



CORRESPONDENCE

Corrigendum to Arcellana *et al.* 2011 *J. Genet.* 90, e90–e93

STEVEN M. CARR

Department of Biology, Memorial University of Newfoundland, St John's, NL A1C 5S7, Canada
 E-mail: scarr@mun.ca.

Received 28 May 2021; revised 28 May 2021; accepted 1 June 2021

Keywords. Philippine islands; MN blood group; Davao del Sur; Palawan.

I wish to bring the attention of *Journal of Genetics* readers a small error in Arcellana A. E. S., Guzman R. M. S. and Fontanilla I. K. C. 2011 Distribution of MN blood group types in local populations in Philippines. *J. Genet.* 90, e90–e93.

The MS reports genotype and allele frequencies for the MN blood group system in eight population samples from various of the Philippine islands, including Matanao, Davao del Sur on the island of Mindanao, and Puerto Princesa, Palawan Island. Genotype frequencies given in figure 2 of that MS for MM, MN, and NN for the Davao del Sur and Palawan samples do not sum to 1.000. Inspection of the data in table 1 and figure 2 suggests the error arises from a simple transposition of the total sample sizes for these two populations, such that values given in table 1 as 52 & 51 should

be reversed to 51 & 52, respectively. In figure 3, allele frequencies for M and N in these two populations are calculated correctly from the correct sample sizes, as are Wright's Inbreeding Coefficients (F) in figure 4.

Table 1 below summarizes figures 2, 3, and 4, and table 1 in Arcellana *et al.* (2011), corrects the genotype frequencies for Davao del Sur and Palawan, confirms all other data, and includes the original blood group counts for all populations as reconstructed from table 1 and the corrected figure 2. Conclusions drawn from these two populations in the original analysis are unaffected. Calculation of Chi-square deviations from Hardy–Weinberg expectations (not corrected for multiple simultaneous comparisons) indicate that the samples from Camarines Sur on Luzon and Butuan on Mindanao show marginal but significant excess and

Table 1. Corrected summary of figures 2, 3, and 4, and table 1 in Arcellana *et al.* (2011).

Group	n	Counts			Frequencies						χ^2
		MM	MN	NN	MM	MN	NN	M	N	F	
Pangasinan	54	15	29	10	0.2778	0.5370	0.1852	0.5463	0.4537	−0.0834	0.3016
Cebu	59	20	35	4	0.3390	0.5932	0.0678	0.6356	0.3644	−0.2806	5.0370
Camarines Sur	54	11	36	7	0.2037	0.6667	0.1296	0.5370	0.4630	−0.3407	6.6458*
Isabela	59	43	7	9	0.7288	0.1186	0.1525	0.7881	0.2119	0.6447	21.4230***
Butuan	49	36	8	5	0.7347	0.1633	0.1020	0.8163	0.1837	0.4556	8.0394*
Davao del Sur'	51	17	23	11	0.3333	0.4510	0.2157	0.5588	0.4412	0.0854	0.3225
Palawan'	52	20	24	8	0.3846	0.4615	0.1538	0.6154	0.3846	0.0250	0.0400
Manila	163	41	86	36	0.2515	0.5276	0.2209	0.5153	0.4847	−0.0562	0.5069

* $P < 0.05$; *** $P < 0.001$.

deficiencies of heterozygotes, respectively, and that the sample from Isabela on Luzon shows a highly significant deficiency, as previously reported. The pooled data for all eight populations show a slight, nonsignificant excess of heterozygotes ($F = -0.0414$, $\chi^2 = 0.888$). Reanalysis of Hardy–Weinberg expectations by the G-test gives the same results.

The data reported by Arcellana *et al.* (2011) are extremely useful for the introduction of population genetic concepts of allele and genotype frequencies for single-locus, two-allele data without dominance, and subsequent tests of Hardy–Weinberg expectations and population structure as shown by F_{ST} and other measures. As such, it is useful to have the record corrected.

Corresponding editor: DURGADAS P. KASBEKAR