File S2:

Expected offspring heterozygosity under central vs. terminal fusion

Expected heterozygosity $H(d)$ at a distance d (in Morgan) from the centromere can be computed in two steps. The first step is to derive expected heterozygosity $H(x)$ for any fixed number x of crossovers between the marker and the centromere. This can be obtained by recurrence. Under terminal fusion, we have

$$H(x+1) = 1 - H(x) + H(x)/2 \qquad \text{(A1)}$$

Indeed, if the marker was homozygous (1-$H(x)$), it becomes heterozygous with an additional crossing over, and if it was already heterozygous, there is only one chance over two that it will remain heterozygous with an additional crossing over ($H(x)/2$). Hence, with $H(0) = 0$ (i.e., terminal fusion), we obtain

$$H(x) = \frac{2}{3}\left(1 - \left(-\frac{1}{2}\right)^{x}\right) \qquad \text{(A2)}$$

This function oscillates (0, 1,$\frac{1}{2}$,$\frac{3}{4}$,$\frac{5}{8}$,$\frac{11}{16}$,$\frac{21}{32}$, ...) and stabilizes at 2/3 after many cross-overs. (Note that heterozygosity under central fusion can be obtained from the result under terminal fusion noting that $H_{\mathrm{cf}} = 1 - H_{\mathrm{tf}}/2$ and that $H_{\mathrm{cf}}(0) = 1$; Engelstädter *et al.* 2011). The second step is to assume that, in absence of interference, the number of crossovers X over a distance d follows a Poisson distribution with mean $2d$ (recalling that 0.5 Morgan corresponds to one cross-over). We obtain

$$H(d) = \sum_{x=0}^{\infty} P(X = x)\frac{2}{3}\left(1 - \left(-\frac{1}{2}\right)^{x}\right) \qquad \text{(A3)}$$

where $P(X = x)$ is given by the Poisson distribution. We find

$$H(d) = \frac{2}{3}\left(1 - e^{-3d}\right) \qquad \text{(A4)}$$

(Engelstädter *et al.* 2011). The equivalent result under central fusion is

$$H(d) = 1 - \frac{1}{3}(1 - e^{-3d}) \tag{A5}$$

(Rizet and Engelmann 1949; Barratt *et al.* 1954). In order to compute $H(d)$ in presence of interference, we propose here to use Conway-Maxwell Poisson distribution (Sellers *et al.* 2012) that generalizes the Poisson distribution allowing for over or underdispersion (positive interference corresponding to underdispersion). This distribution adds a parameter ν to control for the level of dispersion. Its probability density function is

$$P(X = x) = \frac{\lambda^x}{Z(\lambda,\nu)(x!)^\nu} \tag{A6}$$

where $Z(\lambda,\nu)$ is a normalization equal to $\sum_x \lambda^x/(x!)^\nu$, which can be expressed using the generalized hypergeometric function

$$Z(\lambda,\nu) = \ {}_0F_{\nu-1}(\emptyset, \mathbf{1}, \lambda), \tag{A7}$$

where **1** is a vector of 1 of dimension ν-1. Using the probability density (A7) in Eq. (A6) yields an heterozygosity function $H(d)$ for various degree of interference. This is illustrated in Figure 1. Strong interference leads to a non-monotonic mapping function as more evenly spaced cross over events will cause $H(d)$ to reflect the oscillatory behavior of $H(x)$ (Eq. A2). All mapping functions have a slope of two at d=0 and tend to 2/3 for large d. Non monotonicity arises as soon as there is interference, but it becomes noticeably large for $\nu \geq 2$. This method can also be applied to obtain a standard mapping function $M(d)$ expressing the recombination fraction as a function of the genetic distance. For instance using the Mather formula (Mather 1935)

$$M(d) = \frac{1}{2}\big(1 - P(X = 0)\big) = \frac{1}{2}(1 - Z(\lambda,\nu)^{-1}) \tag{A8}$$

In both cases, the mapping requires to express $H(d)$ or $M(d)$ not in terms of λ the parameter of the COM-Poisson distribution, but in terms of d (which is half the expected number of cross over, i.e. half the mean of the COM-Poisson distribution). Here again, the mean of the COM-

Poisson can be expressed in terms of generalized hypergeometric functions, but a simpler approximation is sufficient for most purposes:

$$E(X) = 2d = (1 - e^{-2\lambda})\left(\lambda^{1/\nu} - \frac{\nu - 1}{2\nu}\right) + \lambda e^{-4\lambda} \qquad \text{(A9)}$$

Supporting Figure S2 illustrates this mapping. The case $\nu = 1$ corresponds to Haldane mapping, while $\nu = 3$ is close to the Kosambi mapping used in *Drosophila* (Chen 2013). Note that heterozygosity with interference has already been treated by Barratt *et al.* (1954) for the case of central fusion, however using a less general model (necessitating more restrictive assumptions) than the models based on the COM-Poisson distribution (see also, Nace *et al.* 1970; Zhao and Speed 1998). The latter and other count models (e.g., Zhao *et al.* 1995) are increasingly used also to model interference in classical genetic mapping (e.g., Choi *et al.* 2013).

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