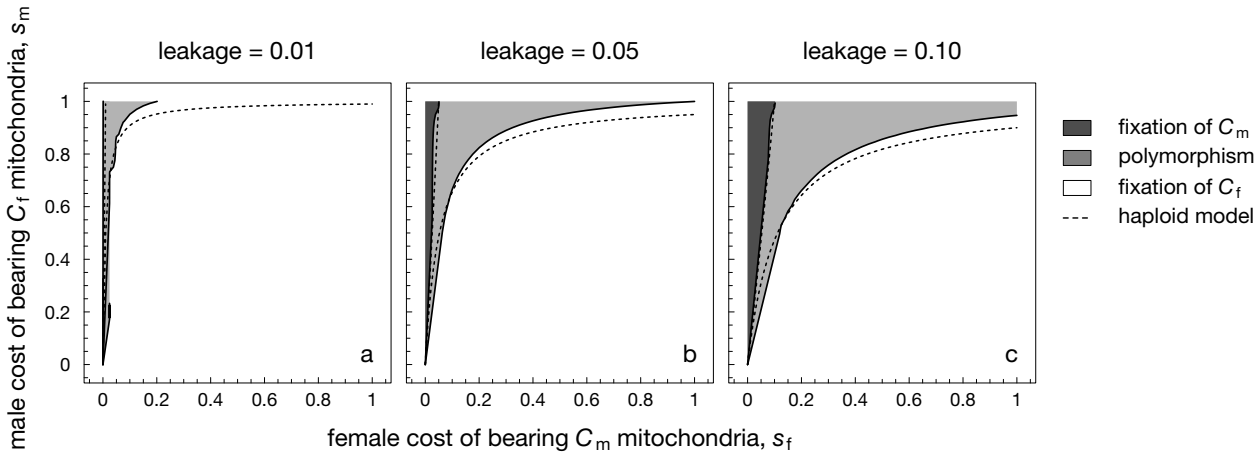

Figure S1:

Figure S1 Cytoplasmic polymorphism with multiple mitochondria per individual and the shape of male and female fitness functions is given by a linear function (additive). The model predicts polymorphism to be slightly less likely in comparison to the haploid model (dashed lines). This is because this model uses a conservative cut-off point of 0.05 to define polymorphism. Parameters: $M = 200$, $\mu = 1 \times 10^{-5}$.

