

# Genetic diversity and structure of fin whales (*Balaenoptera physalus*) in north-western of the Mediterranean Sea

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## Introduction

Because some elements of the fin whale (*Balaenoptera physalus*) ecology in the Mediterranean Sea remain still ignored, WWF-France, the Nicolas Hulot Foundation and the Paul Ricard Oceanographic Institute launched "Objectif/Cap Cétacés": a multi-field program on this species. The aim of this programme consisted in characterization the health of the population and the behavioural ecology of the animal in the liguro-Provençal Mediterranean Sea.

## Material and methods

- Several missions at sea from May to October in 2006, 2007, 2008, 2009 and 2010 totalized 11024 km in effort, 426 sightings of fin whales and 150 biopsies. Samples of three stranding animals from Mediterranean Sea and 12 stranding animals from Atlantic Sea have also been analyzed.
- For sex determination the genes ZF-X and ZF-Y were amplified as described by Bérubé and Palsbøll (1996), and for genetic identification (NJ and "Parenté"), 11 microsatellite markers were highlighted based on Bérubé *et al.*, 1999 and Palsbøll *et al.*, 1997.
- Analyses of Neighbor-Joining (NJ) were carried out with the Darwin software (<http://darwin.cirad.fr/darwin/Home.php>) and the kinship relations with the "Parenté" software (<http://www-leca.ujf-grenoble.fr/logiciels.htm>)
- The samples present capture/recapture of some individuals during the same year or between two years and as well as a mother and her progeny. Those data made it possible to gauge and validate each step of the genetic or contaminant analysis.



## Results

Fig.1 : positions of fin whales observed during missions from 2006 to 2010

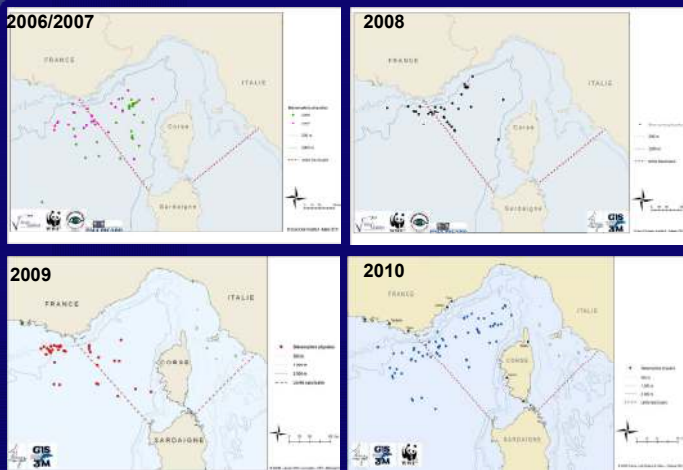


Table 1 : group size, in and out conditions of line transect for five years

	2006	2007	2008	2009	2010
Nb of observations	37	48	38	40	65
Nb of individuals	103	69	49	65	140
Group size	2,8	1,4	1,2	1,6	2,1
Nb of Km	1481	2089	2101	2390	2963
Relative abundance	7 10 <sup>-2</sup> ind.km <sup>-1</sup>	3,3 10 <sup>-2</sup> ind.km <sup>-1</sup>	2,3 10 <sup>-2</sup> ind.km <sup>-1</sup>	2,7 10 <sup>-2</sup> ind.km <sup>-1</sup>	4,7 10 <sup>-2</sup> ind.km <sup>-1</sup>

**2006** : fin whales were in bigger groups (tab.1), localized in the central zone (fig.1) with many social interactions as pursuit, rolling, chasing, breaching. The sex ratio is nearly in balance (tab. 2).

**2007** : fin whales were less numerous, dispersed in small groups (tab.1), never seen in interactions, more often searching for food actively or stationary, performing longer dives and very discrete in surfacing. Le sex ratio is largely with the advantage of the female (tab.2).

**2008** : fin whales were less numerous, most of the time alone (tab.1), mainly traveling, and the sex ratio is in balance (tab.2).

**2009** : fin whales were normally numerous (tab.1), groups were seen more in the west zone (fig.1), and the sex ratio is in balance (tab.2).

**2010** : fin whales were in bigger groups (tab.1), with some social interactions as pursuit and breaching. The sex ratio is nearly in balance (tab. 2).

