54 °C	HQ670729	3	88-108	0.25/0.56
H.sub85	F _(FAM) AGGCAGCTGTAATAATCCAA R TAGTATACACATCTCGCAGC	(CA) ₇	54 °C	HQ670730	3	226-230	0.40/0.46
H.sub61	F _(VIC) AACCCCTTTCCTTGTATATAATC R ATTCATTGAAAATTACACCGAGC	(TC) ₆	54 °C	HQ670731	2	173-175	0.3/0.38
H.sub45	F _(VIC) AGTTGTTATTGACTCCC GTT R CAACAGCTCAACGATCTTAC	(GA) ₉	50 °C	HQ670732	5	242-254	0.5/0.6
H.sub43	F _(VIC) TGAGTGAGCATATTTGCGAG R CAATCGCCGCTTTATTCTCT	(TG) ₇	50 °C	HQ670733	1	325	

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