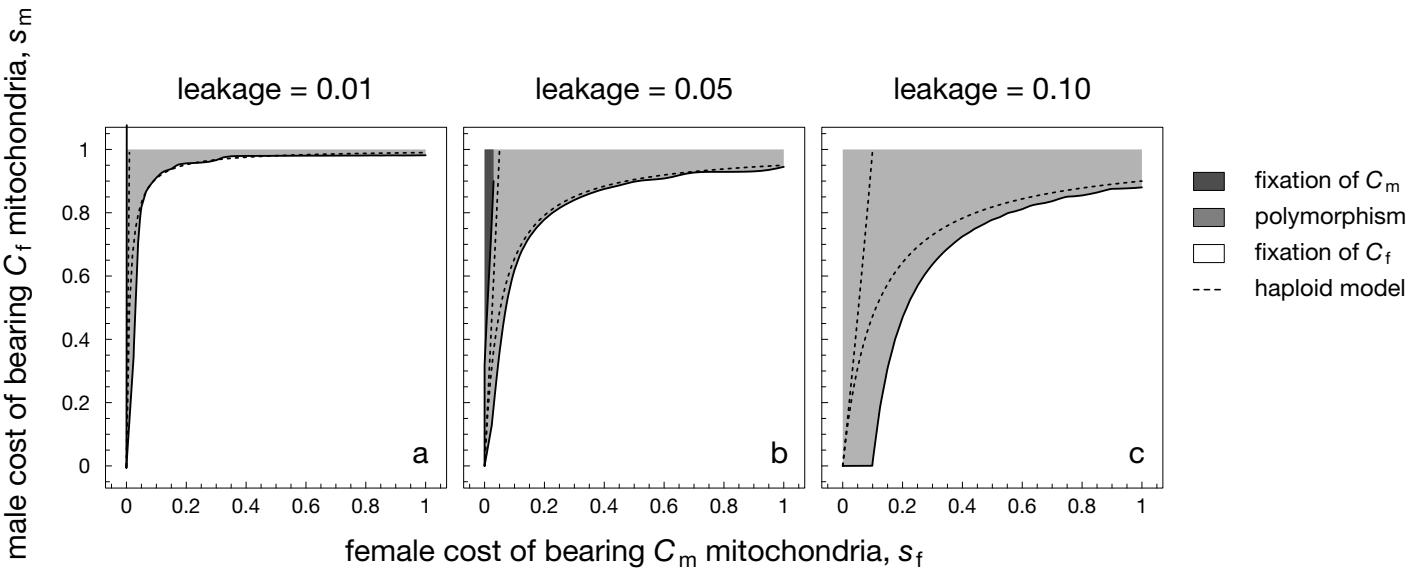

Figure S2:

Figure S2 Cytoplasmic polymorphism when multiple mitochondria per individual are present and the shape of male and female fitness functions is given by a sigmoidal function (see Figure 2D). The region in which a cytoplasmic polymorphism occurs is similar relative to the haploid model (dashed lines). The function of the sigmoidal is given by $w_f = 1 - s_f + s_f \exp\left[-k(M-m)/M\right] / \left\{1 + \exp\left[-k(n = M-m)/M\right]\right\}$ and $w_m = 1 - s_m + s_m \exp\left[k(M-m)/M\right] / \left\{1 + \exp\left[k(M-m)/M\right]\right\}$, where $k = 0.1$. Parameters: $M = 200$, $\mu = 1 \times 10^{-5}$, $B = 200$.

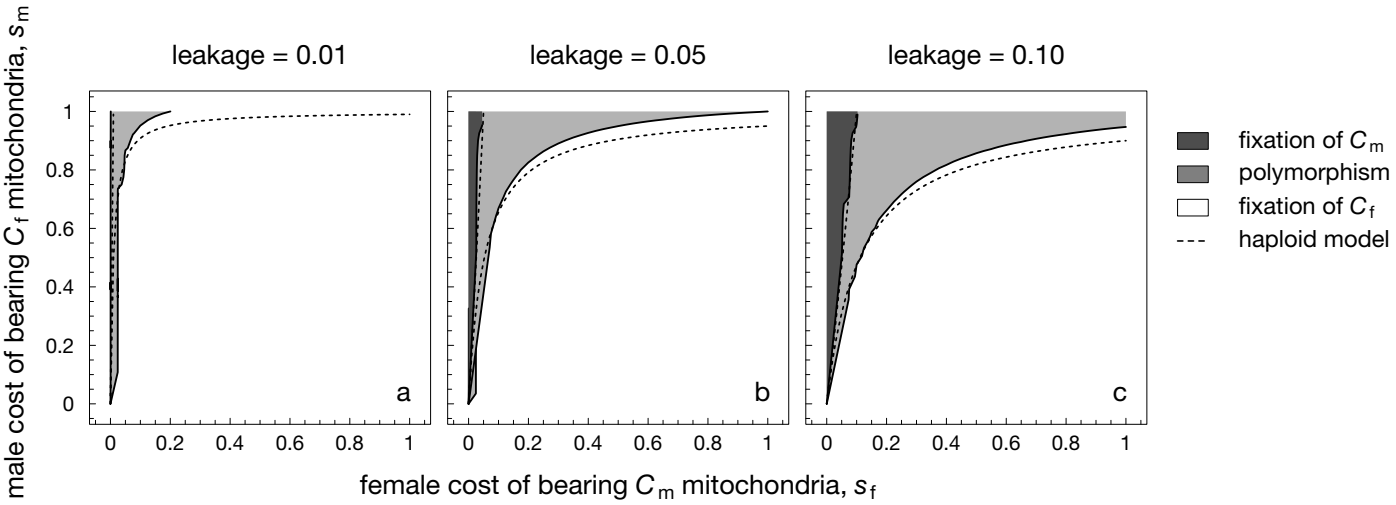

Figure S3:

