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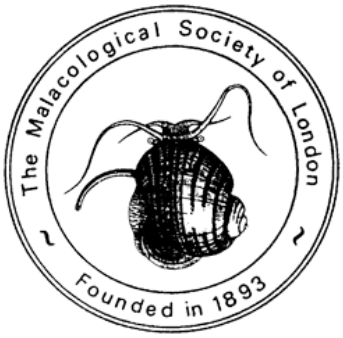


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# Mitochondrial and nuclear DNA phylogeography of two cupped oysters *Crassostrea gigas* and *Crassostrea angulata*

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# Introduction

**1793** *Crassostrea gigas* (Thunberg)

**1819** *Crassostrea angulata* (Lamarck)

**1868** Accidental introduction of *C. angulata* from Portugal into France

**1950's** Up to 100,000 tons per year of *C. angulata* produced in France

**1966** First case of introduction of *C. gigas* into France

**1970** Major mortality leading to disappearance of *C. angulata* by 1973

**1971** Massive introduction of *C. gigas* from Canada and Japan into Europe

**1974** "Portuguese and Japanese oysters are the same species" (Menzel, 1974): they are inter-fertile and morphologically identical.

**1980's** Allozyme-based studies showed no genetic differentiation between *C. angulata* and *C. gigas* (Buroker et al. 1979, Mattuicci & Villani, 1983).

# How do we explain the presence of these two conspecific taxa on opposite sides of the world ?

2 hypotheses:

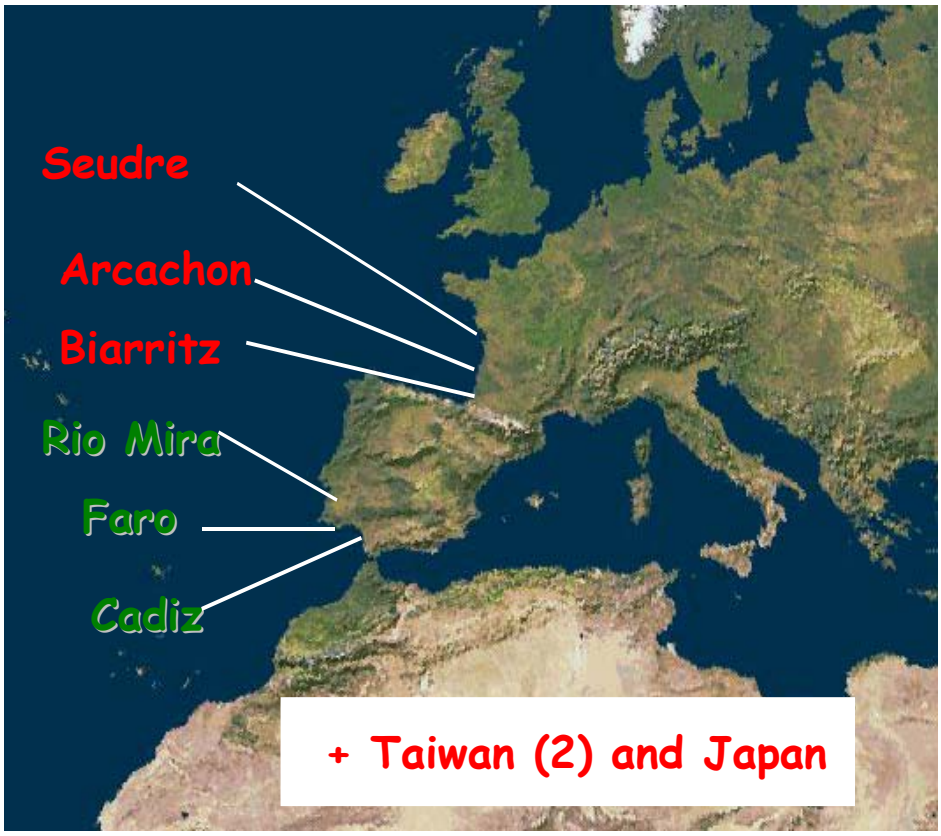
(1) Common ancestry: *C. gryphoides* (Stenzel, 1971; Durve, 1986).

