

MOLECULAR ECOLOGY RESOURCES

Supplemental Information for:

A genomic approach to inferring kinship reveals limited intergenerational dispersal in the yellow fever mosquito

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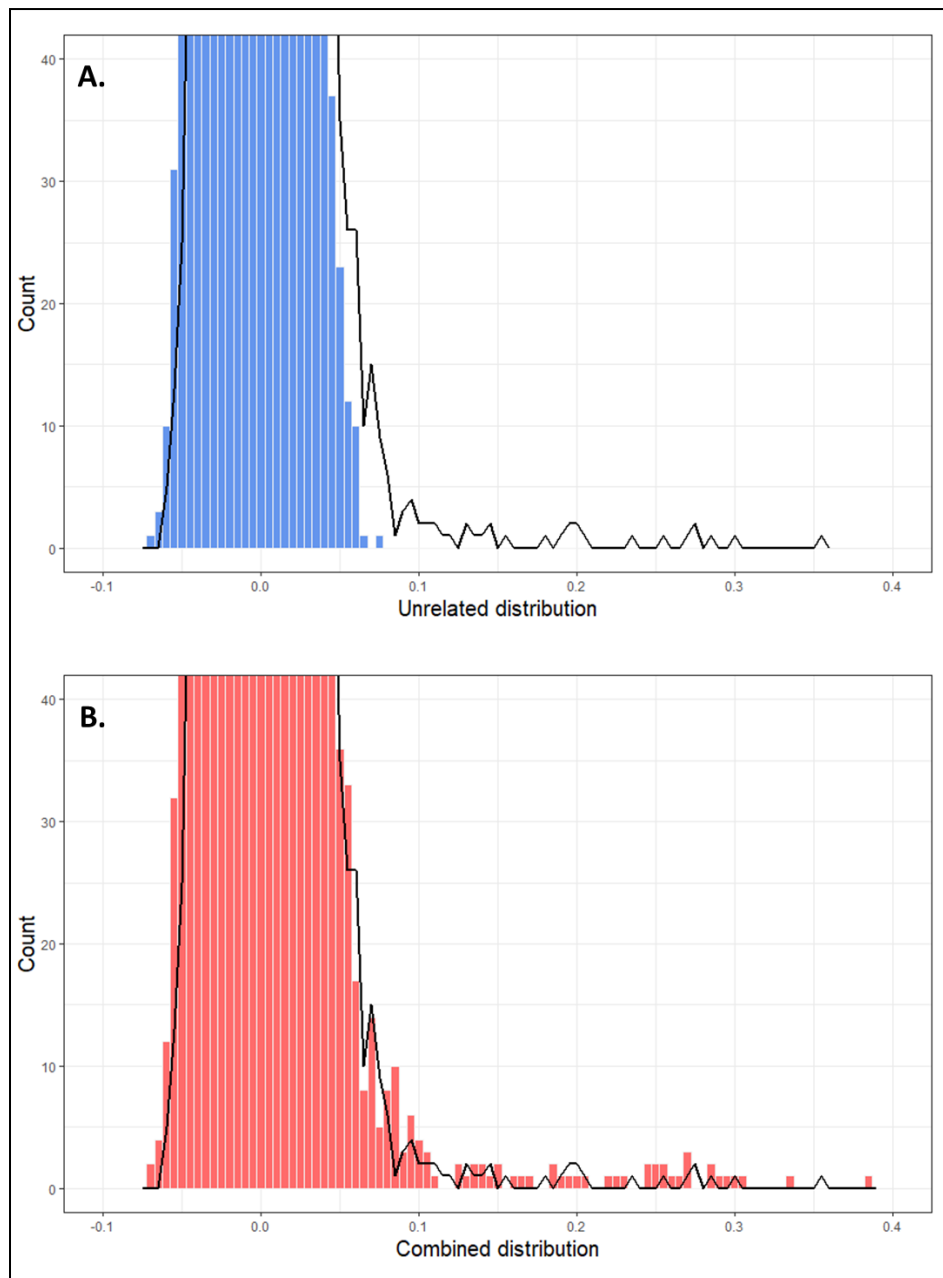
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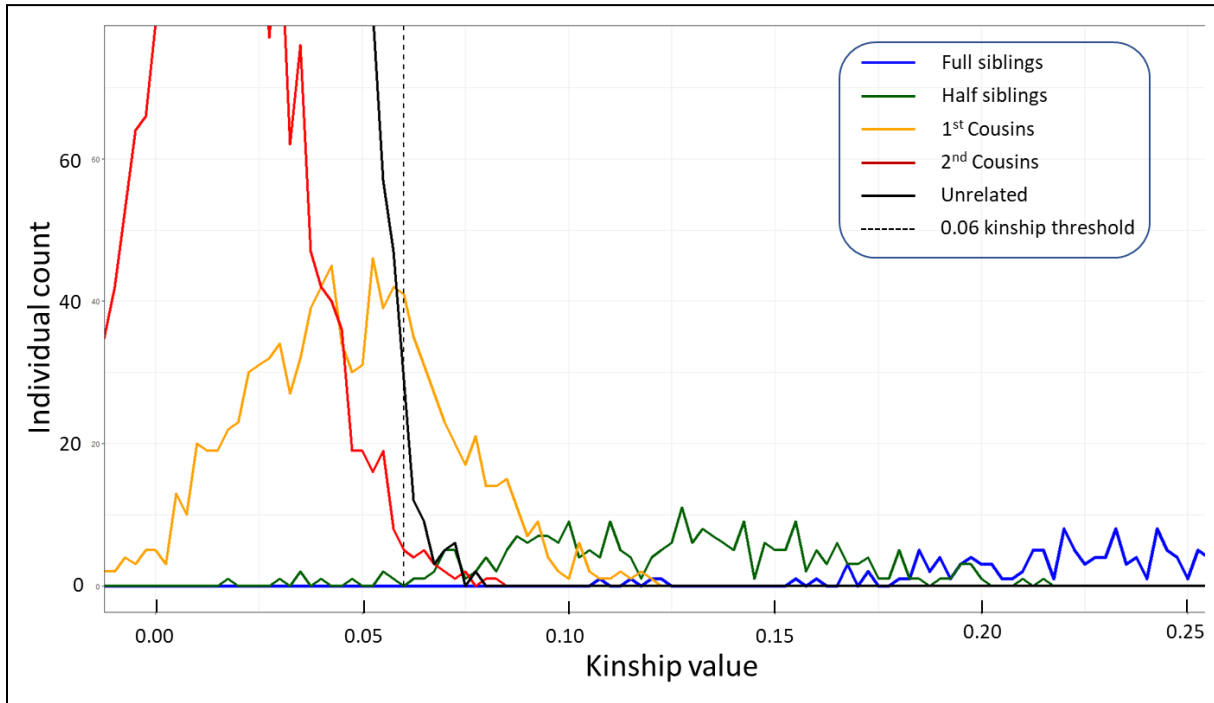


