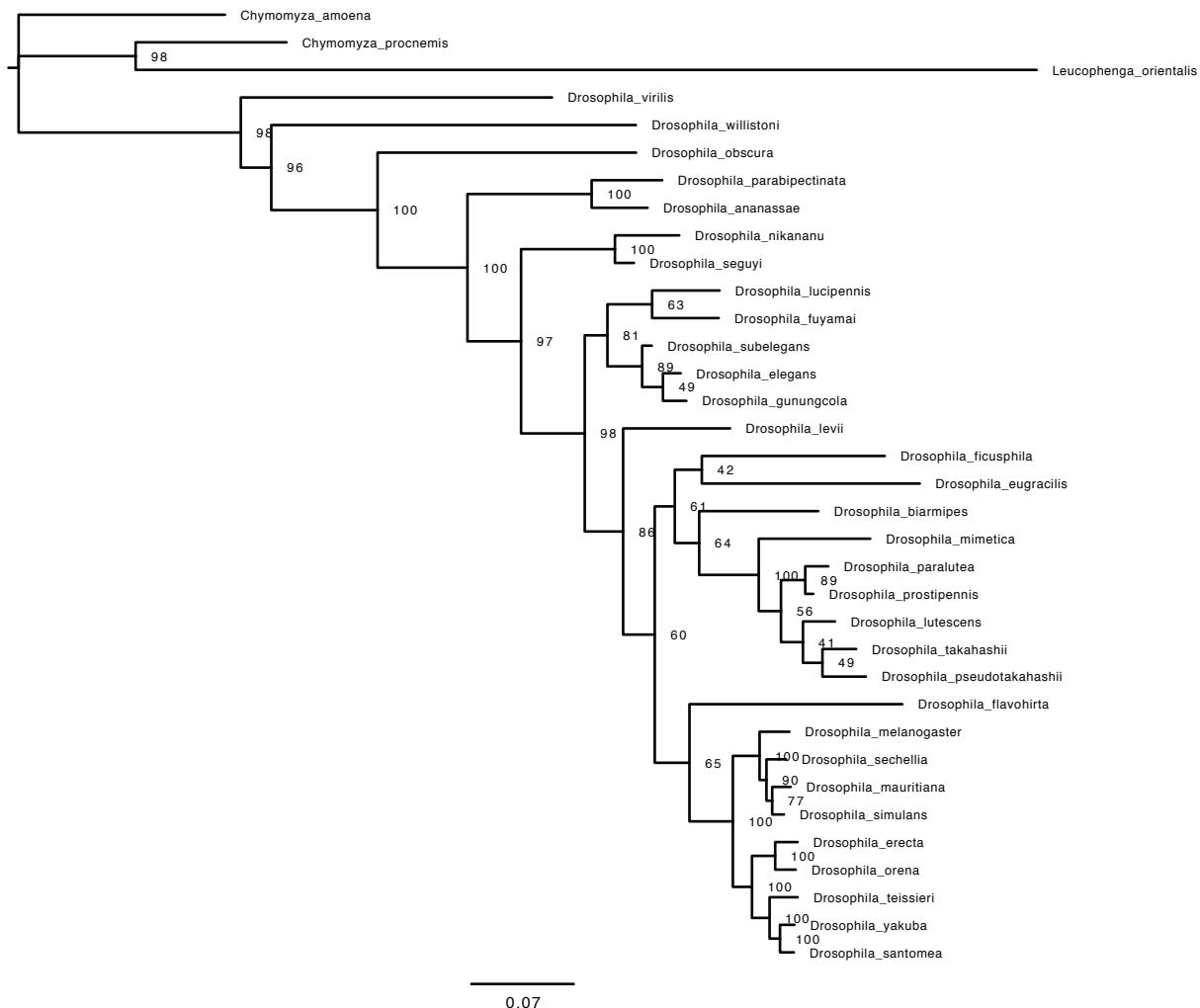
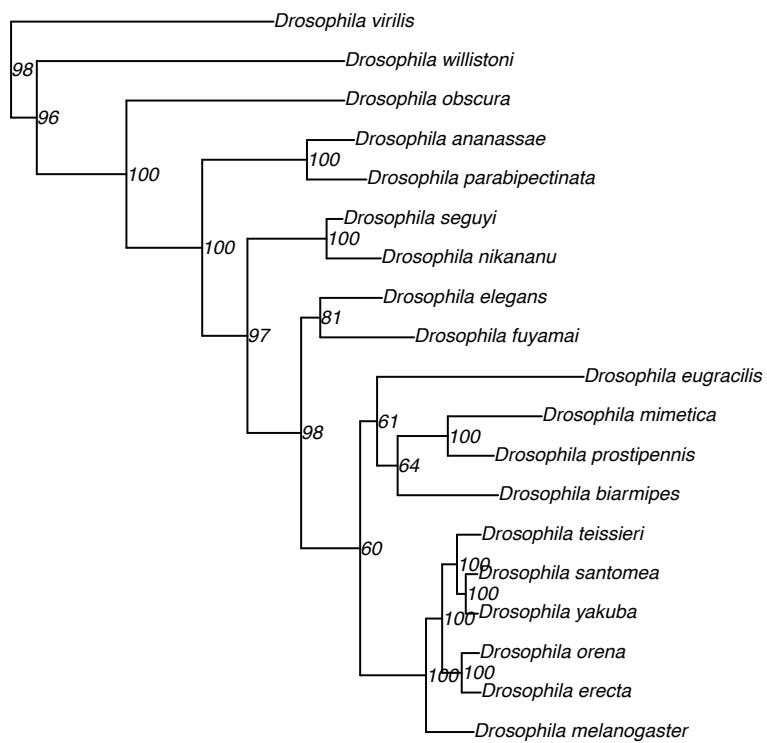


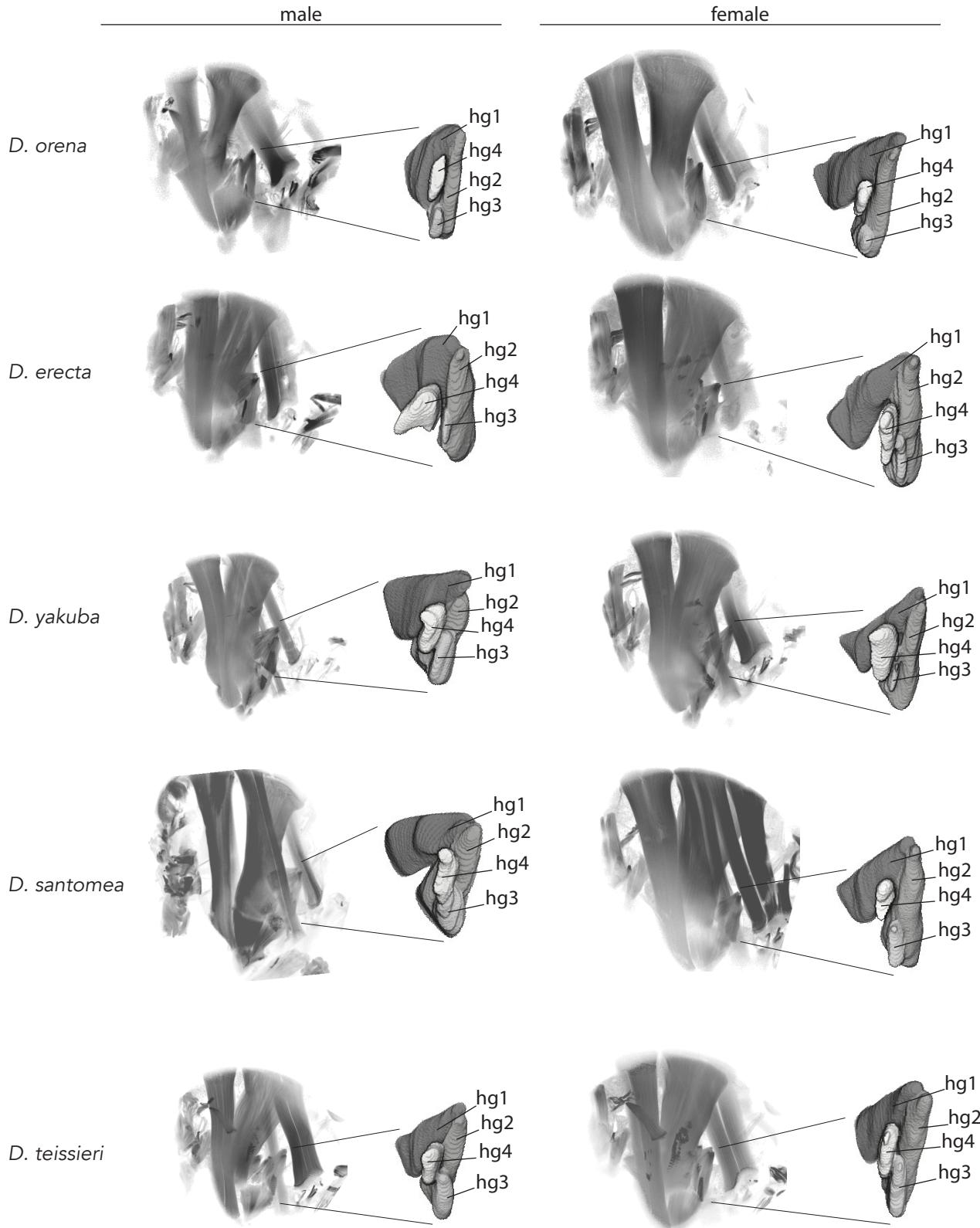
Supplemental Figure 1. Maximum likelihood tree showing phylogenetic relationships among 19 *Drosophila* species. Each ancestral node is numbered. Probabilities of a monomorphic or dimorphic ancestor at each node is shown in Supplemental Table 1.

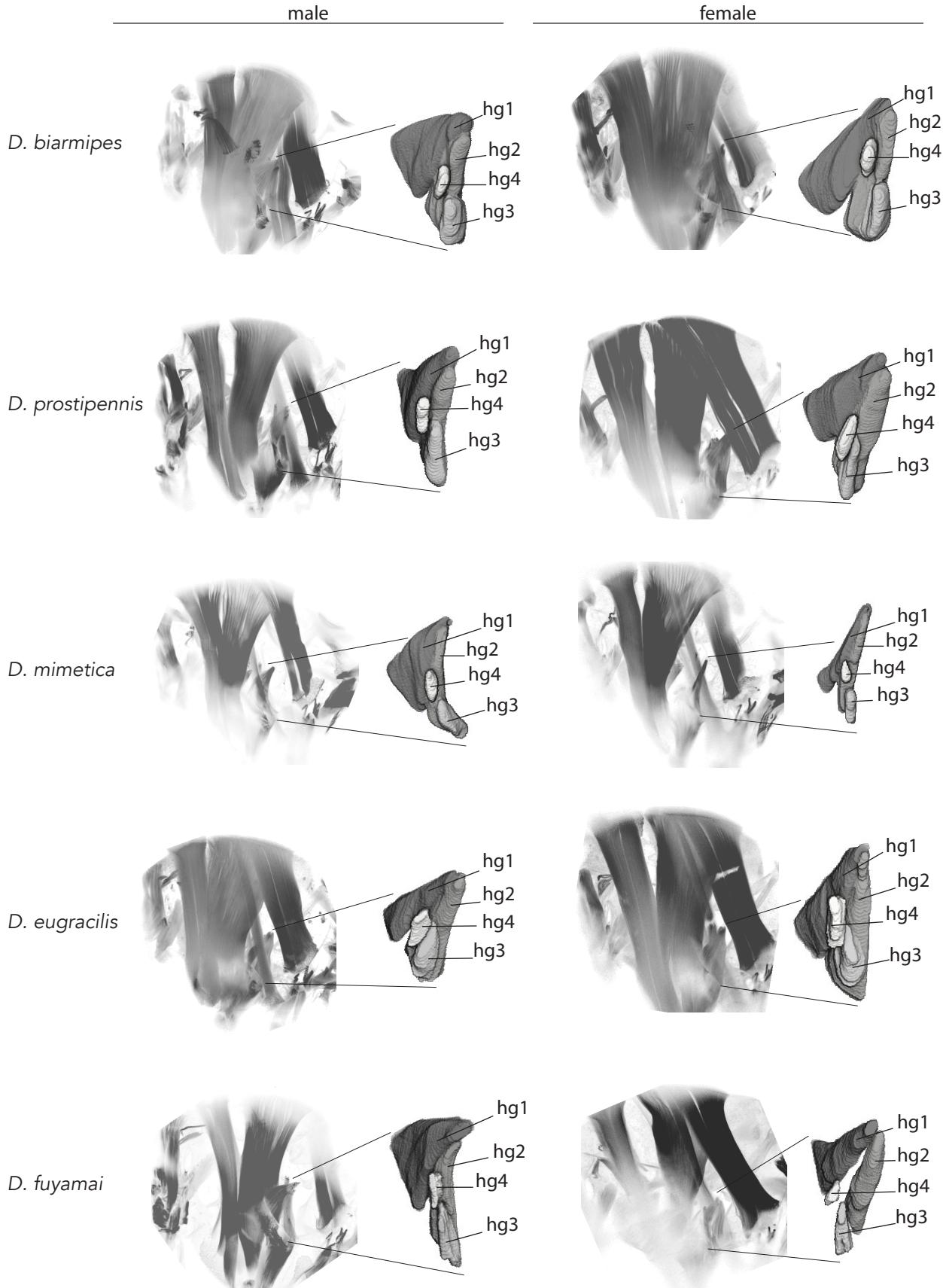


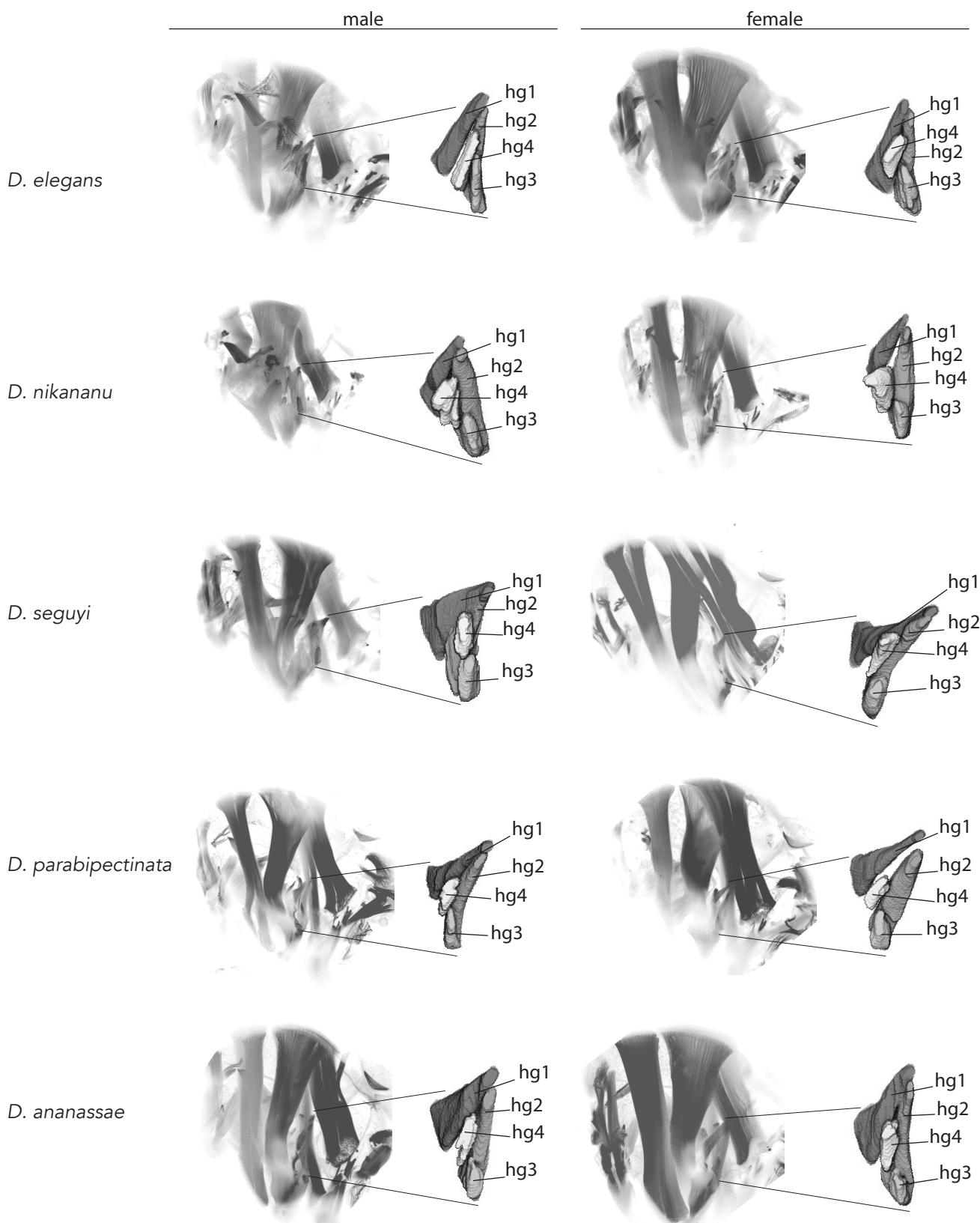
