A note on a mother-foetus pair and alleged father match in the Atlantic fin whale (*Balaenoptera physalus*) off Iceland

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ABSTRACT

The North Atlantic fin whale (*Balaenoptera physalus*) undertakes long-distance annual migration between high-latitude summer feeding locations and low-latitude winter mating locations, like most of the baleen whales. By statistically comparing genotype profiles of mother-foetus pairs (n = 23) to that of the potential alleged father (n = 139) captured at the same feeding location in Iceland, we found a matching pairing of a mother-foetus captured in 2009 and a father captured in 2010. To our knowledge, the present study is the first one to detect a mother-foetus pair matching with an alleged father, caught at exactly the same feeding area one year later.

KEYWORDS: FIN WHALE; ATLANTIC OCEAN; GENETICS; MIGRATION; FEEDING GROUNDS; PATERNITY

INTRODUCTION

Determining lineage and relationships with genetic markers such as microsatellite loci promises to shed light on the patterns of dispersal of marine organisms (Buston *et al.*, 2007; Hedgecock, 2010; Jones *et al.*, 2010). During the last decade, microsatellite loci have proved useful in addressing key empirical questions related to behavioural ecology, biology and mating systems, all of which are relevant in that they are issues that are required in order to understand the dynamics of a species (Bentzen *et al.*, 2001; Fournier *et al.*, 2008; Hedgecock, 2010; Seddon *et al.*, 2005). Since 2009, Iceland has maintained an individual-based DNA registry for the fin whale, *Balaenoptera physalus* (each individual was screened for 15 microsatellite loci and mtDNA). By statistically comparing genotype profiles of mother-foetus pairs (n = 23) to that of the potential fathers (n = 139) captured at the same feeding location, we found a matching pair of a mother-foetus captured in 2009 and a father captured in 2010. Here we report this finding and discuss the results in terms of the migration pattern of the species and population estimates.

MATERIALS AND METHODS

Samples and genotyping

The Icelandic DNA register for the fin whale comprises of 267 genetic profiles collected between and during the years 2009 and 2010, and has been obtained for 15 microsatellite loci (EV001, EV037, GATA028, GATA053, GATA098, GATA417, GT011, GT023, GT195, GT211, GT271, GT310, GT575, TAA023 and GGAA520; see Pampoulie *et al.*, 2008 for the microsatellite characteristics), the control region of mtDNA and a sex-marker (Bérubé and Palsbøll, 1996). From the 267 individual samples genotyped, a total of 23 females carried a foetus for which a genetic sample was also obtained (4 in 2009 and 19 in 2010). A total of 139 males were collected (67 subjects in 2009 and 72 in 2010).

DNA isolation and amplification were performed according to Pampoulie *et al.* (2011).

Statistical analyses

The software WHICHPARENTS (available at *http://www-bml.ucdavis.edu/whichparents.html*) was used to assess potential crosses among mother-foetus and alleged father, using 0–4 potential misses. WHICHPARENTS is an exclusion-based program which presents a moderate level of correction for null alleles, genotyping errors and mutation (handled by misses).

Additional analyses of the possible crosses were performed in the software PATCAN v1.2 (available on request to J.A. Riancho; Riancho and Zarrabeitia, 2003) to assess the paternity probability of the potential father. The standard results reveal the likelihoods and probability of the alleged father being the true father, versus the alternative hypothesis of the true father being an unrelated individual. The software also allows for inclusion of mutation rate at exclusive loci. Paternity tests were also performed using CERVUS 3.0.3 (Kalinowski *et al.*, 2007) for the 23 foetuses collected and the 139 potential fathers genotyped. In the simulation of paternity analyses, the proportion of loci typed was 0.95 for the full set of loci and the simulated genotyping error rate was set at 0.01. Critical values of Delta were assessed for 80 and 95% confidence levels based on simulation of 100,000 offspring.

RESULTS

The exclusion program WHICHPARENTS revealed the presence of one possible cross between a mother-foetus pair and an alleged father when run with a 0 miss procedure, i.e. a 100% match (Table 1).

