The following supplement accompanies the article

Abundance of humpback whales in Oceania using photo-identification and microsatellite genotyping

Rochelle Constantine[1,*], Jennifer A. Jackson[2,12], Debbie Steel[1,3], C. Scott Baker[1,3], Lyndon Brooks[4], Daniel Burns[4], Phillip Clapham[5], Nan Hauser[6], Bénédicte Madon[7,13], David Mattila[8], Marc Oremus[1,11], Michael Poole[9], Jooke Robbins[10], Kirsten Thompson[1], Claire Garrigue[11]

[1]School of Biological Sciences, University of Auckland, Auckland 1142, New Zealand
[2]Marine Research Limited, Southsea, Portsmouth, Hants, PO4 9RN, UK
[3]Marine Mammal Institute and Department of Fisheries and Wildlife, Hatfield Marine Science Center, Oregon State University, Newport, Oregon 97365, USA
[4]Southern Cross University Marine Ecology Research Centre, Lismore, New South Wales 2480, Australia
[5]Alaska Fisheries Science Center/National Marine Mammal Lab, Seattle, Washington 98115, USA
[6]Cook Islands Whale Research, Avarua, Rarotonga, Cook Islands
[7]Department of Statistics, University of Auckland, Auckland 1142, New Zealand
[8]Hawaiian Islands Humpback Whale National Marine Sanctuary, Kihei, Hawaii 96753, USA
[9]Marine Mammal Research Program, Maharepa, Moorea 98728, French Polynesia
[10]Provincetown Center for Coastal Studies, Provincetown, Massachusetts 02657, USA
[11]Opération Cétacés, BP 98802, Noumea, New Caledonia

[12]*Present address:* British Antarctic Survey, Cambridge CB3 0ET, UK
[13]*Present address:* School of Mathematics and Statistics, University of New South Wales, Sydney, New South Wales 2052, Australia

*Email: r.constantine@auckland.ac.nz

Supplement. Additional information

Description of secondary regions

American Samoa

The research in American Samoa focused on the coastal waters of Tutuila (170°0'W, 14°19'S) in 2003 and 2004 (Robbins & Mattila 2006). Densities of whales frequenting these waters (note that Tutuila is the only island surveyed to date) are similar to those found in New Caledonia, Tonga and French Polynesia, which suggests that American Samoa is an important breeding ground for whales in Oceania. There is interchange between whales from American Samoa and other Oceania regions (Garrigue et al. 2012a).

Samoa

Boat-based surveys were conducted in Samoa (173–170°W and 13°S) in 2001. Samoa is approximately 70 km north northwest of American Samoa and has 9 islands and several seamounts. Research was focused in the waters of one of the main islands, Upolu, with low sighting rates of whales compared with American Samoa (Noad et al. 2006b).

Vanuatu

Research was conducted in the southern islands of Vanuatu (168°E, 17°S) in August 2003, with the majority of whales seen near Tanna (Garrigue et al. 2004). Whales identified in Vanuatu have been re-sighted in New Caledonia and Tonga (Garrigue et al. 2012a).

Niue

Research was conducted in Niue (169°52'W, 19°02'S) in the winter of 2001. Whales were infrequently sighted, but mother–calf pairs are observed and whales have been re-sighted in Tonga (Garrigue et al. 2012a).

Fiji

Fiji (178°E, 18°S) has 2 main islands with many small islands scattered throughout. Data were collected from primarily land-based surveys on Lomaiviti Island in 2002 and 2003 (Gibbs et al. 2006). Sighting rates were very low, especially when compared with data collected from the same site in the 1950s, with no other area in Fiji currently highlighted as a high-density humpback area.