Supplemental Figure 2. Complete phylogenetic estimate from Maximum Likelihood analysis of all six nuclear genes concatenated (ADH, amyrel, Ddc, Gphd, Sod, and Xdh). Node labels indicate ultrafast bootstrap support values, with a value of 95 or greater indicating a well supported node.

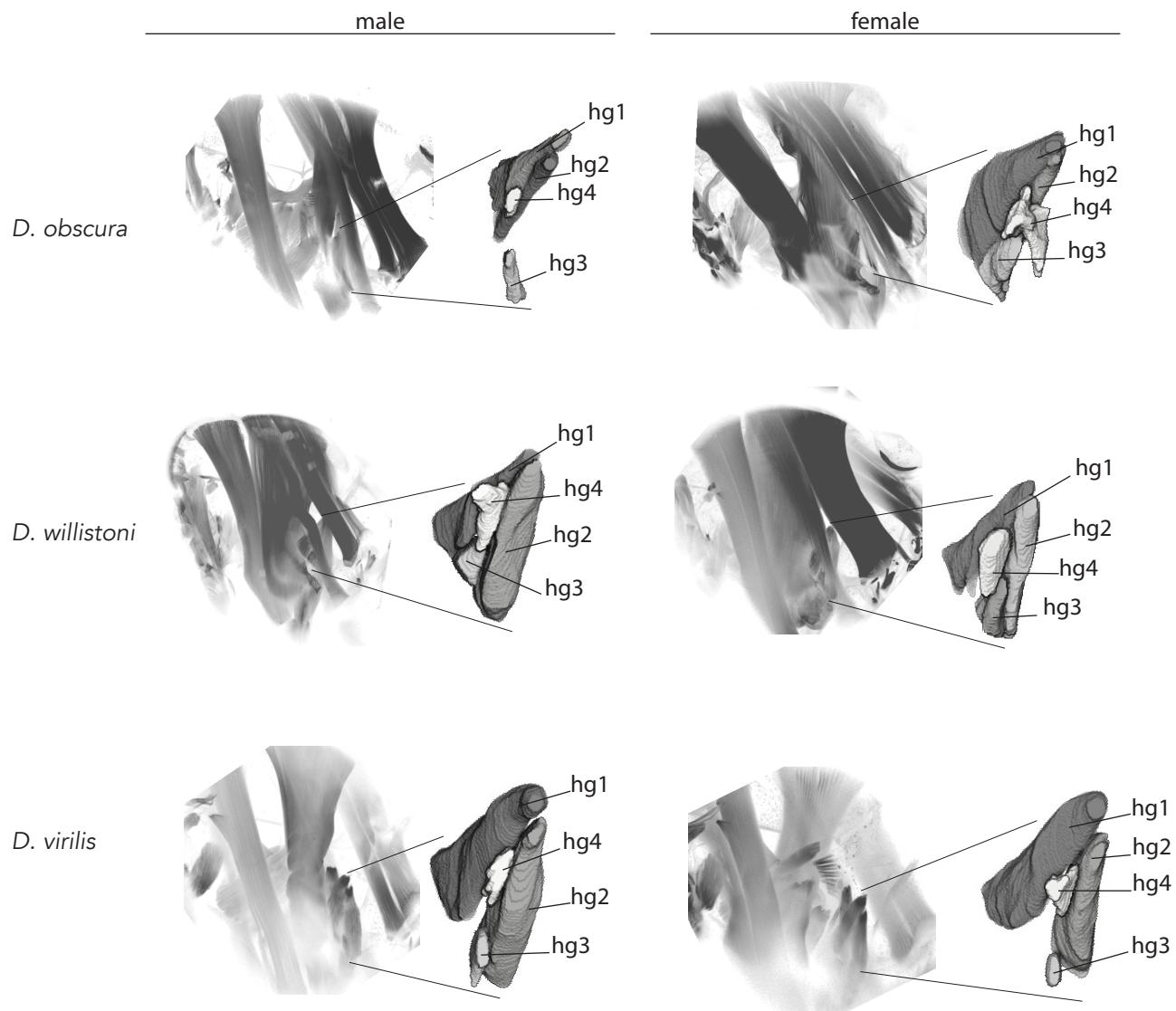


Supplemental Figure 3. Paired down phylogeny used for Ancestral State Reconstructions seen in Figures 3-4. Full phylogeny (Supplemental Figure 2) was paired down to include only species for which muscle volume data was