

Supporting Information

Table S1. Geographic differentiation among populations of *D. quinaria* from PA, NY, and ME. *COI* excludes sequences from flies carrying the mtDNA clade associated with *Wolbachia* infection. Included are two measures of genetic differentiation, K_{ST}^* (Hudson et al. 1992) and S_{nn} (Hudson 2000). Significance was determined using permutation tests, as implemented in DnaSP.

Locus	K_{ST}^*	S_{nn}
<i>COI</i>	0.0652 ($P < 0.0001$)	0.6274 ($P < 0.0001$)
<i>mof</i>	-0.0211 ($P = 0.805$)	0.3626 ($P = 0.248$)
<i>tpi</i>	0.058 ($P = 0.001$)	0.5948 ($P < 0.0001$)
<i>skpA</i>	0.0375 ($P = 0.076$)	0.3918 ($P = 0.092$)
<i>plexA</i>	0.1823 ($P = 0.21$)	0.5424 ($P = 0.145$)

Table S2. Polymorphism in *D. quinaria*. Each locus is separated by population and mtDNA clade. Included here is the number of sampled alleles (N), the total number of sites (L_{All}), the total silent sites (L_{Silent}), and the number of total (S_{All}), silent (S_{Silent}), and nonsynonymous (S_{Nonsyn}) segregating sites. Estimates of polymorphism are shown for all sites (π_{All}) and for silent sites only (π_{Silent}). Tajima's D (D), or the deviation from the site frequency spectrum, is calculated using silent sites only, with numbers in bold those that deviate from neutrality based on coalescent simulations ($P < 0.05$). Divergence for all loci except *RIB* is to *D. innubila*, another member of the quinaria group, and is for silent sites only (Divergence for *RIB* is to *D. palustris*).

Locus	Population/ mtDNA clade		N	L_{All}	L_{Silent}	S_{All}	S_{Silent}	S_{Nonsyn}	π_{All}	π_{Silent}	D_{Silent}	Div_{Silent}
<i>COI</i>	PA / F		4	650	157	3	3	0	0.0031	0.0129	2.01	0.37
	PA / Q		20	650	157	28	25	3	0.0085	0.0334	-0.81	0.35
	PA / Q + F		24	650	157	65	62	3	0.0254	0.1032	0.11	0.35
	PA, ME, NY / Q + F		49	650	157	72	67	3	0.0159	0.0635	-1.10	0.34
	PA, ME, NY / Q		45	650	157	37	34	3	0.0067	0.0271	-1.50	0.34
<i>mof</i>	PA / F		7	636	144	9	9	0	0.0062	0.0271	0.33	0.34
	PA / Q		8	636	144	5	5	0	0.0033	0.0149	0.50	0.33
	PA / Q + F		15	636	144	9	9	0	0.0055	0.0241	0.94	0.33
	PA, ME, NY / Q + F		37	636	144	11	11	0	0.0047	0.0207	0.39	0.33

<i>plexA</i>	PA / F	8	772	180	8	6	2	0.0047	0.0155	0.95	0.39
	PA / Q	12	772	180	9	6	3	0.0046	0.0135	0.87	0.39
	PA / Q + F	20	772	180	10	7	3	0.0048	0.0147	1.12	0.39
	PA, ME, NY / Q + F	30	772	180	11	8	3	0.0045	0.0144	0.86	0.39
<i>RIB</i>	PA, ME, NY / Q + F	14	862	862	0	0	0	0	0	NA	0.10
<i>skpA</i>	PA / F	7	451	94	8	8	0	0.0074	0.0356	0.11	0.27
	PA / Q	4	451	94	7	7	0	0.0049	0.0234	-1.21	0.28
	PA / Q + F	14	451	94	11	11	0	0.0063	0.0305	-0.69	0.28
	PA, ME, NY / Q + F	36	451	94	12	12	0	0.0041	0.0199	-1.12	0.28
<i>tpi</i>	PA / F	8	376	92	7	6	1	0.0082	0.0306	1.02	0.26
	PA / Q	12	376	92	7	6	1	0.0072	0.0242	0.46	0.26
	PA / Q + F	20	376	92	7	6	1	0.0074	0.0259	1.32	0.26
	PA, ME, NY / Q + F	42	376	92	10	9	1	0.0063	0.0215	-0.15	0.25