(2) Introduction: From Japan to Portugal or reverse (Buroker *et al.*, 1971).

This study:

Genetic differentiation among *C. angulata* and *C. gigas* populations using mitochondrial and nuclear DNA markers.

# Sampling of *C. gigas* & *C. angulata*




9 populations

383 individuals

Samples were first classified as *C. angulata* or *C. gigas* according to the information provided by the suppliers.

# Mitochondrial markers

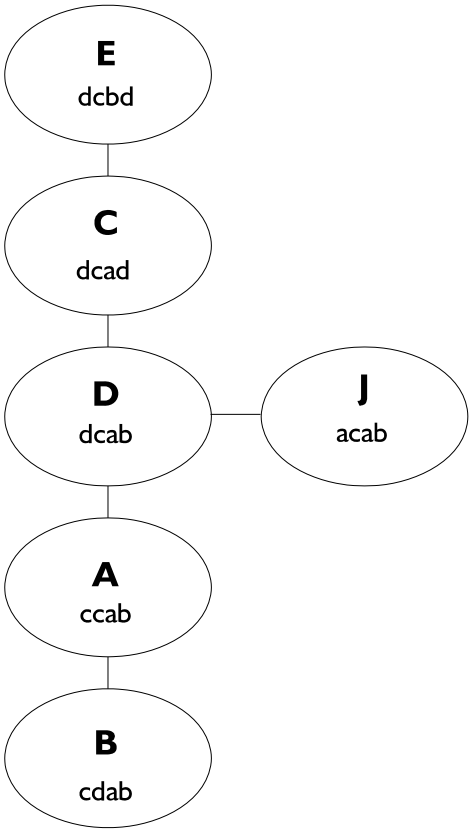
(Boudry *et al.* 1998)

PCR amplification of a 710nt mitochondrial fragment (Cytochrome Oxydase C subunit I)