available for the ancestral state reconstruction. Node labels indicate ultrafast bootstrap support values, with a value of 95 or greater indicating a well supported node. a









Supplemental Figure 4. Reconstructions of the hg1–4 muscles from males and females of the species used in this study. The relative position and shape of the muscles are generally conserved in males and females across all species. In all images, the anterior side of the thorax is to the left and the dorsal side of the thorax is to the top. Maximum projection image of the confocal slices that include the hg muscles is shown to the left of each panel. Reconstructions on the right were generated in Amira.

Node	Hg1		Hg2			Hg3		
	Prob (mono)	Prob (di)	Prob (mono)	Prob (male enlarged)	Prob (female enlarged)	Prob(mono)	Prob (male enlarged)	Prob (female enlarged)
1	0.702	0.298	0.966	0.017	0.017	0.956	0.022	0.022
2	0.719	0.281	0.978	0.011	0.012	0.970	0.015	0.015
3	0.785	0.215	0.990	0.004	0.006	0.989	0.005	0.005
4	0.843	0.157	0.991	0.002	0.007	0.998	0.001	0.001
5	0.811	0.189	0.999	0.000	0.001	0.999	0.001	0.000
6	0.563	0.437	0.999	0.000	0.000	0.992	0.007	0.001
7	0.161	0.839	0.979	0.017	0.004	0.999	0.001	0.000
8	0.018	0.982	1.000	0.000	0.000	1.000	0.000	0.000
9	0.013	0.987	1.000	0.000	0.000	1.000	0.000	0.000
10	0.086	0.914	1.000	0.000	0.000	0.980	0.000	0.019
11	0.001	0.999	1.000	0.000	0.000	1.000	0.000	0.000
12	0.000	1.000	1.000	0.000	0.000	0.990	0.010	0.000
13	0.141	0.859	0.897	0.085	0.018	0.998	0.002	0.000
14	0.081	0.919	0.435	0.473	0.092	0.993	0.006	0.001
15	0.029	0.971	0.169	0.516	0.315	0.885	0.109	0.006
16	0.579	0.421	1.000	0.000	0.000	0.960	0.038	0.003
17	0.990	0.010	1.000	0.000	0.000	1.000	0.000	0.000
18	0.973	0.027	0.871	0.006	0.124	0.999	0.000	0.000

Supplemental Table 1. Results from the ancestral state reconstruction for hg1–hg3 with the probability of each node being monomorphic or dimorphic. Results for hg4 are not shown, as no dimorphisms were present in the dataset (all nodes are inferred to be monomorphic).

