Population Genetic Structure of *Octopus vulgaris*

Octopus vulgaris,
Cuvier, 1797;
photo by J. Lyle

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Introduction

The common octopus *O. vulgaris*, is thought to have a cosmopolitan distribution and can be found worldwide between 50N and 50S (Figure 1). Despite the commercial importance of *O. vulgaris*, its distribution and genetic population structure are relatively unknown.

Studies on the genetic population structure of *O. vulgaris* began with Söller et al. (2000), who concluded that the *O. vulgaris* from Caribbean are phylogenetically closer to *O. bimaculoides* than to *O. vulgaris* from Europe and that is a paraphyletic species. Oosthuizen et al. (2004) compared African and European populations to those in Taiwan and the Caribbean Sea. The study showed little divergence between Europe and Africa. Warnke et al. (2004) suggested that the distribution of *O. vulgaris* extends beyond the Mediterranean and the eastern Atlantic, including the western Atlantic and the northwestern Pacific. The objective of this study was to estimate the connectivity of *O. vulgaris* populations between Caribbean vs. European and African populations.

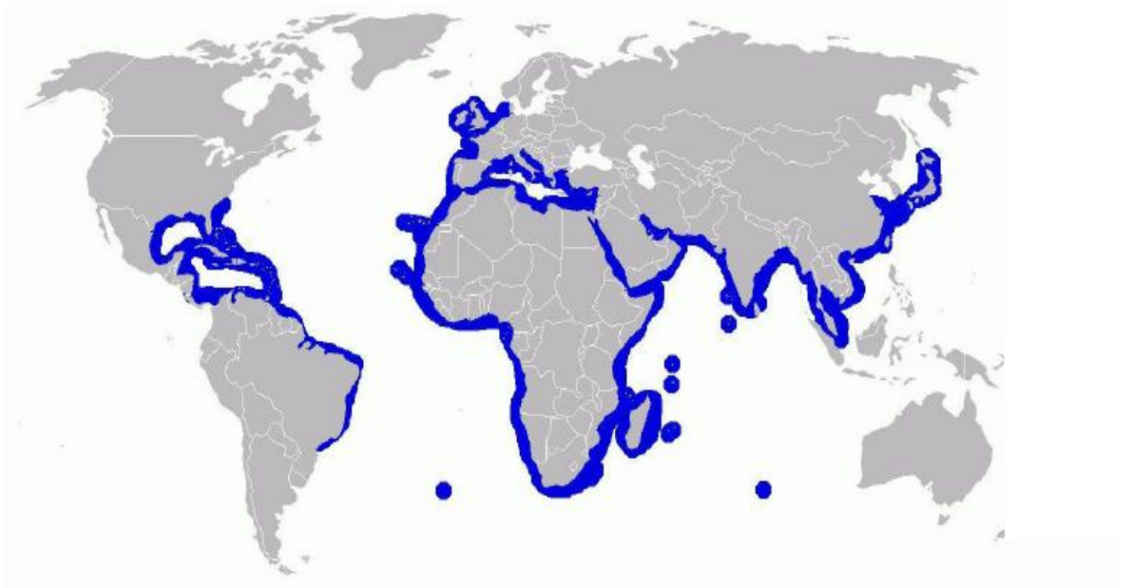


Figure 1. Distribution of *O. vulgaris*. Modified from http://world-map.nl

Materials and methods

Specimens of *Octopus vulgaris* was collected by snorkeling, scuba diving, purchased from fishermen or downloaded from GenBank (Figure2).
Total genomic DNA was extracted using a QIAGEN Dneasy kit, and was purified with the Exosap procedure. DNA trace files were verified in CodonCode Aligner. Aligned sequences were analyzed in DnaSP v5, Arlequin v3.5, jModelTest 3.06, PhyML, PAUP* 4.0b10 and MrBayes v. 3.2.

