

Table S2 Characteristics of marker loci genotyped in polygyne queens and their progeny embryos (male genotypes inferred)

Locus ^a	Number of alleles (N_a)			Expected heterozygosity (H_{exp})			Chromosome	Genome start coordinate ^c
	Queens	Males ^b	Both sexes	Queens	Males ^b	Both sexes		
<i>Bertha</i>	5	3	5	0.653	0.592	0.625	3	3:10321677
<i>Sdag_C27 (C27)</i>	3	3	3	0.327	0.351	0.338	6	6:10867177
<i>Sdag_C294 (C294)</i>	7	6	7	0.642	0.727	0.724	16	16:18429274
<i>Sdag_C536 (C536)</i>	8	8	8	0.820	0.813	0.819	6	6:5725253
<i>cassidy</i>	5	4	5	0.664	0.659	0.661	7	7:12459354
<i>Gp-9</i>	2	2	2	0.500	0.209	0.432	16	16:18579940
<i>Sol_i109 (i_109)</i>	4	4	4	0.736	0.714	0.726	14	14:2617730
<i>Sol_i114 (i_114)</i>	6	6	6	0.713	0.731	0.720	5	5:7887511
<i>Sol_i120 (i_120)</i>	7	6	7	0.711	0.687	0.704	10	10:6961043
<i>Sol_i126 (i_126)</i>	5	4	5	0.751	0.682	0.743	16	16:8362602
<i>Sol_i129 (i_129)</i>	4	3	4	0.286	0.287	0.286	4	4:10716117
<i>red_ant</i>	2	2	2	0.352	0.232	0.294	6	6:18309984
<i>Sol-42f</i>	10	7	11	0.782	0.774	0.778	15	15:6834468
<i>Sol-49</i>	7	5	7	0.758	0.705	0.733	8	8:9915806
<i>sunrise</i>	3	3	3	0.496	0.486	0.490	14	14:5031308

^a All loci except *Gp-9* are microsatellites. Data for supergene-linked loci are highlighted in red shading and font. Abbreviated locus names used in the main text and display items (if any) are shown in parentheses

^b Alleles of mates of polygyne queens were inferred from comparison of maternal and progeny genotypes

^c Based on reference genome build *Si_gnH_C3* of a haploid *SB* male from the USA (Y. Zheng et al., unpublished)