

## CORRIGENDA

In the paper by L. D. HURST and A. POMIANKOWSKI (GENETICS 128: 841–858; August, 1991) entitled “Causes of sex ratio bias may account for unisexual sterility in hybrids: a new explanation of Haldane’s rule and related phenomena,” an entry was omitted

from Table 2. In the third line-pair (“Di . . . Suicide”), the missing top entry of the pair in the final column should be “(1 – L)” while the “(1 – U)\*” entry beneath remains unchanged.

In the paper by M. A. RILEY, M. E. HALLAS and R. C. LEWONTIN (GENETICS 123: 359–369; October, 1989) entitled “Distinguishing the forces controlling variation at the *Xdh* locus in *Drosophila pseudoobscura*,” there were two errors that do not change the conclusions of the paper but need to be corrected for the record.

for the differences among haplotypes. The correct values for Table 3 are given here. When the total variance is substituted in the formula on page 365, we get an estimate of  $4Nc = 172$ . Thus, our estimate of effective population size should be upwardly corrected to  $8.27 \times 10^5$ .

As a result of our errors in the calculation of  $D'$ , the values for this measure given in Figure 6 are all too small. This error is particularly embarrassing because the formula for  $D'$  was originally derived by one of the authors. The correct correlation between  $D'$  and map distance is  $r = 0.009$  ( $p > 0.9$ ). The correct regression equation is  $Y = 0.812 + 1.42 \times 10^{-6} X$  ( $R = 0$ ).

We are grateful to C. F. AQUADRO and W. A. NOON, who detected these errors. In the process, a cautionary tale emerged. After we detected and corrected our overflow error, the results still did not agree with AQUADRO and NOON’s calculation. It then turned out that their program (obtained from someone else) also had an overflow error! Statistical programs written to handle large data sets must be tested on artificial data sets that are *as large as the actual data set and with values with as many digits*.

A second error in the statistical program, resulting in undetected overflows, gave an erroneous variance

**TABLE 3**  
Number of sites differing per genome, within and between localities and electromorphs

	Mean	Variance	N	SE <sup>a</sup>
Within populations	9.0886	11.6743	734	0.1261
Between populations	9.2524	10.7227	919	0.1080
Within electromorphs	8.5509	12.6951	216	0.2424
Between electromorphs	9.2742	10.8523	1437	0.0869
In populations in electromorphs	8.0612	11.4601	98	0.3420
In populations between electromorphs	9.2469	11.5374	636	0.1347
Between populations in electromorphs	8.9576	13.4597	118	0.3377
Between populations between electromorphs	9.2959	10.3211	801	0.1135
Total data	9.1796	11.1451	1653	0.0821

<sup>a</sup> Standard errors are calculated directly from the observed variances in number of site differences among all pairwise comparisons within a given category.