Figure S3 Cytoplasmic polymorphism when the shape of male and female fitness functions is additive and the size of the bottleneck $B = 10$. Although the region of polymorphism is slightly smaller relative to the haploid model, this is due to the conservative demarcation of the region of polymorphism at $p = 0.05$ for the model in which each individual contains multiple cytoplasmic elements. A comparison with relative to Figure S1 (no bottleneck) shows that bottlenecks have little effect when fitness is additive. Parameters: $M = 200,\ \mu = 1 \times 10^{-5}, B = 10$.

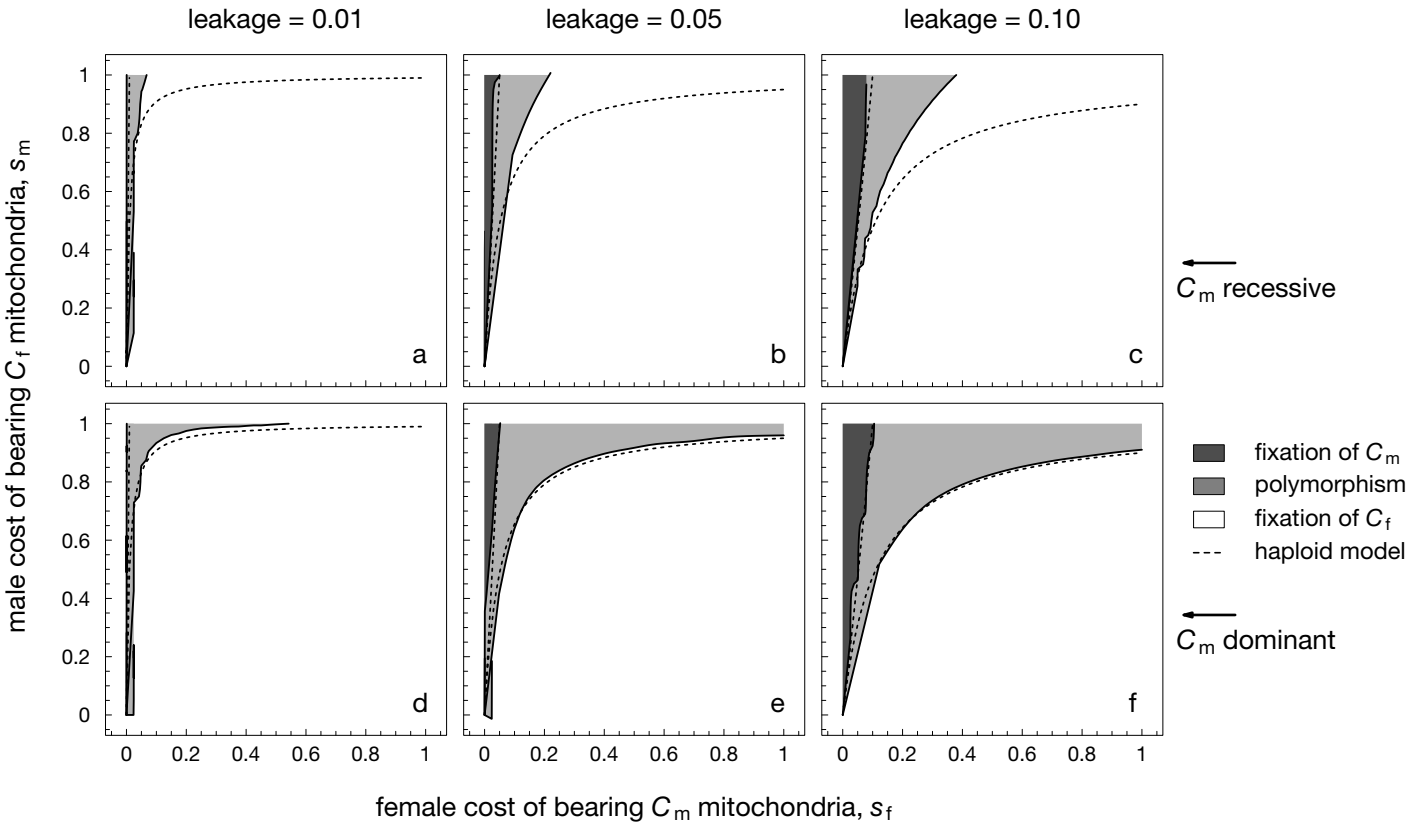

Figure S4:

Figure S4 Cytoplasmic polymorphism when the shape of male and female fitness functions is given by a scenario of constant dominance (solid lines in Figure 2B,C) and the size of the bottleneck $B = 10$. Outcomes are similar to a scenario without bottlenecks in Figure 4. Parameters: $M = 200$, $\mu = 1 \times 10^{-5}, B = 10$.

Supplementary Information to:

Can paternal leakage maintain sexually antagonistic polymorphism in the cytoplasm?

Bram Kuijper, Nick Lane & Andrew Pomiankowski

Model with multiple mitochondria

Following the model by Hadjivasiliou *et al.* (2012), we study a species with separate sexes, whose gametes contain multiple mitochondria. Let M denote the number of mitochondria present in each cell and let j describe the number of mitochondria which carry a C_m-allele ($j \in \{0, 1, \ldots, M\}$), implying that $M-j$ mitochondria in the same cell carry the C_f-allele. The frequency of cells which contain j C_m-mitochondria prior to reproduction is denoted by $p_{0,\mathrm{f}}(j)$ in females and $p_{0,\mathrm{m}}(j)$ in males.