	ADH	amyrel	Ddc	Gphd	Sod	Xdh
<i>Chymomyza amoena</i>	AF059887	AY736544	AY124490	L36961	X61687	AF093217
<i>Chymomyza procnemis</i>	AB026521	-	-	L41252	AF021821	-
<i>Drosophila ananassae</i>	XM001961486	AF024691	-	XM001962674	-	-
<i>Drosophila biarmipes</i>	DQ363229	AF462597	DQ363223	AY098467	-	DQ363235
<i>Drosophila elegans</i>	DQ363230	AF136930	DQ363224	AB032146	-	DQ363236
<i>Drosophila erecta</i>	XM001968861	AF039562	-	XM001968825	AF127156	-
<i>Drosophila eugracilis</i>	AY279326	AF250055	DQ363225	AY098472	-	AY279341
<i>Drosophila ficusphila</i>	DQ363232	AF462600	DQ363226	AB032149	-	DQ363237
<i>Drosophila flavohirta</i>	-	AY733051	-	-	-	-
<i>Drosophila fuyamai</i>	-	-	-	AY098471	-	-
<i>Drosophila gunungcola</i>	AM181670	-	-	AB032145	-	-
<i>Drosophila levii</i>	-	AF491635	-	-	-	-
<i>Drosophila lucipennis</i>	AF459751	AF251138	-	AY098470	-	-
<i>Drosophila lutescens</i>	AY279327	AF491637	-	-	-	AY279343
<i>Drosophila mauritiana</i>	X63953	U96157	-	-	AF127158	-
<i>Drosophila melanogaster</i>	X78384	NM057914	X04661	J04567	X17332	Y00308
<i>Drosophila mimetica</i>	AY279328	AY733058	-	AY098465	-	AY279342
<i>Drosophila nikananu</i>	AF459767	AF251136	-	-	-	-
<i>Drosophila obscura</i>	U90955	AF306713	-	U47881	U47892	-
<i>Drosophila orena</i>	Z00032	U96158	-	DQ167752	AF127155	AY279340
<i>Drosophila parabipectinata</i>	AB194414	AY736489	-	AJ844754	AJ844865	-
<i>Drosophila paralutea</i>	AF459747	-	-	-	-	-
<i>Drosophila prostipennis</i>	AF459748	-	-	AB027282	-	-
<i>Drosophila pseudotakahashii</i>	-	AY736499	-	-	-	-
<i>Drosophila santomea</i>	AY804554	AY736503	-	-	AY804512	AY804550
<i>Drosophila sechellia</i>	XM002035803	AF039558	-	-	AF127157	-
<i>Drosophila seguyi</i>	AF459765	-	-	-	-	-

<i>Drosophila simulans</i>	XM002079432	U96160	AY197770	L41647	X15685	AY279336
<i>Drosophila subelegans</i>	-	AY736507	-	-	-	-
<i>Drosophila takahashii</i>	AF459749	U96161	-	-	-	-
<i>Drosophila teissieri</i>	X54118	AF039557	-	U47809	AF127160	AY279337
<i>Drosophila virilis</i>	XM002057547	XM002048980	AF293749	XM002051332	X13831	AF093215
<i>Drosophila willistoni</i>	XM002066420	AF039560	AF293750	XM002065330	L13281	AF093206
<i>Drosophila yakuba</i>	XM002089270	AF039561	-	XM002089126	AF127159	AY279338
<i>Leucophenga orientalis</i>	AB033638	-	-	-	-	-

Supplemental Table 2. GenBank accession numbers of species used in the phylogenetic analysis. All data was used for the Maximum Likelihood estimation of the phylogeny, and the bolded individuals were the only ones retained on the phylogeny for ancestral state reconstruction.