Correction

GENETICS

Correction for “Triparental inheritance in *Dictyostelium*,” by Gareth Bloomfield, Peggy Paschke, Marina Okamoto, Tim J. Stevens, and Hideko Urushihara, which was first published January 22, 2019; 10.1073/pnas.1814425116 (*Proc Natl Acad Sci USA* 116:2187–2192).

The authors note that Fig. 4 appeared incorrectly. The corrected figure and its legend appear below.

Fig. 4. Lateral transmission of mitochondria in the *Dictyostelium* sexual cycle. (A) We have so far found no evidence for transmission of nuclear DNA from the mutant parent in a three-way cross between HM597, HM598, and the *matA* null strain HM1524; shown here is one representative chromosome from one progeny clone, XGB8. Variants specific to HM597 are shown in magenta, HM598 variants are in green, HM1524 (AX2) variants are in gold; all putative HM1524 variants appear to be false positives. (B) In contrast, lateral transfer of mitochondrial DNA clearly occurred in three of four sequenced progeny. Sequence reads specific to the *matA* null strain were counted at three positions along the mitochondrial genome for the three parent strains and one two-way progeny ("no null control", XGB1), as well as the four three-way progeny. In the three progeny with lateral transmission of mtDNA, all other variants along the mitochondrial chromosome also showed similar contribution from the *matA* null. (C) Three-way fusions were directly observed between an HM598 line expressing GFP-tagged histone 2B (green, *Upper Left*), a AX2 line expressing GFP targeted to the mitochondrial matrix with the TopA N-terminal targeting motif (green, *Upper Left*), and an HM1558 line expressing RFP anchored on the mitochondrial outer membrane using the GemA C-terminal targeting motif (magenta, *Lower Left*). (*Lower Right*) A DIC image is shown. Mitochondria were mixed in the syncytial cytoplasm and were not observed to undergo fusion. (Scale bar, 10 μ m.) (D) The *D. discoideum* mitochondrial genome is unevenly polymorphic: the density of nonsynonymous polymorphisms in protein coding genes across strains used in this study is shown (homing endonuclease genes are omitted). For comparison, the greenbeard genes *tgrB1* and *tgrC1* each have more than 40 polymorphisms per kilobase (31). *atp4* is within the top percentile of polymorphic genes in *D. discoideum* according to this dataset; this gene, along with *atp8*, was found to have the highest dN/dS ratios in a comparison of mitochondrial genes in several social amoeba species (45).

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