Digital supplementary material to

C HAPPELL , P., R OBERTS , K., B AER , B. & H UGHES , W.O.H. 2013: Mating system and population genetic structure of the bulldog ant *Myrmecia pavida* (Hymenoptera: Formicidae). – Myrmecological News 18: 25-32.
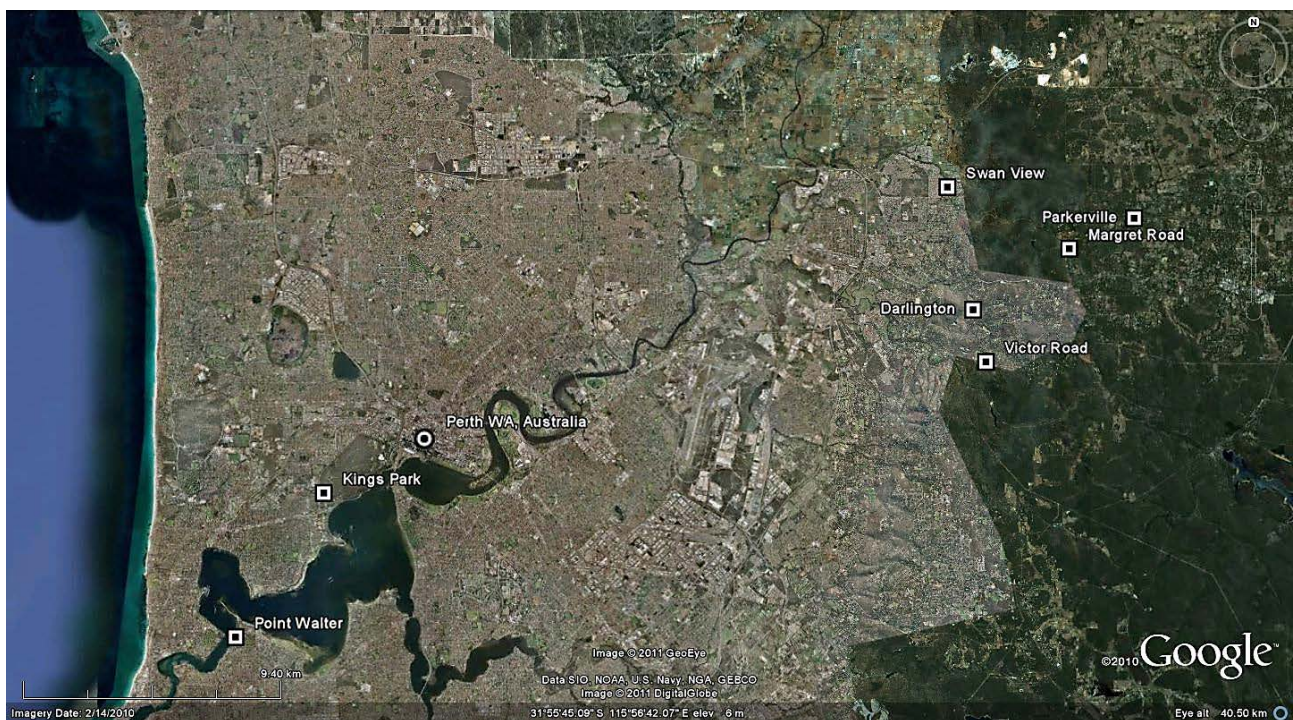

Fig. S1: Locations of sampled areas in South Western Australia (© 2010 Google). Darlington: Nests 1 to 6; Victor Road: Nests 7 to 10; Parkerville: Nests 11 to 13, 20 and 21; Kings Park: Nests 14, 15 and 39 to 45; Margret Road: Nests 16 to 19; Point Walter: Nests 22 to 28; Swan View: Nests 29 to 38, and 46.

Tab. S1: Locations in South Western Australia of the 46 *Myrmecia pavida* colonies studied, with number of individuals collected (C) and genotyped (G) from each nest, and morph.