9 restriction enzymes tested

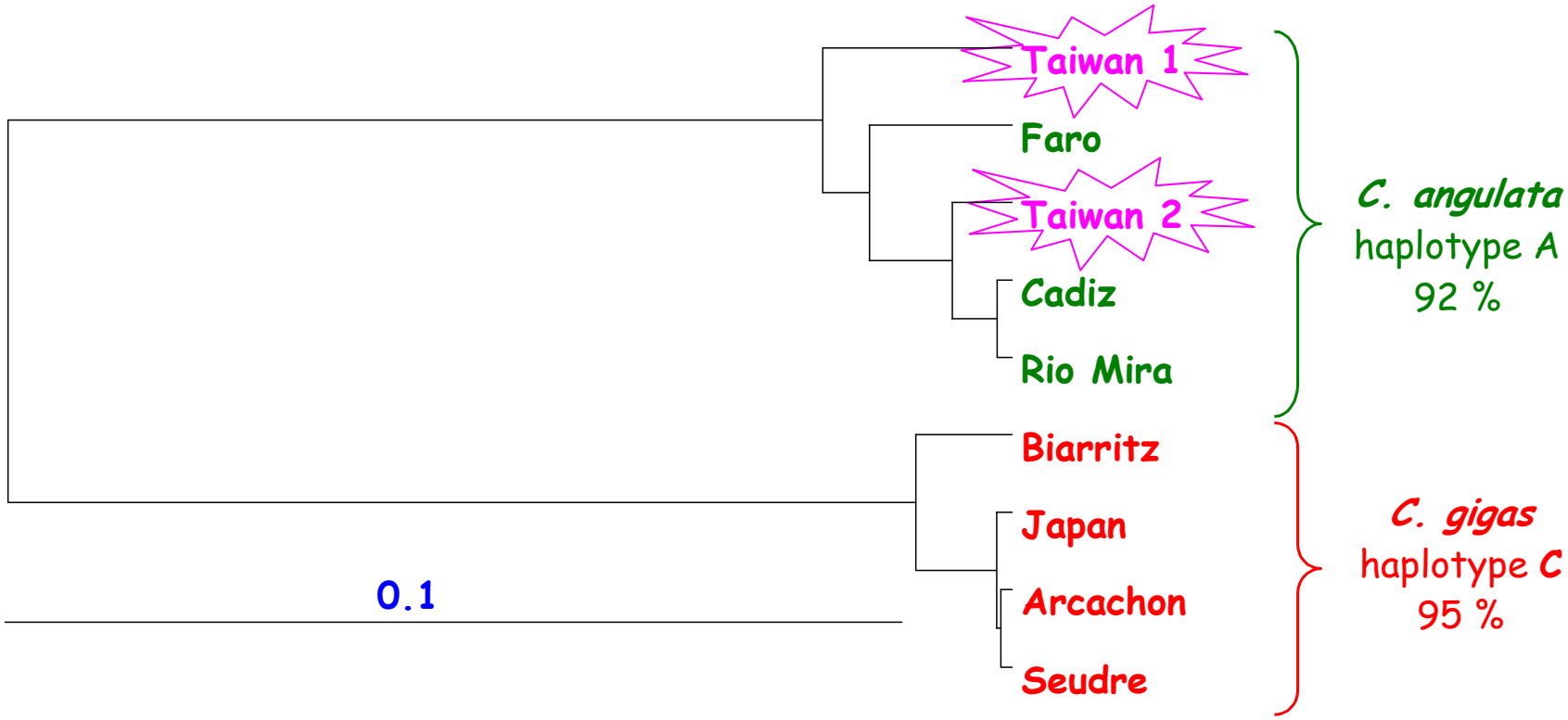
4 restriction enzymes showed polymorphism

6 haplotypes



# Mitochondrial DNA

**Neighbor-joining tree based on Reynolds' genetic distance (Reynolds, 1983)**

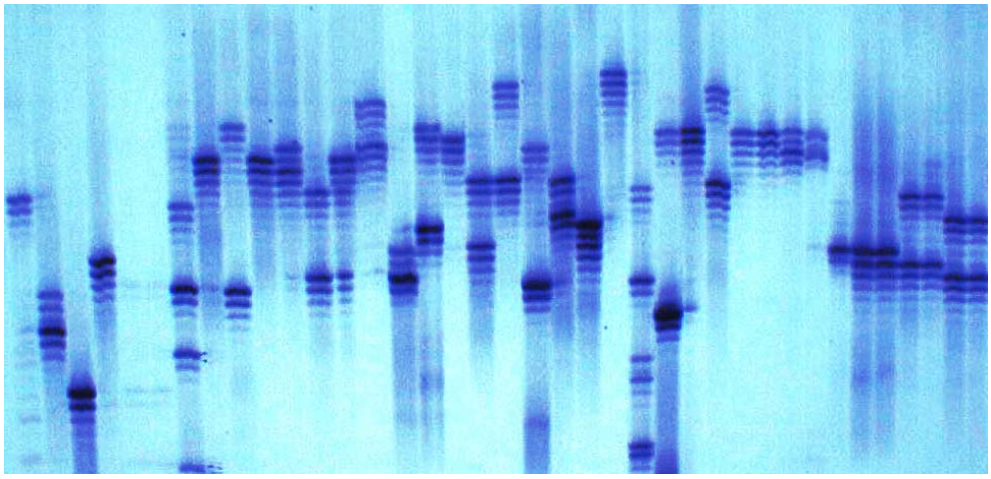


# Microsatellite markers

(Huvet, 1998)

