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Corrigendum

Corrigendum to Genetic identities and local inbreeding in pure diploid clones with homoplasic markers: SNPs may be misleading [Infect. Genet. Evol. 33 (2015) 227–232]



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The authors regret In my paper (De Meeûs, 2015) there is a mistake in Eqs. (3) and (9) and in the text (explanations). The correct equations are, respectively:

$$\begin{split} Q_{I(t+1)} &= (1-u)^2 \big[Q_{I(t)}\big] + 2u(1-u) \bigg[\big(1-Q_{I(t)}\big) \frac{1}{K-1} \bigg] \\ &+ u^2 \Bigg[Q_{I(t)} \frac{1}{K-1} + \big(1-Q_{I(t)}\big) \frac{K-2}{(K-1)^2} \bigg] \end{split}$$

and

$$\begin{split} Q_{S(t+1)} &= (1-u)^2 \left\{ \frac{1}{N} \left[Q_{I(t)} + \left(1 - Q_{I(t)} \right) \times \frac{1}{2} \right] + \left(1 - \frac{1}{N} \right) Q_{s(t)} \right\} \\ &+ 2u(1-u) \left\{ \begin{array}{c} \frac{1}{N} \left[\left(1 - Q_{I(t)} \right) \frac{1}{K-1} \right] \\ + \left(1 - \frac{1}{N} \right) \left[\left(1 - Q_{S(t)} \right) \frac{1}{K-1} \right] \right\} \\ &+ u^2 \left\{ \begin{array}{c} \frac{1}{N} \left[Q_{I(t)} \frac{1}{K-1} + \left(1 - Q_{I(t)} \right) \frac{K-2}{(K-1)^2} \right] \\ + \left(1 - \frac{1}{N} \right) \left[Q_{S(t)} \frac{1}{K-1} + \left(1 - Q_{S(t)} \right) \frac{K-2}{(K-1)^2} \right] \end{array} \right\} \end{split}$$

Indeed, when two alleles mutate, with probability u^2 , if they were identical at generation t, with probability $Q_{I(t)}$ within the same individual (probability 1/N) or $Q_{s(t)}$ in two different individuals (1-1/N), the probability that they become identical by chance is $(K-1)/(K-1)^2=1/(K-1)$ and not $1/(K-1)^2$ as mistakenly written, which is the probability for a specific allelic state among the K-1 possible ones. This error has no consequences in the final results (Eqs. 8 and 17) because the wrong terms belong to parts of the equations that quickly become neglected. Thus this mistake, for which I apologise, does not change the conclusions of the paper.

The authors would like to apologise for any inconvenience caused.

Reference

De Meeûs, T., 2015. Genetic identities and local inbreeding in pure diploid clones with homoplasic markers: SNPs may be misleading. Infect. Genet. Evol. 33, 227–232.