Colony	Number		Coordinates		Location	Morph
	C	G	Longitude	Latitude		
1	32	16	116.07225	-31.91679	Darlington	1
2	32	32	116.07317	-31.9172	Darlington	1
3	31	31	116.07407	-31.9179	Darlington	1
4	32	16	116.07611	-31.91771	Darlington	1
5	20	16	116.07319	-31.91702	Darlington	1
6	40	16	116.07319	-31.91702	Darlington	1
7	34	16	116.07583	-31.92866	Victor Road	1
8	34	16	116.07597	-31.92751	Victor Road	2
9	40	15	116.076	-31.92724	Victor Road	1
10	33	16	116.07597	-31.92695	Victor Road	1
11	14	13	116.13208	-31.88168	Parkerville	1
12	22	15	116.13271	-31.88053	Parkerville	1
13	38	16	116.13271	-31.88041	Parkerville	1
14	23	16	115.81945	-31.97249	Kings Park	3
15	47	16	115.8199	-31.97201	Kings Park	3
16	16	16	116.10717	-31.89579	Margaret Road	1
17	14	14	116.10706	-31.89612	Margaret Road	1
18	53	16	116.1072	-31.89522	Margaret Road	1
19	30	16	116.10765	-31.89542	Margaret Road	1
20	37	16	116.13987	-31.88105	Parkerville	1
21	42	16	116.13961	-31.88097	Parkerville	1
22	18	18	115.78733	-32.0156	Point Walter	3
23	21	15	115.78646	-32.01371	Point Walter	3
24	22	16	115.7863	-32.01591	Point Walter	3
25	34	14	115.78634	-32.01659	Point Walter	3
26	21	16	115.78628	-32.01649	Point Walter	3
27	33	16	115.78502	-32.01944	Point Walter	3
28	21	16	115.78516	-32.01934	Point Walter	3
29	28	16	116.06044	-31.8715	Swan View	1
30	17	16	116.06049	-31.87158	Swan View	1
31	23	16	116.06026	-31.87164	Swan View	3
32	12	12	116.06026	-31.87154	Swan View	1
33	31	16	116.06197	-31.87158	Swan View	1
34	27	16	116.06199	-31.87158	Swan View	1
35	21	21	116.05964	-31.87236	Swan View	1
36	46	15	116.05896	-31.8721	Swan View	1
37	38	16	116.0588	-31.87187	Swan View	1
38	38	15	116.0588	-31.87184	Swan View	1
39	38	16	115.82682	-31.96809	Kings Park	3
40	31	15	115.82682	-31.96809	Kings Park	3
41	35	15	115.82682	-31.96809	Kings Park	1
42	40	16	115.82682	-31.96809	Kings Park	3
43	32	16	115.82682	-31.96809	Kings Park	3
44	31	16	115.82682	-31.96809	Kings Park	3
45	71	29	115.8255	-31.96957	Kings Park	3
46	25	16	116.06049	-31.87158	Swan View	1

Tab. S2: Characteristics of the five microsatellite loci used in the study of *Myrmecia* populations from South Western Australia and genetic diversity indexes for the three morphs studied (A) and overall (B). Number of individuals (N), Number of populations (N_p), Number of alleles (N_a), frequency of the most common allele (f), Observed heterozygosity (H_o) and Expected Heterozygosity (H_e).

A.	Size (bp)	Morph 1 $N = 491$, $N_p = 29$				Morph 2 $N = 16$, $N_p = 1$				Morph 3 $N = 274$, $N_p = 16$			
		N_a	f	H_o	H_e	N_a	f	H_o	H_e	N_a	f	H_o	H_e
Nmac1	186 - 211	4	0.509	0.680	0.636	2	0.781	0.438	0.353	5	0.477	0.619	0.651
Nmac115	282 - 320	5	0.815	0.319	0.320	2	0.500	1.000	0.516	4	0.829	0.319	0.289
Nmac23	327 - 350	8	0.483	0.694	0.680	2	0.556	1.000	0.513	8	0.438	0.760	0.744
Nmac53	366 - 475	40	0.094	0.908	0.952	3	0.500	1.000	0.643	18	0.361	0.759	0.833
Nmac18	234 - 275	23	0.147	0.916	0.919	3	0.500	1.000	0.613	18	0.259	0.873	0.852
Mean				0.704	0.702			0.888	0.528			0.666	0.674
s.d.				0.243	0.255			0.252	0.114			0.214	0.229
Average gene diversity		0.623 ± 0.372				0.531 ± 0.338				0.630 ± 0.376			

B.	Size (bp)	Overall $N = 491$, $N_p = 29$			
		N_a	f	H_o	H_e
Nmac1	186 - 211	7	0.504	0.65270	0.71809
Nmac115	282 - 320	6	0.813	0.33424	0.32054
Nmac23	327 - 350	10	0.469	0.72301	0.76264
Nmac53	366 - 475	42	0.196	0.85411	0.94382
Nmac18	234 - 275	26	0.194	0.90257	0.91183
Mean				0.69333	0.73138
s.d.				0.22423	0.24881
Average gene diversity		0.638919 ± 0.402397			

Tab. S3: Two level AMOVA results produced as a weighted average over loci with related *F*-statistics calculated by Arlequin 3.5 when testing for different population structures. Analyses tested for structure using either worker genotypes, with nests treated as either one, three or seven populations, or the inferred genotypes of the parent queens or males. Significance was tested over 1023 permutations.

Data based on	Tested structure / Source of variation	% variation	F_{ST}	P
Workers	One population			
	Among nests	12.76	0.12	< 0.001
	Within nests	87.24		
Workers	Three populations (grouped by morph)			
	Among morphs	0.94	0.009	0.038
	Within morphs	99.06		
Workers	Seven populations (grouped by collection sites)			
	Among sites	1.81	0.018	0.019
	Within sites	98.19		
Queens	Seven populations (grouped by collection sites)			
	Among sites	3.73	0.037	0.712
	Within sites	96.27		
Males	Seven populations (grouped by collection sites)			
	Among sites	5.81	0.058	0.019
	Within sites	94.19		