Description of goodness of fit tests carried out using U-CARE

Tests 3.SR and 3G.SR test the hypothesis that there is no difference in the probability of being later re-encountered between 'new' and 'old' individuals encountered on a given occasion i. Tests 3.Sm and 3G.Sm test the hypothesis that there is no difference in the expected time of re-encounter between the 'new' and 'old' individuals encountered on occasion i (in state n) and seen again at least once. Tests 2.CT and M.ITEC test the hypothesis that there is no difference in the probability of being re-encountered (in a different state) on future occasion $i+1$ between those encountered and not encountered at occasion i, conditional on presence at both occasions. Test 2.CL tests the hypothesis that there is no difference in the expected time of next re-encounter between the individuals encountered and not encountered at occasion i, conditional on presence at occasions i and $i+2$. Test M.LTEC tests the hypothesis that there is no difference in the expected time and

state of next re-encounter between the individuals in the same state at occasion i that were not encountered at occasion $i+1$ whether encountered or not encountered at occasion i, conditional on presence at both occasions i and $i+2$. 'Where before, where after' (WBWA) tests the null hypothesis that there is no difference in location between 2 successive encounters in the multi-strata model.

Global tests were also implemented for the multi-strata data set. Test 3G assumes behavioural equivalence of individuals in each stratum, regardless of their capture history. Test M tests the 'equivalence' of recaptured individuals, conditional on whether they are captured at the present occasion. Test JMV tests whether the fully time-dependent Jolly-Move model (t*p*stratum) is a better fit than the standard (single-stratum model), i.e. do animals behave differently in different strata?

LITERATURE CITED

Garrigue C, Dodemont R, Steel D, Baker CS (2004) Organismal and 'gametic' capture-recapture using microsatellite genotyping confirm low abundance and reproductive autonomy of humpback whales on the wintering grounds of New Caledonia. Mar Ecol Prog Ser 274:251–262

Garrigue C, Constantine R, Poole M, Hauser N and others (2012) Movement of individual humpback whales between wintering grounds of Oceania (South Pacific), 1999 to 2004. J Cetacean Res Manag Spec Issue 3:269–274

Gibbs N, Paton DA, Childerhouse S, Clapham PJ (2006) Assessment of the current abundance of humpback whales in the Lomaiviti Island Group of Fiji and a comparison with historical data. Paper SC/A06/HW34. International Whaling Commission, Cambridge

Noad MJ, Paton DA, Gibbs NJ, Childerhouse SJ (2006) A combined visual and acoustic survey of humpback whales and other cetaceans of Samoa. Paper SC/A06/HW28. International Whaling Commission, Cambridge

Robbins J, Mattila DK (2006) Summary of humpback whale research at American Samoa, 2003–2005. Paper SC/58/SH5. International Whaling Commission, Cambridge

Table S1. Thermocycling conditions for all microsatellite loci used to individually identify humpback whales from Oceania and the

Antarctic. The PCR profile listed is for a 96-well format; an extra 5 cycles were added for 384-well format PCRs

Loci	Label	Co-load group	Size range	No. of alleles	$[Mg^{2+}]$ (mM)	PCR profile
464/465	FAM	4	131–149	8	2.5	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 30 s) ×35, 72°C 10 min
Ev1	NED	1	123–129	4	4	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 30 s) ×35, 72°C 10 min
Ev14	VIC	1	125–145	10	2.5	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 40 s) ×35, 72°C 30 min
Ev21	FAM	1	107–119	7	1.5	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 30 s) ×35, 72°C 10 min
Ev37	NED	3	192–230	20	3.5	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 30 s) ×35, 72°C 10 min
Ev94	FAM	3	202–220	9	2.5	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 40 s) ×35, 72°C 30 min
Ev96	FAM	3	147–173	12	1.5	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 40 s) ×35, 72°C 30 min
Ev104	FAM	1	143–153	5	2.5	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 30 s) ×35, 72°C 10 min
GATA 28	NED	2	143–191	12	2.5	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 40 s) ×35, 72°C 30 min
GATA 417	FAM	2	183–282	23	2.5	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 40 s) ×35, 72°C 30 min
GT 211	FAM	2	98–120	12	2.5	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 30 s) ×35, 72°C 10 min
GT 23	VIC	4	101–123	9	2.5	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 40 s) ×35, 72°C 30 min
GT 575	FAM	2	137–177	12	1.5	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 30 s) ×35, 72°C 10 min
rw31	FAM	3	106–122	9	1.5	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 40 s) ×35, 72°C 30 min
rw4-10	VIC	2	192–216	12	3	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 30 s) ×35, 72°C 10 min
rw48	NED	3	108–120	7	2.5	94°C 3 min, (94°C 30 s, 50°C 30 s, 72°C 30 s) ×35, 72°C 10 min