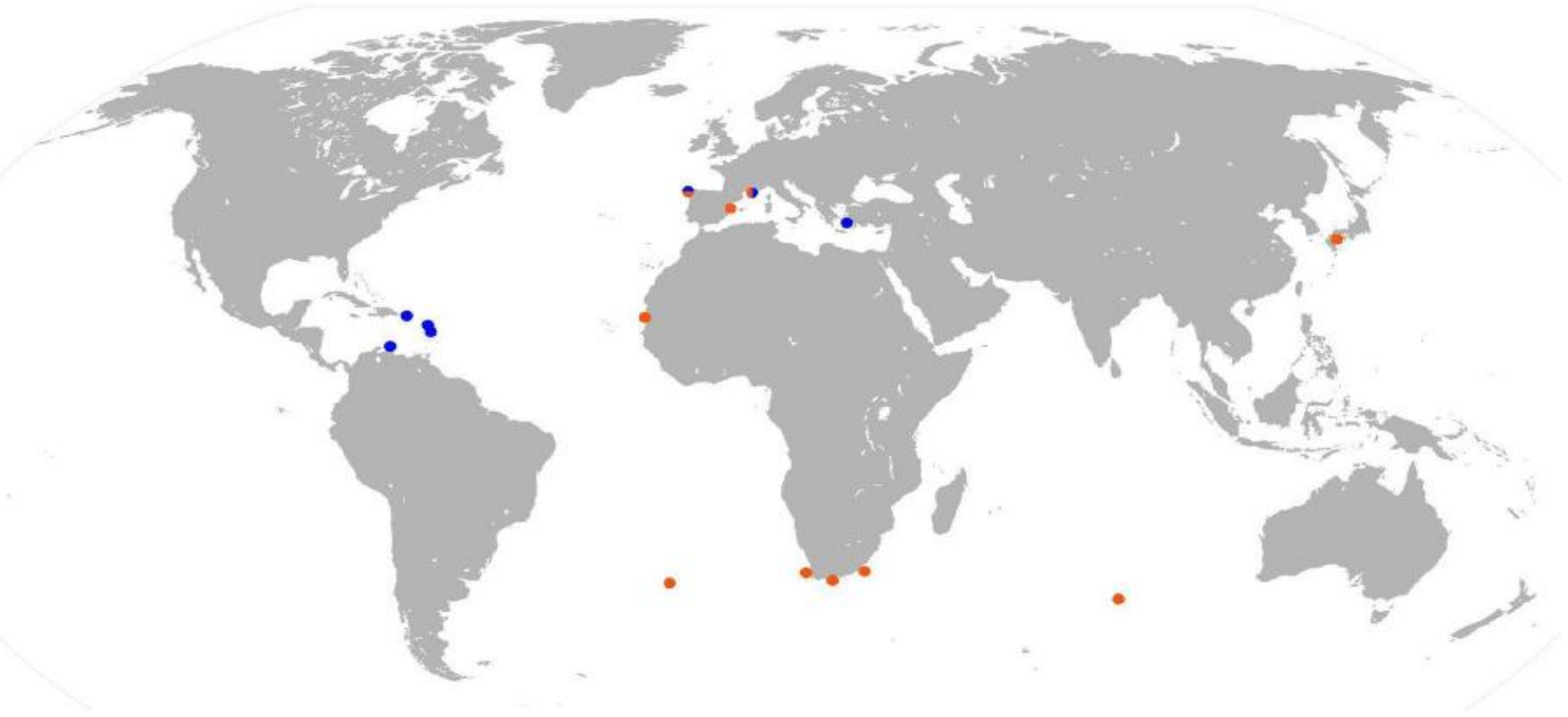


Figure 2. Origin of *O. vulgaris* analyzed in this study. The blue dots represent new locations. The orange dots represent locations of publicly available sequences. Modified from http://world-map.nl.

Results

A 467 bp portion of the mitochondrial gene COI was analysed from 92 specimens from Mediterranean, Eastern Atlantic, greater Caribbean area, Indian Ocean and Pacific Ocean (Figure 2). Seventeen haplotypes were identified, four of which originated in the Caribbean (Figure 3). Thirteen of the haplotypes were singletons. The highest values of haplotype diversity were observed in the Japanese and E. Atlantic specimens.

