GENETIC AND DEMOGRAPHIC INVESTIGATION OF POPULATION STRUCTURE AND SOCIAL SYSTEM IN FOUR DELPHINID SPECIES

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Thesis Abstract

Population structure, genetic diversity and social system were investigated in four species of dolphins, thought to present contrasting habitat preferences and social organisation: spinner dolphins, rough-toothed dolphins, long-finned and short-finned pilot whales. To overcome methodological limitations, I combined molecular markers (mitochondrial DNA, -or mtDNA-, and microsatellite loci) and observational data (photo-identification and mass strandings) where possible. Genetic samples were obtained from skin biopsies of free-ranging (n = 243) and stranded (n = 375) dolphins.

As with many species of delphinids, spinner dolphins (*Stenella longirostris*) form communities in which social and reproductive boundaries are poorly understood. In French Polynesia, capture-recapture analyses based on photographs of distinctly marked individuals (DMIs) and microsatellite genotypes (12 loci) indicated a community of about 150 dolphins around Moorea that is relatively closed on a generational time scale. Distinct communities, likely to follow a similar demographic pattern, were observed around neighbouring islands (Tahiti, Raiatea, Huahine and Bora Bora), as indicated by photo-identification data and restricted gene flow (F_{ST} = 0.143, n = 154). Surprisingly high levels of insular mtDNA genetic diversity (average π = 1.44%, suggesting N_{ef} ~ 100,000) contrasted with demographic characteristics of these communities. There was no evidence for a recent bottleneck effect, suggesting that this pattern is the result of metapopulation structure, based on numerous insular communities connected through male and female gene flow.

Investigation of the worldwide mtDNA diversity and phylogeography of long-finned and short-finned pilot whale species revealed a complex evolutionary history (*Globicephala melas*, n = 434; and *G. macrorhynchus*, n = 134, including published and unpublished sequences). Strong genetic differentiation between long-finned pilot whales from the North Atlantic (*G. m. melas*) and Southern Hemisphere (*G. m. edwardii*) indicated severely restricted gene flow, although shared haplotypes suggested some recent contact between the two subspecies. Low genetic distances among haplotypes and a star-like phylogeny suggested a recent worldwide expansion for this species. Higher levels of diversity (although low compared to other cetaceans) were found in short-finned pilot whales, in particular among samples from around Japan. Phylogeographic studies suggested that Japanese samples originate from three distinct populations, one of which could be the ancestral population of the species. Overall, my results confirmed that worldwide mtDNA diversity is low in the two species, probably due to a recent worldwide population expansion and, potentially, to a matrilineal social structure.

The molecular ecology of the mass strandings of long-finned pilot whales around New Zealand was investigated to test the hypothesis that individuals stranding together are part of an extended matrilineal group. Analyses of mtDNA sequences indicate that more than one haplotype was found in five of the seven mass strandings

investigated (n = 275), demonstrating that groups are sometimes composed of unrelated maternal lineages. This was further supported by analyses of relatedness within and between strandings based on microsatellites (14 loci). These analyses discount kinship as the only factor causing large mass strandings in long-finned pilot whales. Parentage analyses confirmed some aspects of previous studies in the North Atlantic, suggesting a social system with at least some level of male and female philopatry to the maternal group, and infrequent paternities within the group. In a detailed study of a large mass stranding (Stewart Island 2003, n = 122), there was no correlation between position of the whales on the beach and genetic relatedness (based on 20 microsatellite loci), discounting the assumption that kinship bonds are maintained during these traumatic events. This was further supported by the striking separation of stranded mothers and dependant calves. This disruption of kinship bonds could help explain the behavioural distress of stranded individuals and the tendency of many whales to re-strand even after being re-floated.

Finally, a study of rough-toothed dolphins (*Steno bredanensis*) in the Society Archipelago, French Polynesia, provided new insights in the ecology of this poorly-known species. Although traditionally viewed as a pelagic dolphin, analyses supported a pattern of local communities, in some ways similar to spinner dolphins, with fine-scale population genetic structure (F_{ST} = 0.60, $p < 0.001$ based on mtDNA, n = 65) and local fidelity. These communities also showed a low level of mtDNA haplotype diversity (four unique haplotypes at Moorea compared to 18 for spinner dolphins), suggesting the potential influence of a matrilineal social structure similar to long-finned pilot whales.

Dedication

To my parents
Bernadette and Jean-Louis OREMUS

For always being here for me

Acknowledgments

During the first weeks of my thesis, preparing my fieldwork at Moorea, I have to say that I felt very lonely far from home and family left behind in France. As my next three (to five…) years were meant to be spent in French Polynesia and New Zealand, I had the first impression that I was about to live a great but rather solitary experience. Instead, it did not take very long for me to realise that I would not go anywhere in this endeavour alone. From fixing holes in the inflatable boat (which is pretty much how I started my PhD) to the last proof readings of my chapters, I received continuous and tremendous help and support from many many people that I wish to thank here.

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