Table S2. Summary of results from U-CARE tests of goodness-of-fit between the data and various Cormack-Jolly-Seber models. Tests that are significant at p < 0.05 are indicated by an asterisk. With the statistic for trap dependence, positive values indicate 'trap shyness' and negative values 'trap happiness'. M: males; F: females

Test type	Genotype SYN		Photo-ID SYN	New Caledonia	Tonga	French Polynesia
	Male	Female				
3.SR						
N(0,1) statistic for transience	4.38*	1.39	2.60*	M: 3.98* F: 1.66	M: 0.90 F: 0	M: 0 F: 0
Log odds ratio statistic for transience	4.20*	1.10	2.50*	M: 3.69* F: 1.32	M: 1.65* F: 0.16	M: 0 F: 0.36
χ^2 overall	21.65*	2.89	13.2*	M: 17.81* F: 3.85	M: 1.61 F: 0	M: 0 F: 0
χ^2 2000	5.78*	0	2.18	M: 4.19* F: 0	M: 0 F: 0	M: 0 F: 0
χ^2 2001	5.17*	1.52	10.80*	M: 5.49* F: 1.77	M: 0 F: 0	M: 0 F: 0
χ^2 2002	1.69	0.22	0	M: 2.03 F: 0.57	M: 0 F: 0	M: 0 F: 0
χ^2 2003	8.07*	1.14	0.19	M: 5.57* F: 1.51	M: 1.61 F: 0	M: 0 F: 0
χ^2 2004	0.95	0		M: 0.52 F: 0	N/A	M: 0 F: 0
G2	21.65*	2.89	11.7*	M: 17.33* F: 3.85	M: 1.61 F: 0	M: 0 F: 0
G2 2000	5.78*	0	2.18	M: 4.19* F: 0	M: 0 F: 0	M: 0 F: 0
G2 2001	5.17*	1.52	9.28*	M: 5.49* F: 1.77	M: 0 F: 0	M: 0 F: 0

G2 2002	1.69	0.22	0	M: 2.03 F: 0.57	M: 0 F: 0	M: 0 F: 0
G2 2003	8.07*	1.14	0.18	M: 5.10* F: 1.51	M: 1.61 F: 0	M: 0 F: 0
G2 2004	0.95	0		M: 0.52 F: 0	N/A	M: 0 F: 0

3.Sm

χ^2 overall	2.24	0.44	0.70	M: 1.51 F: 0.66	M: 0 F: 0	N/A
χ^2 2000	0.36	0.36	0	M: 0.37 F: 0	M: 0 F: 0	M: 0 F: 0
χ^2 2001	1.25	1.25	0.14	M: 0.36 F: 0.66	M: 0 F: 0	M: 0 F: 0
χ^2 2002	0.63	0.63	0.56	M: 0 F: 0	M: 0 F: 0	M: 0 F: 0
χ^2 2003	0	0		M: 0.79 F: 0	N/A	M: 0 F: 0
G2 overall	2.24	0.44	0.70	M: 1.51 F: 0.66	M: 0 F: 0	N/A
G2 2000	0	0	0	M: 0.37 F: 0	M: 0 F: 0	M: 0 F: 0
G2 2001	0.44	0.44	0.14	M: 0.36 F: 0.66	M: 0 F: 0	M: 0 F: 0
G2 2002	0	0	0.56	M: 0 F: 0	M: 0 F: 0	M: 0 F: 0
G2 2003	0	0		M: 0.79 F: 0	N/A	M: 0 F: 0

