CORRIGENDA

In the paper by HELENA SANTOS-ROSA and ANDRÉS AGUILERA (GENETICS **139**: 57–66; January, 1995) entitled “Isolation and genetic analysis of extragenic suppressors of the hyper-deletion phenotype of the *Saccharomyces cerevisiae* *hpr1Δ* mutation,” on page 59 in Table 1, the genotypes of all 15 “SS” strains should include the *hpr1Δ3::HIS3* mutation.

In the paper by BRUCE RANNALA and J. A. HARTIGAN (GENETICS **139**: 429–437; January, 1995) entitled “Identity by descent in island-mainland populations,” on page 430, equation (5) should read

$$\varphi[z] = \left(\frac{\lambda - \mu}{\lambda \exp[(\lambda - \mu)t] - \mu} \right)^{\phi/\lambda} \times \left(1 - z \frac{\lambda(\exp[(\lambda - \mu)t] - 1)}{\lambda \exp[(\lambda - \mu)t] - \mu} \right)^{-\phi/\lambda}.$$

On page 431, equation (9) should read

$$P[N] = \binom{\frac{\phi}{\lambda} + N - 1}{N} \left[1 - \frac{\lambda}{\mu} \right]^{\phi/\lambda} \left[\frac{\lambda}{\mu} \right]^N.$$

On page 432, column two should begin, “over, the entire collection of populations. For the BDI demographic model, f_0 is given by $(f_1\phi + \lambda)/(\phi + \lambda)$ as shown above (equation 21).”

In the paper by MONTGOMERY SLATKIN (GENETICS **139**: 457–462; January, 1995) entitled “A measure of population subdivision based on microsatellite allele frequencies,” The ABSTRACT was omitted. It follows:

A new measure of the extent of population subdivision as inferred from allele frequencies at microsatellite loci is proposed and tested with computer simulations. This measure, called R_{ST} , is analogous to WRIGHT’s F_{ST} in representing the proportion of variation between populations. It differs in taking explicit account of the mutation process at microsatellite loci, for which a generalized stepwise mutation model appears appropriate. Simulations of subdivided populations were carried out to test the performance of R_{ST} and F_{ST} . It was found that, under the generalized stepwise mutation model, R_{ST} provides relatively unbiased estimates of migration rates and times of population divergence while F_{ST} tends to show too much population similarity, particularly when migration rates are low or divergence times are long.

In the paper by THOMAS NAGYLAKI (GENETICS **139**: 473–485; January, 1995) entitled “The inbreeding effective population number in dioecious populations,” a computer error after final proofreading replaced some, but not all, of the symbols $\mathcal{E}$ and $\mathcal{P}$ with E and P, respectively. Thus, both $\mathcal{E}$ and E denote expectation, and both $\mathcal{P}$ and P denote probability.