Supplementary Figure 1

A Histogram of unrelated sampling distribution (blue) compared to that of field data (black line).

B Histogram of combined sampling distribution (red) compared to that of field data (black line). The combined sampling distribution approximates the field data much more closely than does the unrelated.

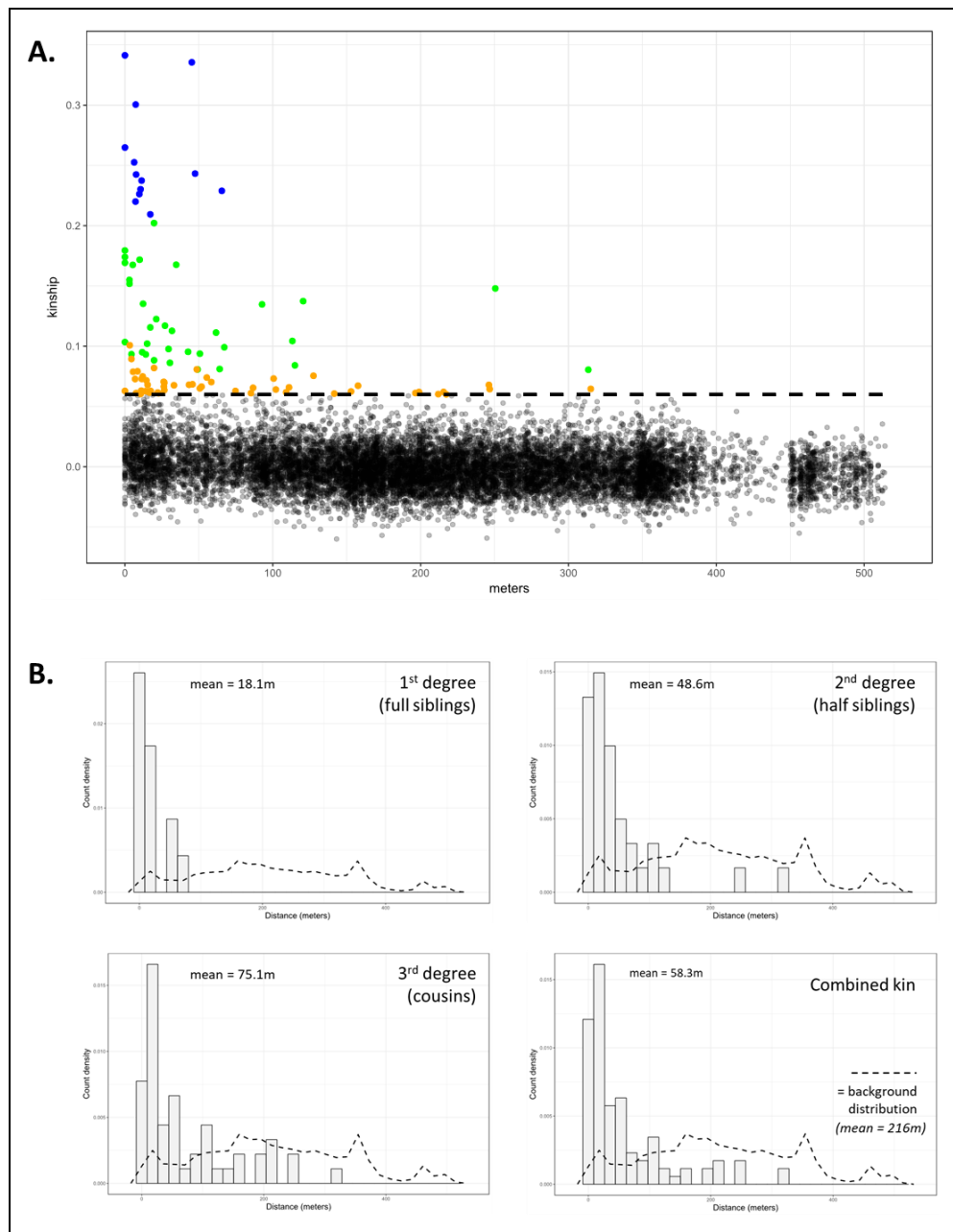
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Supplementary Figure 2

Frequency polygons showing distributions of simulated kinship (k) scores. Colours indicate unrelated (black), second cousins (red), first cousins (orange), half-siblings (green), and full-siblings (blue). Dotted vertical line shows the $k = 0.06$ lower bound for first cousins. Based on these distributions, we no longer considered second cousins.