The analysis of this possible family, involving the mother F09-091, her foetus (F09-091F) and the alleged father (F10-

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Table 1

Allele sizes at each microsatellite loci of the mother-foetus pair number F09-091 and of the alleged father (F10-100). The alleged father was collected in 2010 while the mother-foetus pair was collected in 2009.

Locus	Mother	Foetus	Alleged father
EV1	157/163	159/163	159/171
EV37	193/193	193/193	193/193
GT011	127/131	125/131	117/125
GT023	127/129	125/129	125/129
GT195	161/175	161/169	169/173
GT211	120/120	116/120	116/116
GT271	114/118	114/118	118/118
GT310	106/112	106/112	112/112
GT575	154/156	154/154	152/154
GATA028	199/219	199/215	215/227
GATA053	262/262	262/270	258/270
GATA098	100/100	096/100	096/108
GATA417	269/277	269/269	269/285
GGAA520	201/223	207/223	207/219
TAA023	086/086	086/086	086/086

Table 2

Bayesian analysis of the mother-foetus pair F09-091 and the alleged father F10-100 by the software PATCAN (Riancho and Zarrabeitia, 2003). The values represent the likelihood and the probability associated with the hypothesis that the alleged father is the true biological father versus the competing hypothesis that the father is an unrelated animal. PI depicts the paternity index.

Prior probability (%)	Prior odds	PI	Posterior odds	Posterior probability
0.1	0.001001	$>10^6$	2.6×10^8	100
1	0.010101	$>10^6$	2.6×10^9	100
10	0.111111	$>10^6$	2.6×10^{11}	100
50	1	$>10^6$	2.6×10^{12}	100
70	2.333333	$>10^6$	6.2×10^{12}	100
90	9	$>10^6$	2.4×10^{13}	100
95	19	$>10^6$	5.1×10^{13}	100

100), using the software PATCAN revealed a high likelihood and probability (cumulative $Pw = 1$; cumulative $PI > 2.7 \times 10^{12}$) associated with the hypothesis that the alleged father was the true biological father of the foetus F09-091F (Table 2). The paternity analysis performed with the program CERVUS predicted a very low success rate of paternity assignment (Table 3) but slightly higher than the simulated data (not shown), at least for the father alone set-up.

DISCUSSION

The fin whale (*Balaenoptera physalus*) is believed to undertake long-distance migration between high-latitude feeding areas in the summer and low-latitude mating locations in the winter, like most of the baleen whales; in spite of this, little is known about the actual migration pattern and dynamic of this species. Although several genetic studies have been performed over the last few decades, there is no consensus upon the potential numbers of breeding grounds or on the migration pattern of the species (IWC, 2009).

Here, despite the low number of available samples, searching within the Icelandic DNA registry for a potential match between a mother-foetus pair and an alleged father enabled us to find a highly significant match between a mother-foetus pair caught in 2009 and an alleged father caught in 2010.

Although this match might be incidental and be due to the low number of loci employed, at least two hypotheses can still be considered to explain the observed trio-match:

(1) The detected mating pair occurring at the same mating location exhibited a similar migration habit during the winter. Sighting surveys revealed that fin whales are most commonly seen alone or in ‘pairs’ (Víkingsson *et al.*, 2009) and relatedness analyses tended to confirm that related individuals (Parent-offspring and half-sibling) more commonly occur at the same feeding location (Skaug *et al.*, 2009).

(2) The detected mating pair may originally belong to two different populations (or mating locations) among which gene flow may not be restricted, which might indicate that individual fin whale from different mating location may roam across the North Atlantic during the winter feeding migration as was suggested by a previous genetic study (Pampoulie *et al.*, 2008).

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Table 3

Number of paternity assignment among the 23 foetus with known mother calculated in CERVUS.

Confidence level of assignment	Father alone			Father given known mother		
	Critical delta	Observed assignment	Expected assignment	Critical delta	Observed assignment	Expected assignment
95%	3.92	1 (5%)	3 (15%)	0	2 (9%)	3 (16%)
80%	0.93	4 (18%)	4 (19%)	0	2 (9%)	3(16%)
Unassigned	–	18 (82%)	18 (81%)	–	20 (91%)	19 (84%)
Total	–	22 (100%)	22 (100%)	–	22 (100%)	22 (100%)

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Date received: January 2012
Date accepted: February 2012