Electronic supplementary material to accompany submission

Marker variation

All loci used in the study were polymorphic, with the number of alleles varying between four and 34 and with observed heterozygosity ranging from 0.37 to 0.87 (Table 1). No locus combinations exhibited significant linkage disequilibrium after correcting for multiple tests with sequential Bonferroni. Three loci (FE8, FE49, FE37) did not conform to Hardy-Weinberg proportions after applying sequential Bonferroni corrections. Analysis of null allele frequencies using MICRO-CHECKER revealed low (0.004 to 0.145) null allele frequency estimates for nearly all loci (except FE19 and FE51 where no nulls were calculated to occur) and it is possible that these deviations simply reflect population structuring across the 4km site (significant population sub-structuring was detected within the Mull site: $Fst = 0.15$; $p < 0.0001$). All loci were therefore included for further analyses. Any bias due to the non-detection of alleles would be the same for all colonies.

Table 1 Characteristics and amplification conditions of loci examined for Mull samples (see text for further information). "Multi" indicates that these loci were simultaneously co-amplified. * indicates these loci were amplified for all samples at all sites.

Locus	Annealing temp (# cycles)	5' dye label	number of alleles	Observed Heterozygosity
FE7*	57° (32) Multi	FAM	16	0.78
FE8*	60° (34)	FAM	17	0.85
FE11*	58° (30)	TET	11	0.73
FE17*	50° (35)	HEX	14	0.83
FE19*	57° (32) Multi	FAM	5	0.61
FE21	50° (35)	HEX	6	0.56
FE37*	57° (32) Multi	TET	7	0.72
FE38*	57° (32) Multi	HEX	24	0.87
FE42	55° (28)	TET	4	0.51
FE49*	52° (34)	FAM	34	0.81
FE51*	57° (32) Multi	FAM	9	0.77
FL12	58° (30)	TET	6	0.37