2.CT

N(0,1) statistic for trap dependence	1.05	2.84*	0.04	M: 0.21 F: 1.85	M: 0 F: 0	M: 0 F: 0
Log odds ratio statistic for trap dependence	1.30	2.69*	–0.09	M: 0.21 F: 1.80	M: 0.48 F: 0.61	M:-0.95 F: 1.34
χ^2 overall	4.13	9.10	2.91	M: 1.58 F: 5.03	M: 0 F: 0	M: 0 F: 0
χ^2 2000	1.46	0.32	1.22	M: 0 F: 0	M: 0 F: 0	M: 0 F: 0
χ^2 2001	0.63	2.97	0.06	M: 0.42 F: 0,56	M: 0 F: 0	M: 0 F: 0

χ^2 2002	0.08	3.47	1.63	M: 0 F: 2.97	M: 0 F: 0	M: 0 F: 0
χ^2 2003	1.96	2.33	N/A	M: 1.16 F: 1.50	N/A	M: 0 F: 0
G2	4.27	9.38	2.99	M: 1.58 F: 5.08	M: 0 F: 0	M: 0 F: 0
G2 2000	1.46	0.32	1.22	M: 0 F: 0	M: 0 F: 0	M: 0 F: 0
G2 2001	0.65	3.01	0.06	M: 0.42 F: 0.56	M: 0 F: 0	M: 0 F: 0
G2 2002	0.08	3.54	1.71	M: 0 F: 2.97	M: 0 F: 0	M: 0 F: 0
G2 2003	2.09	2.51	N/A	M: 1.16 F: 1.55	N/A	M: 0 F: 0
2.CL						
χ^2	0.66	4.68	0.53	M: 0.19 F: 0.22	M: 0.54 F: 0	N/A
G2	0.66	4.95	0.53	M: 0.19 F: 0.22	M: 0.54 F: 0	N/A

Table S3. Jolly-Move goodness-of-fit tests (and variants) for multi-strata models (New Caledonia, Tonga/Cook Islands and French Polynesia). Asterisks indicate significance at $p < 0.05$.

	SYN by sex – males		SYN by sex – females		ALL by sex – males		ALL by sex – females	
	Statistic	DF	Statistic	DF	Statistic	DF	Statistic	DF
WBWA	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3G.SR	17.44*	9	3.85	9	17.58*	9	3.85	9
3G.Sm	1.20	5	0	4	1.20	5	0	4
M.ITEC	1.67 (χ^2)	3	3.35 (χ^2)	3	2.45	4	3.20	3
	2.04 (G2)	3	3.63 (G2)	3	3.28	4	3.50	3
M.LTEC	1.89 (χ^2)	3.43			2.16	2	3.43	2
	2.58 (G2)	3.49 (G2)						
Global tests								
3G	18.64	14	3.85	13	18.78	14	3.85	13
M	3.56	5	6.78	5	4.61	6	6.63	5
JMV	22.20	19	10.63	18	23.38	20	10.48	18

Table S4. Summary of the best AIC-supported Cormack-Jolly-Seber models applied to the genotype SYN and ALL (by sex) data sets. Models are described in terms of survival (ϕ) and capture probability (p). ΔAIC is the difference in AIC value between each model and the best fitting model, whereas AIC$_c$ weight is the weighting given to that model during model averaging. #P is the number of parameters used in the model. ϕm1 refers to a time since marking (TSM) model of survival, where m1 is estimated from the initial capture period of all male cohorts (or fully time dependent, varying across all cohorts as m1t), and the subsequent ϕ term represents survival estimated from all other cohorts (male and female). Capture probability 'sexc' denotes use of a coefficient to estimate female capture probabilities as a logit-transformed function of male capture probabilities. The most parameter-rich, fully identifiable model (**) was chosen in each case for the estimation of median c-hat

