Figure S1  Decay of linkage disequilibrium ($r^2$) with genetic distance in the Ohio sample of *C. remanei*. Data for 20 loci are superimposed in the figure. Solid red line indicates a stiff spline fit of the data, while orange lines represent a loose spline fit. Histograms on the top and side indicate the distribution of pairwise distances and $r^2$ values, respectively.
Figure S2  Correction of synonymous-site diversity for its correlation with codon usage bias. (A) Data shown for Ohio population only, but a similar correlation was observed for all C. remanei populations and adjusted accordingly. Synonymous-site diversity (Jukes Cantor corrected; $\pi_{\text{syn-JC}}$) is reduced in loci with strong codon bias (i.e. high $F_{\text{OP}}$). A value of $F_{\text{OP}} = 0.36$ represents the expectation in the absence of selection on codon usage. (B) $\pi_{\text{neu}}$ values are uncorrelated with codon bias, following adjustment of $\pi_{\text{syn-JC}}$. 

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Supporting Tables

Tables S1-S5

Tables S1-S5 are available for download as Excel files at
http://www.genetics.org/content/suppl/2012/05/25/genetics.112.140418.DC1.