S1.1 Mitochondrial mutation

Analogous to recent models of sexually antagonistic polymorphisms in nuclear genomes (e.g., Connallon & Clark, 2012; Mullon *et al.*, 2012), we assume the presence of recurrent mitochondrial mutation. Specifically, each mitochondrial allele mutates with probability μ. Hence, in order to compute the relative frequency of each genotype $p_{x,1}(j)$ in sex $x \in \{\mathrm{m}, \mathrm{f}\}$ subsequent to mutation, we need to assess the probability of mutation from all possible other genotypes $k \neq j$. Writing the genotype frequencies $p_x(j)$ in vector form, $\mathbf{p}_0 = [p_\mathrm{m}(0), p_\mathrm{m}(1), \ldots, p_\mathrm{m}(n), p_\mathrm{f}(0), p_\mathrm{f}(1), \ldots, p_\mathrm{f}(M)]^\mathrm{T}$ (where T denotes transposition) , we have

$$\mathbf{p}_1 = \mathbf{U}\mathbf{p}_0, \tag{S1}$$

where $\mathbf{U} = \left[\begin{smallmatrix} \mathbf{u} & \mathbf{0} \\ \mathbf{0} & \mathbf{u} \end{smallmatrix}\right]$ is a $2(M+1) \times 2(M+1)$ block diagonal matrix of which entry $u(k, \ell)$ describes the probability of mutating from genotype ℓ to genotype k. Following Hadjivasiliou *et al.* (2012), we assume that each mitochondrial gene only mutates once during an individual's lifespan. Hence, given a probability

of mutation of μ for each gene, the entry $u_{k\ell}$ is given by

$$u_{k\ell} = \sum_{g_2=0}^{M-\ell} \sum_{g_1=0}^{\ell} \mathrm{Binom}\,(x = g_1, \mu, \ell)\,\mathrm{Binom}\,(x = g_2, \mu, M-\ell)\,\delta_{\ell-g_1+g_2=k}, \tag{S2}$$

where Kronecker's delta indicates that only those combinations are incorporated which result in the desired number of k C_m alleles.