Model	# P	SYN AIC$_c$	ΔAIC$_c$	AIC$_c$ weight	Model likelihood	Deviance	ALL AIC$_c$	ΔAIC$_c$	AIC$_c$ weight	Model likelihood	Deviance
ϕ(m1) ϕ(.) p(t*sexc)	9	916	0	0.25	1.00	103	955	0.70	0.21	0.71	103
ϕ(m1) ϕ(sex) p(t*sex) p1=7	13	917	1.63	0.11	0.44	98	958	3.46	0.06	0.18	98
ϕ(m1) ϕ(.) p(t*sex) p1=7	12	917	1.63	0.11	0.44	98	956	1.60	0.13	0.45	98
ϕ(mt1-4,5-6) ϕ(.) p(t*sexc)	13	917	1.68	0.11	0.43	99	959	4.83	0.03	0.09	99
ϕ(m1) ϕ(sex) p(t*sexc)	10	918	2.04	0.09	0.36	103	957	2.45	0.09	0.29	103
ϕ(m1-2,3-4,5-6t (clustered into 2-yr	12	918	2.09	0.09	0.35	101	958	4.21	0.04	0.12	101

groups)) φ(sex) p(t*sexc)

φ(m1-2,3-4,5-6t (clustered into 2-yr groups)) φ(.) p(t*sexc)	11	918	2.13	0.09	0.34	101	957	2.60	0.08	0.27	101
φ(m1) φ(.) p(t*sex) female p1=p2	13	918	2.28	0.08	0.32	97	**954	0	0.29	1.00	97
φ(mt1,2,3,4) φ(.) p(t*sexc)	9	919	3.75	0.04	0.15	99	959	4.75	0.03	0.09	99
**φ(mt1-4,5-6) φ(sex) p(t*sexc)	8	921	5.77	0.02	0.06	98	959	5.24	0.02	0.07	96
φ(m1t) φ(sex) p(t)	7	925	9.12	0	0.01	112	959	4.66	0.03	0.10	109
φ(m1) φ(.) p(t)	7	928	11.88	0	0	117	964	10.12	0	0.01	115
φ(.) p(t)	8	932	16.61	0	0	124	970	16.11	0	0	123
φ(.) p(t) p1=7	9	930	14.57	0	0	124	968	14.07	0	0	123
φ(sex) p(t) p1=7	8	932	16.12	0	0	123	970	15.51	0	0	122
φ(sex) p(t)	7	936	20.21	0	0	123	972	17.54	0	0	122
φ(sex) p(t*sexc)	8	938	22.18	0	0	123	972	17.46	0	0	122
φ(.) p(t*sexc)	8	934	18.45	0	0	124	974	19.48	0	0	122

Table S5. Numbers of individuals captured and recaptured by year and total numbers of

recaptures across all survey regions (ALL). (A) Genotype database summary; (B) photo-ID

data set summary

A. Genotypes

Year	1999	2000	2001	2002	2003	2004	2005
Individuals captured	50	115	182	130	231	95	162
Cumulative individuals captured	50	162	333	446	640	719	843

Year of initial capture	1999	2000	2001	2002	2003	2004	2005
1999	X	3	7	3	6	2	2
2000		X	6	5	11	3	6
2001			X	9	20	7	10
2002				X	8	2	12
2003					X	4	17
2004						X	5
2005							X

Total recaptures	1	2	3				Total
No. of individuals	99	14	4				117

B. Fluke photographs

Year	1999	2000	2001	2002	2003	2004
Individuals captured	108	124	135	115	171	128
Cumulative individuals captured	108	226	341	437	570	660

Year of initial capture	1999	2000	2001	2002	2003	2004
1999	X	6	13	5	8	8
2000		X	9	8	13	10
2001			X	9	13	13
2002				X	11	3
2003					X	13
2004						X
Total recaptures	1	2	3			Total
No. of individuals	82	18	1			101

Table S6. Total genotype captures and recaptures across synoptic regions for males and females

Males	1999	2000	2001	2002	2003	2004	2005
Individuals captured	25	72	117	84	129	41	88
Cumulative individuals captured	25	94	204	278	386	422	487