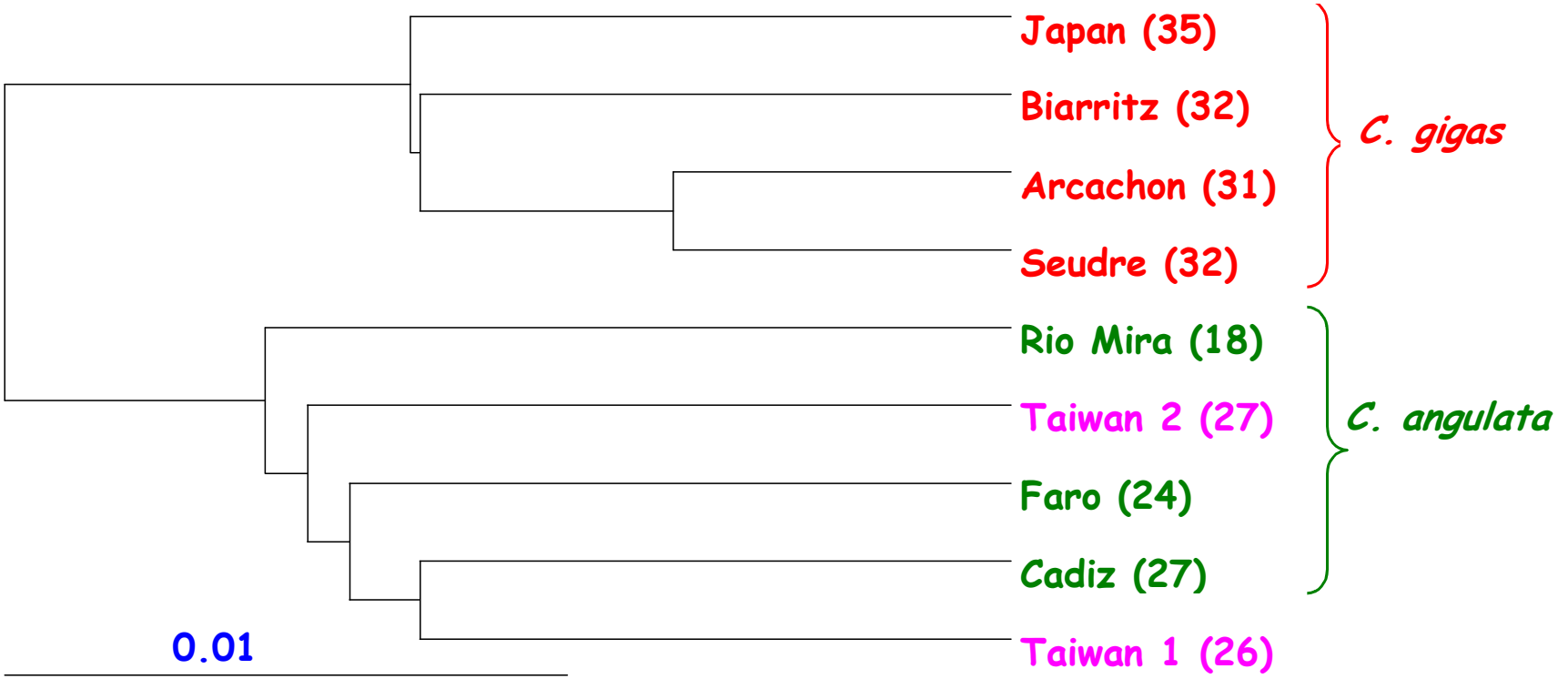
PCR amplification of 3 polymorphic loci (Magoulas *et al.*, 1998)

| | *CG44* | *CG49* | *CG108* |
|---|---|---|---|
| **Total number of alleles** | **52** | **52** | **54** |
| **Alleles/population** | **18-29** | **17-38** | **20-40** |
| **Observed heterozygosity (*Ho*)** | **0.5-0.9** | **0.4-1** | **0.8-1** |
| **Gene diversity (*He*)** | **0.9** | **0.9** | **0.9** |