S1.2 Fitness

See main text for a description of the fitness effects.

Recursions The frequencies $p_{2,\mathrm{m}}(j)$ and $p_{2,\mathrm{f}}(j)$ of mitochondrial type j after selection in males and females respectively subsequent to selection are given by

$$p_{2,\mathrm{m}}(j) = \frac{w_\mathrm{m}(j)p_{1,\mathrm{m}}(j)}{\bar{w}_\mathrm{m}} \tag{S3a}$$

$$p_{2,\mathrm{f}}(j) = \frac{w_\mathrm{f}(j)p_{1,\mathrm{f}}(j)}{\bar{w}_\mathrm{f}}, \tag{S3b}$$

where $\bar{w}_x = \sum_{j=0}^{n} p_{1,x}(j)w_x(j)$ is the mean fitness for sex x.

S1.3 Bottlenecks

First, M mitochondria are sampled without replacement down to B mitochondria. Subsequently, in the newly divided cell, mitochondria are randomly selected with replacement to divide again until a number of M is restored. Let the vector $\mathbf{p}_3$ denote the frequency distribution of mitochondrial genotypes after the bottleneck. We then have

$$\mathbf{p}_2 = \mathbf{A}\mathbf{p}_2$$

where $\mathbf{A} = \begin{bmatrix} \mathbf{b} & \mathbf{0} \\ \mathbf{0} & \mathbf{b} \end{bmatrix}$ is again a block diagonal matrix with entry $b_{k\ell}$ given by

$$b_{\ell \to k} = \sum_{h_2=0}^{M} \sum_{h_1=0}^{B} P_{B_1}(\ell \to h_1) P_{B_2}(h_1 \to k)$$

where $P_{B_1}(\ell \to h_1)$ is the transition probability from a cell that contains ℓ alleles preceding the bottleneck and h_1 alleles afterwards, according to a hypergeometric distribution

$$P_{\text{Bottleneck}}(\ell \to h_1) = \frac{\binom{\ell}{h_1}\binom{M-\ell}{B-h_1}}{\binom{M}{B}}$$

wheres $P_{B_2}(h_1 \to k)$ reflects the transition probability from h_1 C_{m} alleles following the bottleneck to k alleles after re-sampling back to M mitochondria. This is given by a binomial distribution with

$$P_{B_2}(h_1 \to k) = 1, \quad \text{when } k = 0 \text{ and } h_1 = 0$$
$$P_{B_2}(h_1 \to k) = \binom{M}{k} \left(\frac{h_1}{B}\right)^k \left(\frac{B-h_1}{B}\right)^{M-k}$$

S1.4 Meiosis I and II

Meiosis I In meiosis I, each mitochondrion is duplicated and then two daughter cells are formed by random segregation. Each receives a random sample of the $2M$ mitochondria present in the parent cell. Let $a_{k\ell}$ reflect the probability that a mother cell with ℓ mitochondria gives rise to a daughter cell with k mitochondria. Again we have a similar block matrix dynamic as previously

$$\mathbf{p}_5 = \mathbf{E}_1 \mathbf{p}_4,$$

in which element $\varepsilon_{1,k\ell}$ in the diagonal blocks of the matrix $\mathbf{E}_1$ is given by

$$\varepsilon_{1,k\ell} = \frac{\binom{2\ell}{k}\binom{2(M-\ell)}{M-k}}{\binom{2M}{M}}.$$

