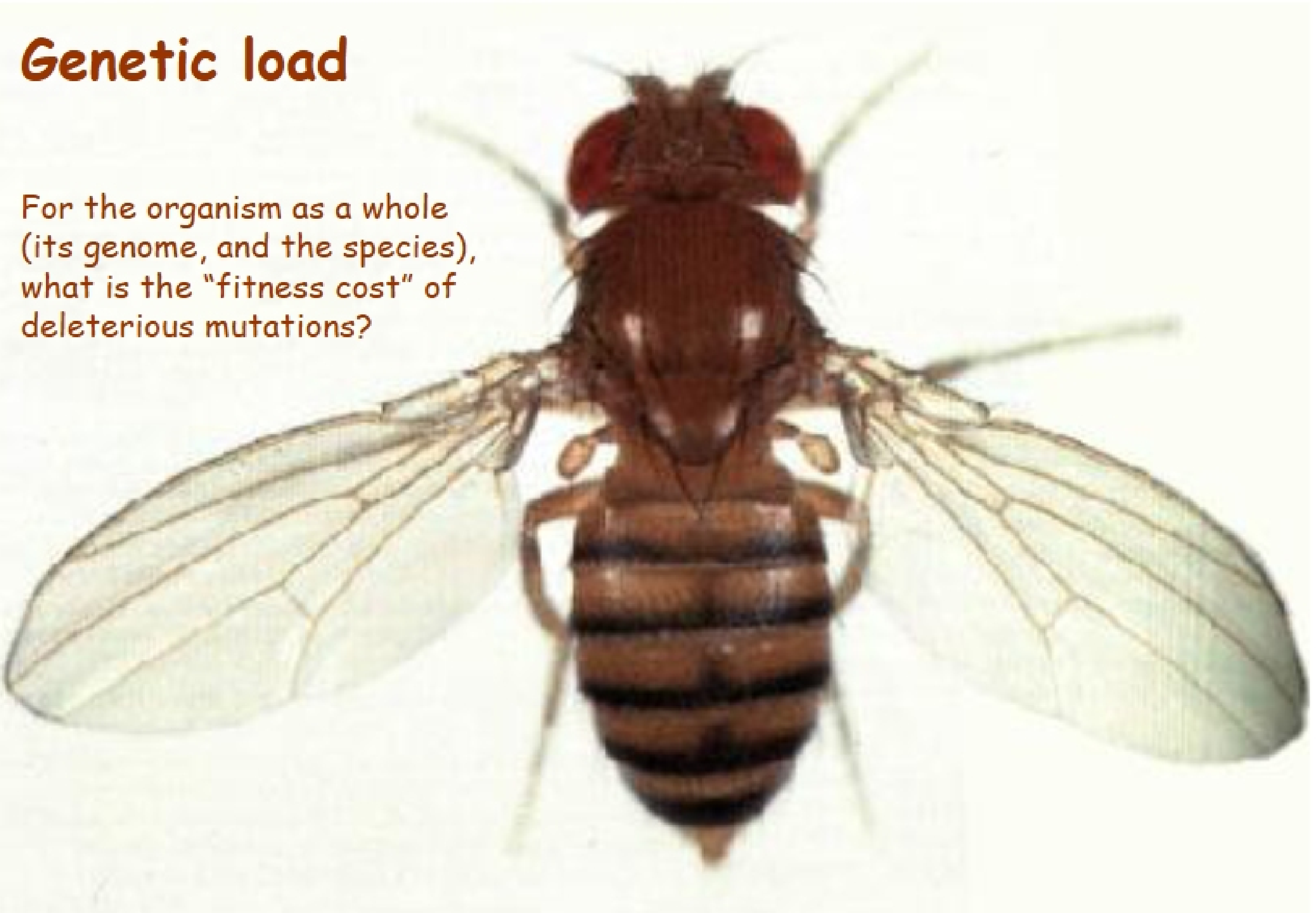
Genetic load

For the organism as a whole (its genome, and the species), what is the "fitness cost" of deleterious mutations?



We saw that the expected frequency of deleterious alleles is

$$\boxed{\hat{q} \approx \frac{u}{hs}}$$

How much is *average fitness* depressed, as a result?

$$\begin{aligned}
\bar{w} &= 1 - 2\hat{p}\hat{q}hs - \hat{q}^2 s \\
&\approx 1 - 2\hat{q}hs && \text{(because } q^2 \approx 0 \text{ and } p \approx 1\text{)} \\
&\approx 1 - 2u && \text{(because } qhs \approx u\text{)}
\end{aligned}$$

So the dominance (h) and the selection coefficient (s) don't matter!

Just the (diploid) rate of deleterious mutation ($2u$)!

Why?

The *load* is the reduction relative to an "unloaded" genotype.

$$L = \frac{w_{\max} - \bar{w}}{w_{\max}}$$

Thus at any given locus where the mutation probability is *u* per copy,

$$L = \frac{1 - (1 - 2u)}{1} = 2u$$

In other words, the load is equal to the diploid mutation rate.