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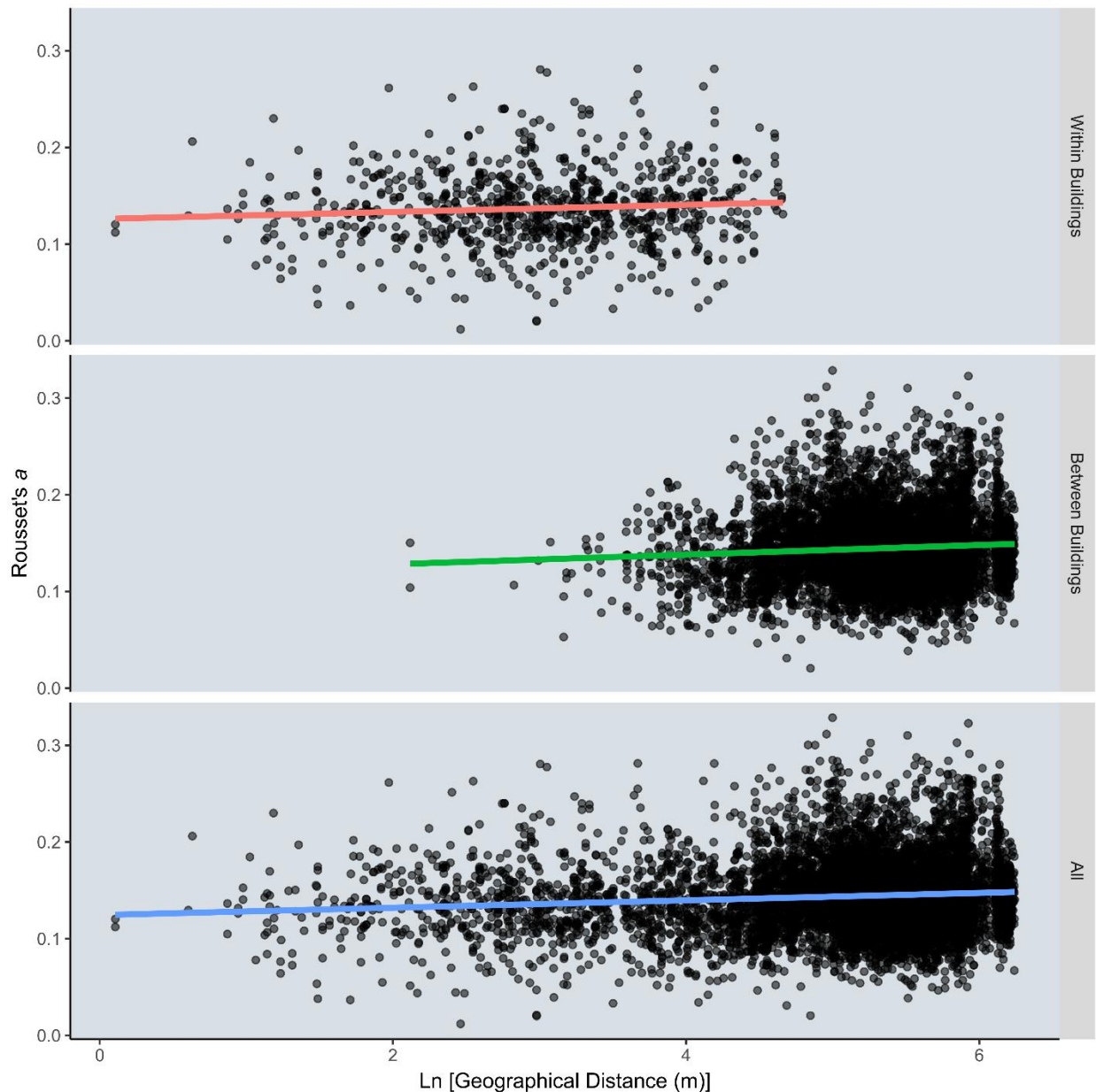
Supplementary Figure 3

Kin assignment and distribution across distance.

A Pairwise Loiselle's k scores between all individuals relative to distance of separation. Blue = full-siblings, green = half-siblings, orange = cousins, black = unrelated. Dotted line at $k = 0.06$ shows the lower bound for first cousins.

B Histograms of density of each order of kinship (and combined) relative to distance (m). The density distribution of all possible pairwise combinations is shown as a dotted line in each panel for reference.

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Supplementary Figure 4

Regressions of pairwise genetic distance (Rousset's a) and the natural logarithm of geographical distance for all non-sibling pairs. Regressions for all non-sibling pairs ($P < 2e^{-16}$; $R^2 = 0.0090$; slope = 0.0037), all non-sibling pairs within the same building ($P = 0.012$; $R^2 = 0.0062$; slope = 0.0041), and all non-sibling pairs in different buildings ($P = 1.3e^{-09}$; $R^2 = 0.0048$; slope = 0.00484) all showed significant positive associations between geographical and genetic distances.