Hi Joe,

Here's all the info I think you might need for the paper.

There are 18 loci on the attached spreadsheet. I have included ZcCgDh1.8 here, but this was left out of the analysis in the paper I'm about to resubmit, as it's predominantly only one or two alleles and one of the reviewers (rightly) raised concerns about it's inclusion. It didn't change the population-wide statistical inference at all, but I'll leave it up to you whether you want to include it in your work or not.

The references for the microsatellite loci and the pop stats data (excluding the locus mentioned above) are in the table attached and the table legend pasted below. Note the info I'm pasting below references 1205 individuals, while there are 1300-ish in the spreadsheet, this is because I left pre-2001 samples out of my analyses (for various, non-science-related reasons!). The table is from the paper I'm about to resubmit (hopefully early next week!). I have also attached a map of sampling locations, again a figure from the paper I'm resubmitting. Below I've pasted sampling info (from the paper.....!) and also the tests of population differentiation I performed (there was no structure). I'm guessing that your paper won't be ready to submit until the one I'm resubmitting is in press? I assume that as long as yours isn't published before the reviewers re-read mine, we're all good!! I'll let you know if there are any hold-ups but I'm sure we'll be fine.

I think that's everything, let me know if I've forgotten anything or if there's anything else I can do!

Best wishes,

Amy

Sampling

The New Zealand sea lion sample used here includes 1205 individual animals collected between the 2000/2001 and 2006/2007 Austral summer breeding seasons (Table 1). All NZSL samples in this study were collected from sites within the Auckland Islands group (Figure 1, 50°42′S 166°5′E). The majority of NZSL samples were collected from Sandy Bay on Enderby Island, which is the most intensively monitored site. A proportion of pup samples were also collected during the 2003/2004 breeding season from Dundas Island (n = 42), South East Point on Enderby Island (n = 32) and Figure of 8 Island (n = 24) in the Auckland Islands group (Figure 1). Pups were predominantly sampled from marked females in each year of the study.

Population differentiation

Live pups from the 2003/2004 breeding season were used to test for population differentiation, from four different breeding beaches: Sandy Bay, Enderby Island n = 77; Dundas Island, n = 42; Figure of 8 Island, n = 24 and South East Point, Enderby Island n = 32. To investigate population substructuring, the true K (number of populations) was inferred from the data. The data was subjected to a burnin period of 5000 and 50000 Markov chain Monte Carlo (MCMC) repeats, and this was performed 20 times for each of 6 hypothesised K = 1 to K = 6. When K is approaching its true value, the log likelihood for each K (L(K)) plateaus, and has a high variance between runs. The most likely K was inferred using the delta K method (Evanno et al., 2005), Supplementary Table 4). While delta K cannot evaluate K=1, the mean Ln P(D) (probability of the data) suggests that K=1. In addition, for K>1, the high variance in mean Ln P(D) for all other values of K except 1 imply that there is no structure in the dataset (Hubisz et al., 2009).

Pairwise comparisons of the fixation index FST (Weir and Cockerham, 1984) found no evidence of structuring based on microsatellite genotype data between the different breeding sites (Supplementary Table 5, (Wright, 1978)), again indicating the lack of substructure in the NZSL population.

Figure and table legends:

Figure 1 – Breeding distribution of the NZSL. There are three recognised breeding areas: two in the Auckland Islands, one on Campbell Island Motu Ihupuku and also a colony on the Otago Peninsula (Chilvers and Wilkinson, 2008). Sampling locations used in this study are Sandy Bay on Enderby Island, Figure of Eight Island, South East Point, and Dundas Island. Figure from Robertson and Chilvers (2011).

Table 2 - Microsatellite variation using samples spanning seven breeding seasons (2000/2001 to 2006/07). N, number of NZSL genotyped at each locus; k, number of alleles; HO, observed heterozygosity; HE, expected heterozygosity; HWE, Bonferroni-corrected p-value of significance of Hardy Weinberg equilibrium. References: 1.(Allen et al., 1995), 2.(Gelatt et al., 2001), 3.(Davis et al., 2002), 4.(Hoelzel et al., 1999), 5.(Buchanan et al., 1998), 6.(Goodman, 1997), 7.(Coltman et al., 1996), 8.(Hernandez-Velazquez et al., 2005), 9.(Wolf et al., 2006).