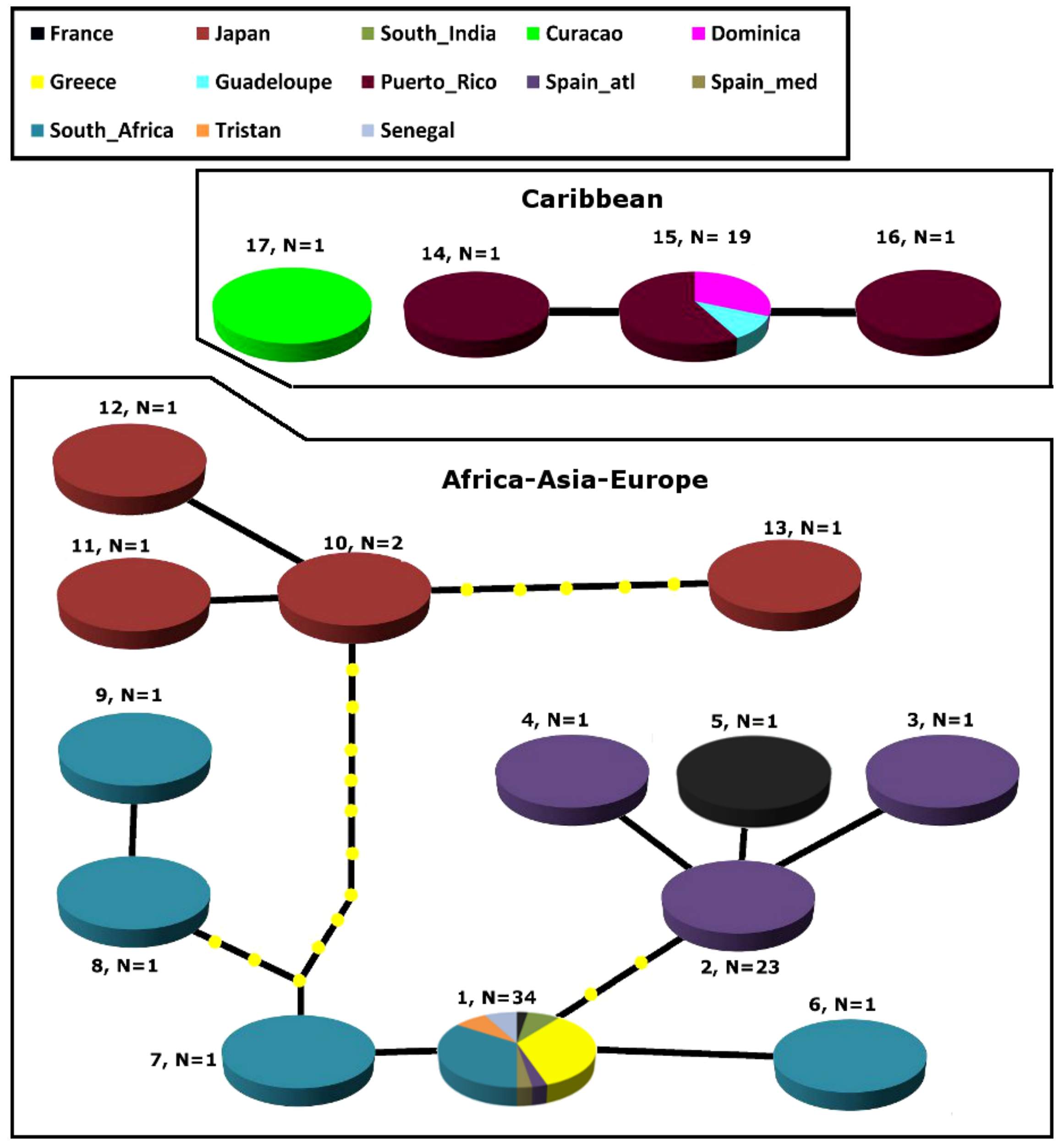
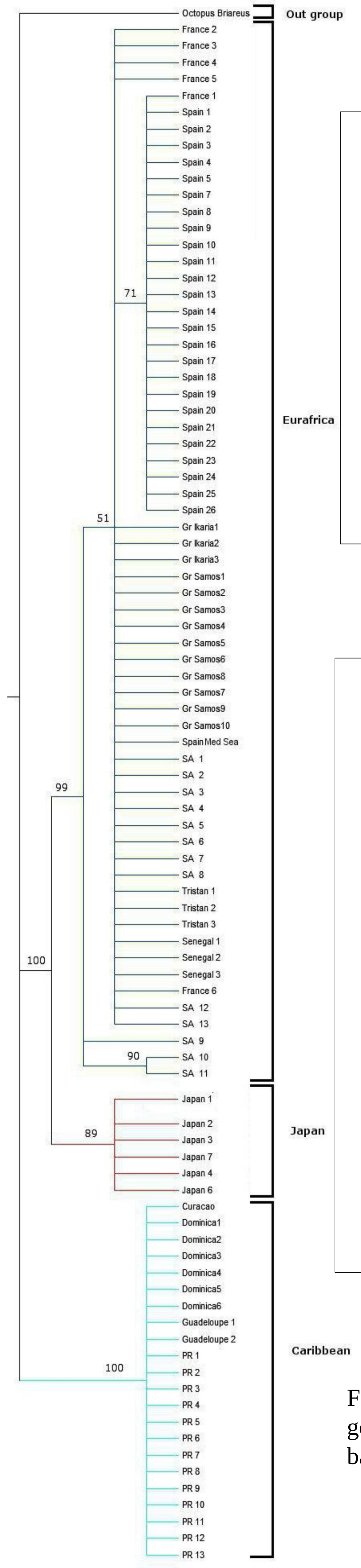


