



Erratum

Corrigendum to “Genetics and taxonomy of Chilean smooth-shelled mussels, *Mytilus* spp. (Bivalvia: Mytilidae)” [C. R. Biol. 335 (2012) 51–61]Philippe Borsa^{a,*}, Vincent Rolland^b, Claire Daguin-Thiébaud^c^a Institut de recherche pour le développement (IRD), UR 227 « Biocomplexité des écosystèmes récifaux », 911, avenue Agropolis, 34032 Montpellier cedex, France^b Aptiv Solutions, Clinical Database Programming, Allschwil, Switzerland^c Centre national de la recherche scientifique (CNRS), Université Pierre et Marie Curie, UMR 7144, « Adaptation et diversité en milieu marin », Station biologique de Roscoff, Roscoff, France

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1. Introduction

After publication, we noticed a typographical error regarding the assignation of alleles at the *mac-1* locus in the smooth-shell mussel sample CBL from Tasmania. The alleles at this locus were typical *E* alleles and not *G* alleles as written erroneously in Table 2 of the published article. The corrected Table 2 is presented here.

2. Corrected Table 2

Table 2

Smooth-shelled *Mytilus* spp. Summary of genetic characteristics at nuclear-DNA loci *mac-1* and *Glu-5'* ([16,22, 29] and unpublished data) and mitochondrial locus *COI* [21] of two samples from Chile (*CHL*, *MAU*) and reference samples (*CBL*, *FLØ*, *GIL*, *KER*, *SET*), all analysed morphometrically (Fig. 4). *Allozymes*: genetic characterization of samples from the same or nearby locations, previously analyzed at 7–8 allozyme loci [5,24,30,31]; *E*, *G*: compound alleles characteristic of *M. edulis* and *M. galloprovincialis*, respectively; *N_A* bulk of the *N* clade that includes all Northern-Hemisphere *M. edulis*, and a proportion of Northern-Hemisphere *M. galloprovincialis* female *COI* haplotypes; *N_D* well-supported subclade of the *N* clade that exclusively comprises Northern-Hemisphere *M. galloprovincialis* female *COI* haplotypes [19,21].

Sample	Marker											
	mac-1			Glu-5'			COI					Allozymes
	<i>E</i>	<i>G</i>	(<i>N</i>)	<i>E</i>	<i>G</i>	(<i>N</i>)	<i>N_A</i>	<i>N_D</i>	<i>S₁</i>	<i>S₃</i>	(<i>N</i>)	
CHL	0.04	0.96	(76)	–	1.00	(48)	0.22	0.78	–	–	(9)	nd
MAU	1.00	–	(52)	–	1.00	(28)	–	–	1.00	–	(7)	<i>E</i>
CBL	1.00	–	(32)	–	1.00	(29)	–	–	–	1.00	(5)	<i>G</i>
FLØ ^a	1.00	–	(47)	1.00	–	(35)	1.00	–	–	–	(20)	<i>E</i>
GIL	1.00	–	(26)	1.00	–	(16)	nd	nd	nd	nd	nd	<i>E</i>
KER	1.00	–	(83)	0.35	0.65	(79)	–	–	1.00	–	(83)	<i>E</i>
SET ^b	0.03	0.97	(68)	0.06	0.94	(39)	0.65	0.35	–	–	(17)	<i>G</i>

N: sample size; nd: no data.

^a *COI* data from sample “Tjärnö, Sweden” [25].

^b Female-mitochondrial composition determined from 16S RFLP haplotypes of sample *G-Fr* [27].

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