				Year of recapture			
Year of initial capture	1999	2000	2001	2002	2003	2004	2005
1999	X	3	4	0	3	0	1
2000		X	5	3	8	2	6
2001			X	7	12	3	7
2002				X	4	0	6
2003					X	1	11
2004						X	3
2005							X

Females	1999	2000	2001	2002	2003	2004	2005
Individuals captured	25	43	62	46	85	38	65
Cumulative individuals captured	25	68	126	165	235	265	317

	Year of recapture						
Year of initial capture	1999	2000	2001	2002	2003	2004	2005
1999	X	0	3	3	3	2	1
2000		X	1	2	3	1	0
2001			X	2	8	3	3
2002				X	3	2	5
2003					X	1	5
2004						X	2
2005							X

Table S7. Summary of the best AIC-supported POPAN open population models applied to the genotype SYN and ALL data sets. Models are described in terms of survival (ϕ), capture probability (p) and entry probability (PENT). ΔAIC is the difference in AIC value between each model and the best-fitting model, whereas AIC_c weight is the weighting given to that model during model averaging. #P is the number of parameters used in the model

Model	# P	SYN				ALL			
		AIC_c	ΔAIC	AIC_c weight	Model likelihood	AICc	ΔAIC	AIC_c weight	Model likelihood
ϕ(.) p(t), p1=p7, PENT(.) N(sex)	10	1007	0.00	0.44	1.00	1049	0.00	0.40	1.00
ϕ(sex) p(t), p1=p7, PENT(.) N(sex)	11	1009	1.35	0.22	0.51	1051	1.63	0.18	0.44
ϕ(.) p(t * sexc), p1=p7, PENT(.) N(sex)	11	1009	1.87	0.17	0.39	1050	1.35	0.20	0.51
ϕ(sex) p(t * sexc), p1=p7, PENT(.) N(sex)	12	1011	3.40	0.08	0.18	1052	3.35	0.07	0.19
ϕ(.) p(t), p1=p7, PENT(t) N(sex)	14	1012	4.56	0.04	0.10	1054	4.61	0.04	0.10
ϕ(sex) p(t), p1=p7, PENT(t) N(sex)	15	1014	6.28	0.02	0.04	1053	3.89	0.06	0.14
ϕ(.) p(t * sex coefficient), p1=p7, PENT(t) N(sex)	15	1014	6.54	0.02	0.04	1054	4.61	0.04	0.10
ϕ(sex) p(t * sex coefficient), p1=p7, PENT(t) N(sex)	16	1016	8.31	0.01	0.02	1056	7.00	0.01	0.03

Table S8. POPAN annual estimates of population abundance, derived from the genotype data sets using the Delta method of variance estimation in the program MARK. Data obtained by model averaging of p(t) models are shown in Table S7. Estimates from the initial and final years of data collection have been removed as they are non-interpretable. N: population estimate; CV: coefficient of variation

Year	ALL		SYN		ALL Males		SYN Males		SYN (no 2004) males	
	N	CV	N	CV	N	CV	N	CV	N	CV
2000	1788	0.55	1793	0.56	973	0.27	959	0.25	843	0.33
2001	2444	0.20	2241	0.18	1254	0.22	1201	0.18	1124	0.27
2002	2286	0.22	2289	0.22	1445	0.18	1393	0.16	1300	0.22
2003	2399	0.21	2298	0.21	1640	0.18	1593	0.17	1471	0.22
2004	2797	0.20	2711	0.21	1856	0.20	1798	0.19	N/A	N/A

Table S9. Estimates of apparent survival (ϕ) and apparent population growth (λ) estimated for Oceania genotype and photo-ID ALL data sets. Capture probabilities over time (p_t) for each data set were estimated from the best-fitting AIC_c-weighted Pradel model in MARK. Standard errors are given in parentheses. Abundance was derived by dividing the number of animals captured by the estimated capture probability. Confidence intervals (CI) were derived from the 95% CIs of each capture probability

