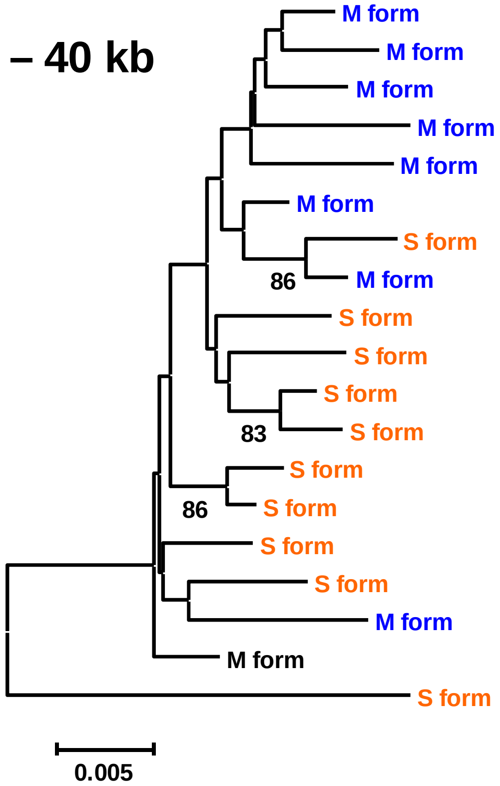
Supporting Figure S3: Alleles 5 kb, 10 kb, 20 kb and 40 kb to either side of *APL1* gene cluster do not show strong genealogical structuring between the M and S molecular forms. Whereas the *APL1* genes show strong subdivision between M and S and very little diversity within the M form, alleles from M and S form alleles become progressively more genealogically interspersed and the M form shows greater genealogical depth with increasing physical (recombinational) distance from the *APL1* locus. These data indicated that the structuring observed at *APL1* is restricted to that locus, and is not a general property of M/S differentiation, consistent with a recent selective sweep at *APL1* in the M form, purging diversity from the M form but not the S form. All mosquitoes in these figures were collected in Bancoumana, Mali. The plotted genealogies are neighbor joining trees, drawn in MEGA 3.1 [54] using uncorrected p-distance. Nodes with greater than 50% bootstrap support are indicated, scale bar indicates nucleotide divergence.

– 40 kb



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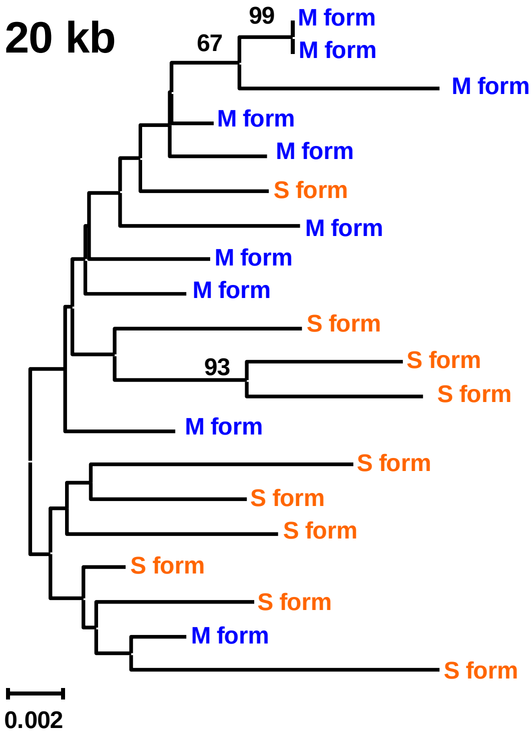

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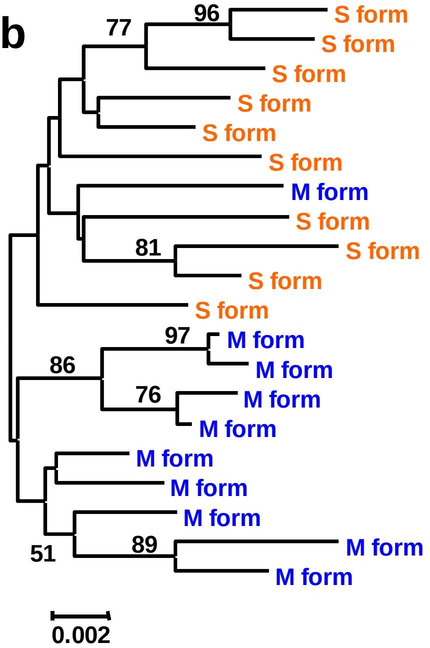

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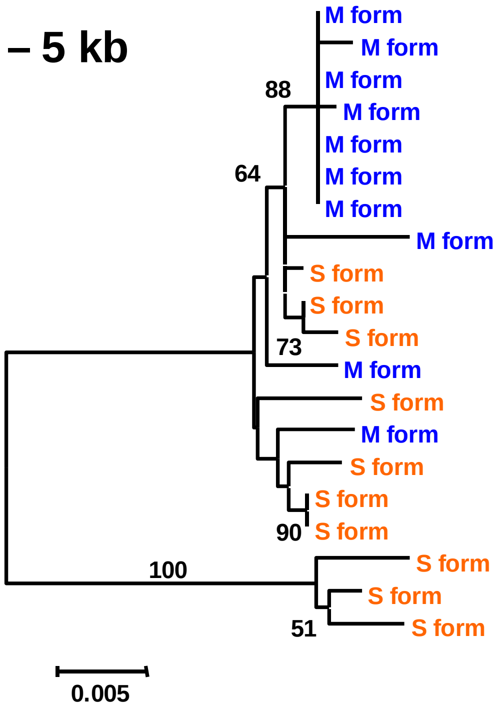