# Microsatellite markers

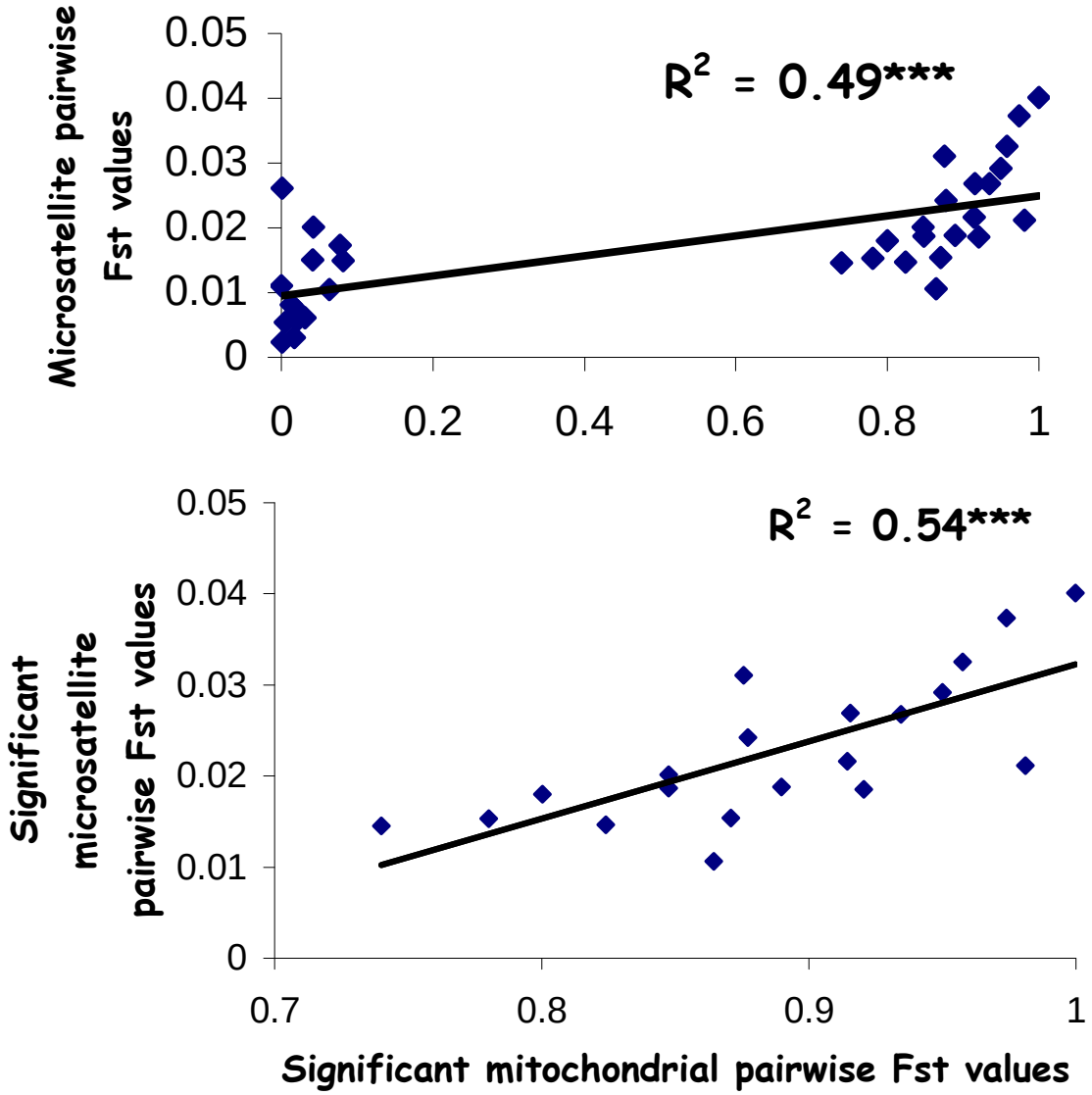
Neighbor-joining tree based on Reynolds' genetic distance (Reynolds, 1983)