	Genotype ALL (overall)		Photo-ID ALL	
ϕ	0.94		0.96	
SE (CI)	0.07 (0.59–1.00)		0.07 (0.38–1.00)	
λ	1.04		1.00	
SE (CI)	0.07 (0.91–1.19)		0.07 (0.87–1.16)	
Year	p_t	N_t (CI)	p_t	N_t (CI)
1999	0.023 (0.007)	2157 (1188–3952)	0.062 (0.017)	1732 (1015–3018)
2000	0.051 (0.012)	2240 (1407–3612)	0.071 (0.016)	1737 (1122–2732)
2001	0.077 (0.015)	2352 (1609–3484)	0.078 (0.015)	1741 (1201–2556)
2002	0.054 (0.010)	2416 (1689–3483)	0.066 (0.012)	1746 (1215–2535)
2003	0.092 (0.017)	2510 (1770–3604)	0.098 (0.020)	1751 (1193–2613)
2004	0.036 (0.008)	2607 (1687–4059)	0.073 (0.018)	1756 (1095–2867)
2005	0.059 (0.015)	2724 (1659–4545)		

Table S10. Summary of the best AIC-supported Pradel open population models applied to the genotype SYN (by sex), ALL (by sex) and SYN no 2004 (by sex) data sets. Models are described in terms of survival (ϕ), capture probability (p) and growth (λ). The best-fitting AIC models are shown in bold for each data set. ΔAIC is the difference in AIC value between each model and the best-fitting model, and Wt is the weighting given to that model during model averaging. L is the model likelihood. Correction for over-dispersion was applied to the SYN no 2004 data set only

Model	#P	SYN				ALL				SYN no 2004[a]			
		AICc	ΔAIC	Wt	L	AICc	ΔAIC	Wt	L	AICc	ΔAIC	Wt	L
ϕ(.) p(t) λ(.)	**9**	**3921**	**0**	**0.33**	**1.00**	**4101**	**0**	**0.33**	**1.00**	**2935**	**0**	**0.36**	**1.00**
ϕ(.) p(t) λ(sex)	10	3923	1.25	0.18	0.54	4103	1.86	0.13	0.40	2937	1.67	0.16	0.43
ϕ(.) p(t*sexc) λ(.)	10	3923	1.93	0.12	0.38	4103	1.41	0.16	0.49	2937	2.01	0.13	0.37
ϕ(sex) p(t) λ(.)	10	3923	1.95	0.12	0.38	4103	1.77	0.14	0.41	2937	1.91	0.14	0.38
ϕ(sex) p(t) λ(sex)	11	3924	2.99	0.07	0.22	4105	3.48	0.06	0.18	2939	3.68	0.06	0.16
ϕ(.) p(t*sexc) λ(sex)	11	3924	3.00	0.07	0.22	4104	3.08	0.07	0.21	2939	3.72	0.06	0.16
ϕ(sex) p(t*sexc) λ(.)	11	3925	3.98	0.04	0.14	4105	3.37	0.06	0.19	2939	3.90	0.05	0.14
ϕ(sex) p(t*sexc) λ(sex)	12	3926	5.02	0.03	0.08	4106	5.08	0.03	0.08	2941	5.67	0.02	0.06
ϕ(.) p(t*sex) λ(.)	16	3927	5.88	0.02	0.05	4108	6.88	0.01	0.03	2943	7.17	0.01	0.03
ϕ(sex) p(t*sex) λ(.)	17	3929	7.92	0.01	0.02	4110	8.92	0	0.01	2944	9.13	0	0.01
ϕ(.) p(t*sex) λ(sex)	17	3929	7.96	0.01	0.02	4110	8.91	0	0.01	2945	9.16	0	0.01
ϕ(sex) p(t*sex) λ(sex)	18	3931	9.97	0	0.01	4112	10.90	0	0	2947	11.20	0	0.01

[a]Number of parameters for this data set all (#P-1)