Figure 3. Parsimony network of 17 haplotypes of *O. vulgaris* based on COI. Each circle represents a unique haplotype. Each haplotype has a numerical identifier and the number of samples sharing a particular haplotype is indicated. The minimum inferred number of mutational steps is represented by the yellow dots.

	Caribbean	Japan	S. Indian Ocean	Mediterranean	Atl. Spain	S. Africa	Tristan
Caribbean	--						
Japan	0.95134***	--					
S. Indian Ocean	0.95583***	0.85516*	--				
Mediterranean	0.96803***	0.92009***	-0.19403	--			
Atl. Spain	0.97355***	0.94469***	0.88406**	0.84912***	--		
S. Africa	0.95768***	0.85045***	-0.11472	0.06882	0.75281***	--	
Tristan	0.95583***	0.85516	0	-0.19403	0.88406***	-0.11472	--
Senegal	0.95583***	0.85516	0	-0.19403	0.88406***	-0.11472	0

Table 1. Pair-wise Φ_{ST}s based on *Octopus vulgaris* COI sequences. Tristan = Tristan da Cunha. Asterisks indicate significant differences (*P<0.05, **P<0.01, ***P<0.001).



Uncorrected average pairwise differences among populations indicated that the Caribbean is 11.6-11.7% divergent compared to Mediterranean, Atlantic and Japanese samples of *O. vulgaris*
The sequence divergence between Japan and Mediterranean and E. Atlantic was 3.1%, indicating a close genetic relationship between these two regions. All *O. vulgaris* populations were at least 14.5% divergent from the closely related *O. briareus.*

The Japanese octopi formed a monophyletic clade which is more closely related to the octopi from those in Mediterranean, E. Atlantic, Tristan da Cunha and three specimens from St. Paul and Amsterdam Islands in the South Indian Ocean (Figures 2, 4). All specimens from the Mediterranean Sea (Spain, France and Greece) together with those from Senegal, Tristan da Cunha and some from South Africa formed a non-differentiated clade (Figure 4). Within that clade, all octopi from Atlantic Spain formed a tightly clustered clade. Two specimens from South Africa formed a sister clade of the Mediterranean/E. Atlantic clade (Figure 4).

Figure 4. Maximum Likelihood genealogy of *Octopus vulgaris* based on COI.

Conclusions

The most important finding was the significant population divergence we observed between western and Eastern Atlantic (including Mediterranean) populations, which were previously thought as panmictic. The Caribbean lineage represents a lineage of *Octopus vulgaris* that is more genetically distant to all other *O. vulgaris* populations but still less divergent between any *O. vulgaris* and the congeneric species *O. briareus*.

The Caribbean *O. vulgaris* represents a distinct genetic lineage within the *O. vulgaris* species complex. Most likely the most southern distribution of the Caribbean lineage is North Brazil and the most northern limits of its distribution are the Carolinas. A new study with a higher number of samples is needed to decipher the population structure within Caribbean.

Our data agrees with the assertion that the common octopus *O. vulgaris* is a complex of several closely related, rather indistinguishable species in tropical to temperate waters (Norman, 2003).

Literature cited

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For further information

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