Table 2 : sex ratio for five years

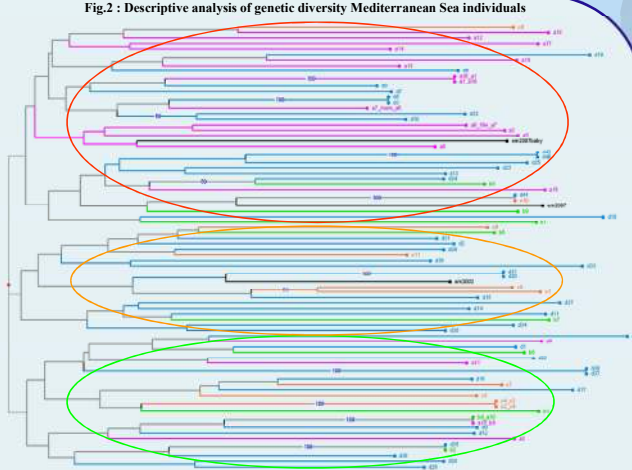
	2006	2007	2008	2009	2010
N	18	9	10	39	74
Female	45 %	78 %	50 %	51%	47%
Male	55 %	22 %	50 %	49%	53%

Fig.2 : Descriptive analysis of genetic diversity Mediterranean Sea individuals

The NJ method builds a tree by connecting the closest operational taxonomic units by nodes which represent a common ancestor, based on the integration of the allelic data of 11 microsats of the individuals of 2006 to 2010 and 3 stranded animals (em, black).

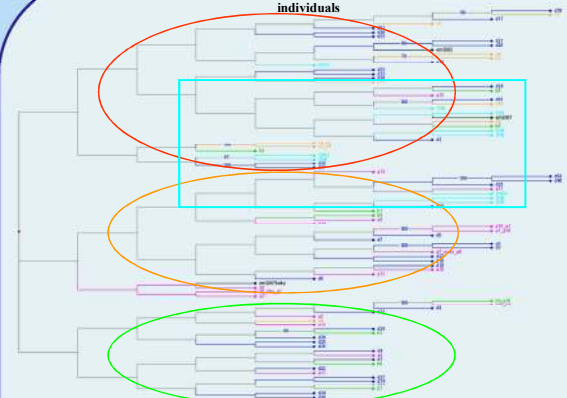
The tree (Fig.2) shows a clear structure in three groups, whatever the year of the biopsy. There is a homogeneous distribution of the males and females between the groups.

On a total of 86 individuals sampled in 2006 to 2009, four of them were met at least twice during the same year (A1 in June and A16 in October) or from one year to another (a10/b4, b2/d35; c10/d41).



The calculation of kinship relations, which integrates the allelic frequencies and their force, gives a probability of relation "mother/daughter" of 98% for A7/A6, 97% for C1/C8 and 82% for C7/D17. Two other relations are also highlighted, "father of" with 95% for D12/D9 and 75% for D7/A3.

Fig.3 : Descriptive analysis of genetic diversity between Mediterranean and Atlantic Sea individuals



Allelic data of 6 microsats for the stranded animals from Atlantic Sea were integrated with those Mediterranean Sea in analyses of Neighbor-Joining (NJ). The structuring of the resulting tree (Fig. 3) is clear and always highlights a classification of the individuals in three groups. Atlantic Sea individuals are distributed in two of these groups, forming a sub-groups marked well (light blue) which is made up only females.

## Discussion-Conclusion

The results of sex ratio, behaviour, size of group and distribution vary according to the years, which is probably the reflection of the availability of the trophic resource. This could explain that in 2006 and 2010 animals were in bigger groups and could take time to socialise.

Genetic analyses show the fin whale population of Mediterranean Sea structured in 3 sub-groups. There is a homogeneous distribution of the individuals in each sub-group either the year of the biopsy or either the sex. Animals of two of the sub-groups share allelic combinations with those of Atlantic Sea. That suggests a genetic mixing of populations close following the migration to animals through Gibraltar in the two directions as that is observed in situ

From genetic information resulting from the new samples of 2010, capture-recapture genetic, kinship relations and by using numerical models which were applied successfully to the gray whales (Alter *et al.*, 2007) us should be able to establish two particularly interesting parameters in term of conservation and management: initial size of this population as well as the "effective" size in lower part of which it could be put in danger.

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## Acknowledgement

We wish to acknowledge the CRMM and the GECEM for the samples of stranded animals