Population (mean number of alleles)

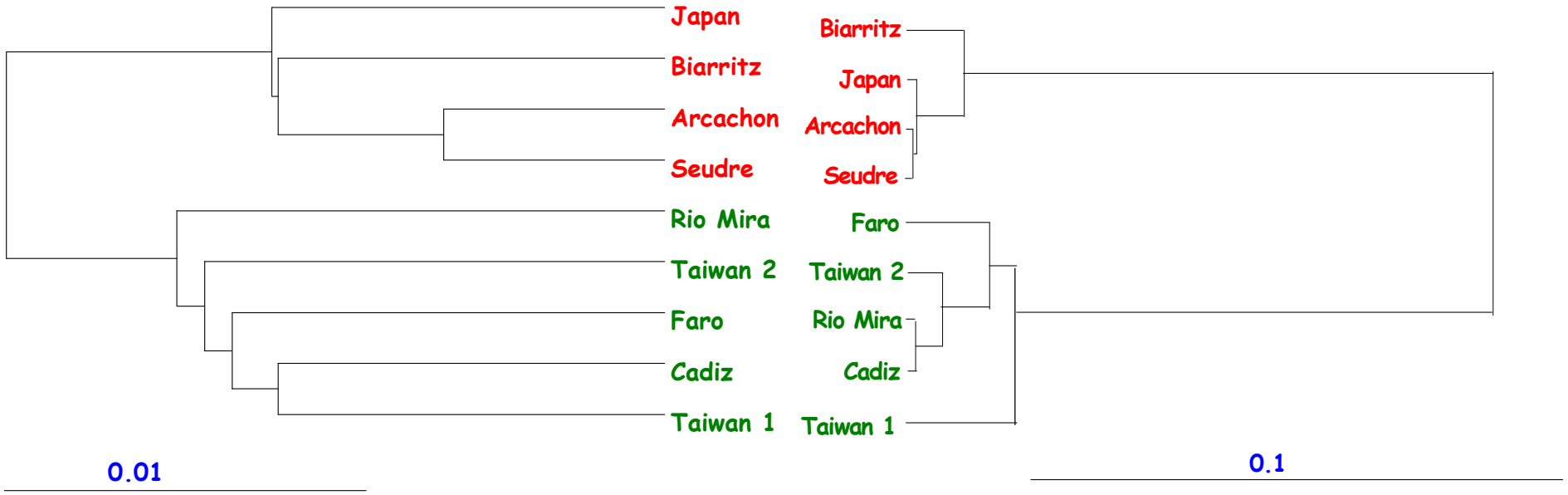
# Comparison between mitochondrial and microsatellite data

| | Global Fst |
|---|---|
| Mitochondrial DNA | 0.81 |
| Microsatellites | 0.017 |



# Comparison between mitochondrial and microsatellite data

## Neighbor-joining tree based on Reynolds' genetic distance (Reynolds, 1983)



# Conclusion

Portuguese oysters originated from Asia, probably from Taiwan.

The Asian origin of *C. angulata* was supported by *mt*DNA sequence data and the divergence date between *C. angulata* and *C. gigas* was estimated at 1 to 2 million years (O'Foighil *et al.* 1998).

Portuguese oysters were probably transported by ships from "Formosa", reached by European seafarers during the XVII$^{th}$ century. These naturalised in Southern Europe and then were described by Lamarck.

Microsatellite markers show no evidence of drift following this introduction.

Mitochondrial and markers give qualitatively but not quantitatively congruent results, probably due to different evolutionary forces on these markers (drift, mutation).

## Distribution of allele frequencies in terms of allele size for the locus *CG44*