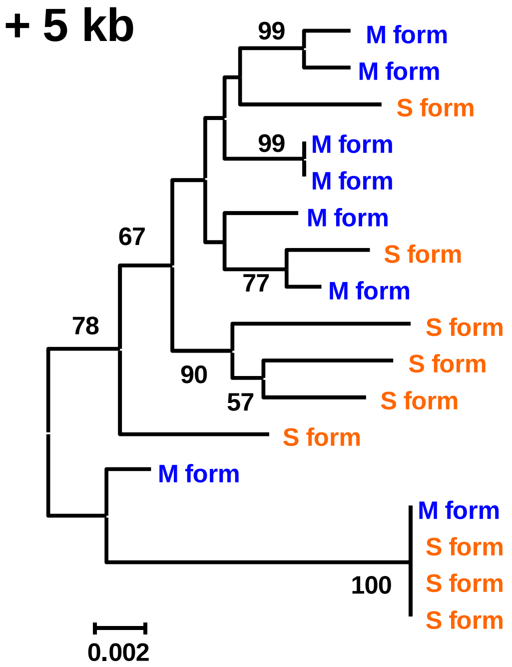
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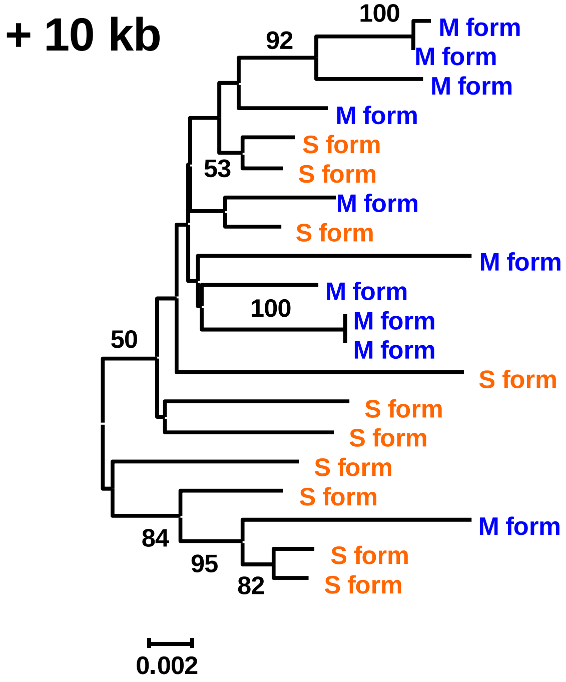
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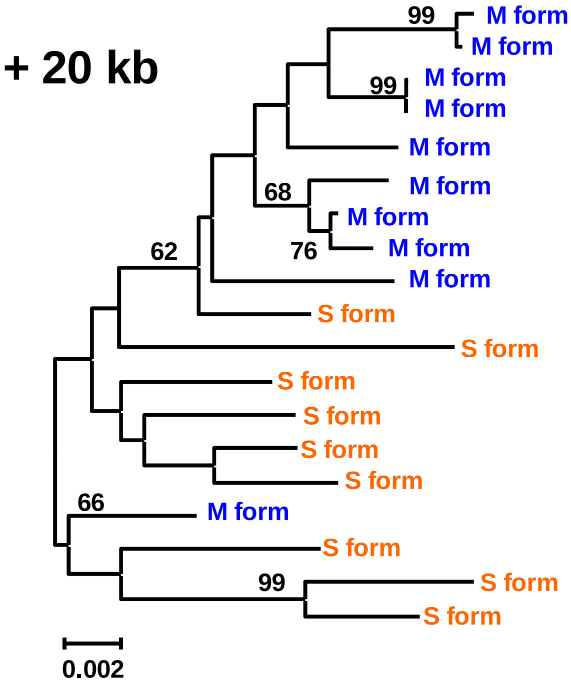
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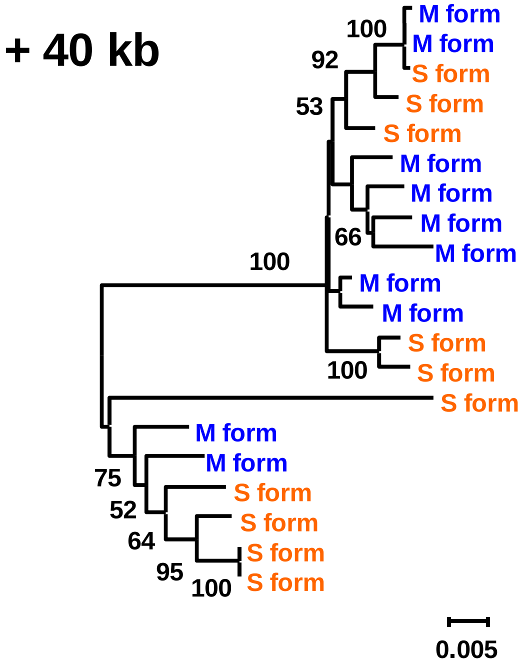
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