Meiosis II In meiosis II, each newly formed diploid daughter cell now divides into two gametes, each containing $M/2$ mitochondria through random segregation. The vector $\mathbf{p}_6$ is the distribution of mitotype numbers after meiosis II, which contains zeros for frequencies $p_{\mathrm{f}}(j)$ and $p_{\mathrm{m}}(j)$ where $j > M/2$. Given the dynamic $\mathbf{p}_6 = \mathbf{E}_2\mathbf{p}_5$, the transition matrix $\mathbf{E}_2$ is given by

$$\mathbf{E}_2 = \begin{bmatrix} \mathbf{e} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{e} \\ \mathbf{0} & \mathbf{0} \end{bmatrix}$$

with elements

$$\varepsilon_{2,k\ell} = \frac{\binom{\ell}{k}\binom{M-\ell}{M/2-k}}{\binom{M}{M/2}}$$

S1.5 Syngamy

Uniparental inheritance We assume that the mitochondrial genome of one parent is discarded, and that of the other is doubled through sampling with replacement. The distribution of genotypes is then given by the vector $\mathbf{p}_7 = \mathbf{S}\mathbf{p}_6$, where

$\mathbf{S} = \left[\begin{smallmatrix} \mathbf{0} & \mathbf{s} \\ \mathbf{0} & \mathbf{s} \end{smallmatrix}\right]$ .Elements of the sub-matrices $\mathbf{s}$ are given by

$$s_{k\ell} = \binom{M}{k}\binom{2\ell}{M}^{k}\binom{M-2\ell}{M}^{M-k}.$$

Paternal leakage Given paternal leakage, $0 < \pi < \frac{M}{2}$ denotes the number of mitochondria inherited from the father, so $0 < 1-\pi < \frac{M}{2}$ mitochondria are inherited from the mother. After syngamy, the resulting set of $M/2$ mitochondria is duplicated until the required number of M zygotic mitochondria is reached. Consider a sperm cell that has a number of r_{m} C_{m} mitochondria, whereas the egg contains r_{f} C_{f} mitochondria. Let $0 < j_{\mathrm{m}} < \pi$ be the number of C_{m} mitochondria among those mitochondria that are inherited through sperm. Similarly, let $0 < j_{\mathrm{f}} < 1-\pi$ be the number of C_{m} mitochondria that are inherited

through the egg, where the total contribution of C_{m} mitochondria is $k = j_{\mathrm{f}} + j_{\mathrm{m}}$. Hence, we have

$$p_7(k) = \sum_{j_{\mathrm{m}}=0}^{\pi} \sum_{r_{\mathrm{m}}=0}^{M/2} \sum_{r_{\mathrm{f}}=0}^{M/2} p_{\mathrm{m6}}(r_{\mathrm{m}})\, p_{\mathrm{f6}}(r_{\mathrm{f}})\, \epsilon(r_{\mathrm{m}} \to j_{\mathrm{m}}, \pi)\, \epsilon(r_{\mathrm{f}} \to k - j_{\mathrm{m}}, 1-\pi)$$

where $\epsilon(r \to j, x)$ reflects the probability that a gamete cell containing a number of r C_{m}-mitochondria contributes $0 \leq j \leq x$ C_{m} mitochondria to the zygote. Hence, $\epsilon(r \to j, x)$ is given by

$$\epsilon(r \to j, x) = \frac{\binom{r}{j}\binom{M/2-r}{x-j}}{\binom{M/2}{x}}.$$

Subsequently, the $M/2$ mitochondria are duplicated by re-sampling until the required number of n zygotic mitochondria is achieved, or

$$p_8(k) = \sum_{z=0}^{M/2} p_7(z) \binom{M}{k} \left(\frac{2z}{M}\right)^k \left(\frac{M-2z}{M}\right)^{M-k}$$

S1.6 Analysis

We numerically iterated recursions for $\mathbf{p}$ by coding a system of $2(M+1) \times 2(M+1)$ recursion equations in C. We assumed that equilibria are reached when the differences in mitotype frequencies between subsequent time steps are smaller than 1×10^{-7}.