

# The taxonomic status and origin of the Portuguese oyster *Crassostrea angulata* (Lamarck, 1819)

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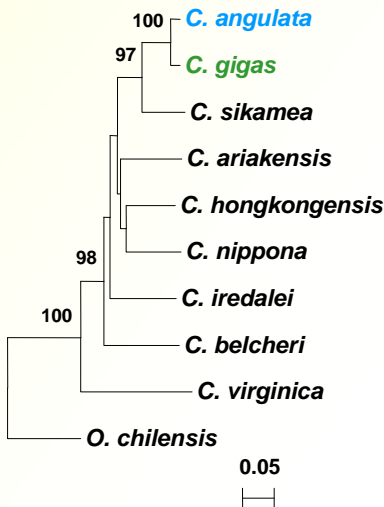
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## 1. TAXONOMIC STATUS

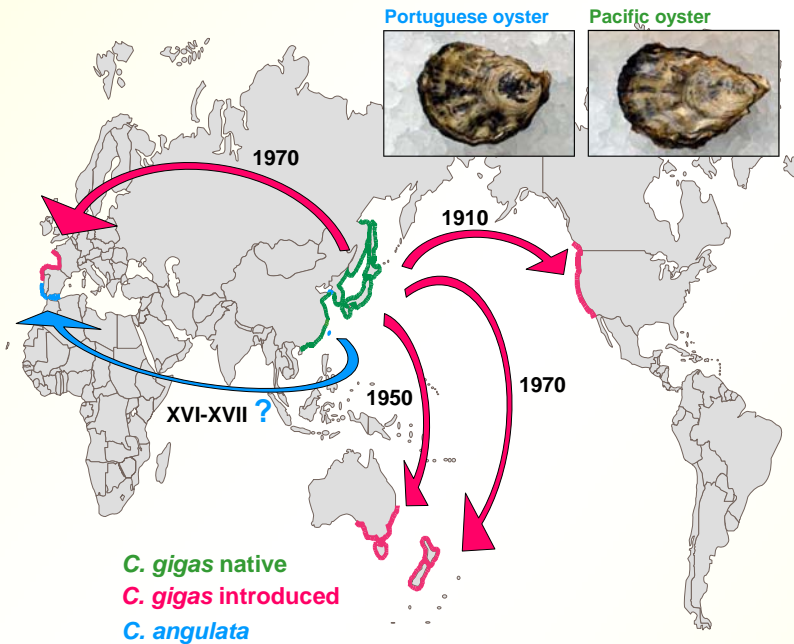
The taxonomic status of the Portuguese oyster, *Crassostrea angulata*, and the Pacific oyster, *Crassostrea gigas*, has been a matter of controversy. Based on larval shell morphology, experimental hybridisation and electrophoretic studies of enzyme polymorphism several authors have considered these two species as being synonymous (1, 2).

## 2. PHYLOGENETICS ANALYSIS AND GEOGRAPHIC ORIGIN

During the last years, several genetic studies based on mitochondrial DNA (3, 4) and microsatellites (5) data have provided accumulating evidences that the two taxa are genetically distinct although close related. Phylogenetic analyses firmly place both Portuguese and Pacific oysters within an Asian *Crassostrea* clade supporting the hypothesis of the introduction of *C. angulata* from Asia to Europe. Pure populations of *C. angulata* were observed in Taiwan as well as presumed mixed populations of *C. angulata* and *C. gigas* in Northern China.

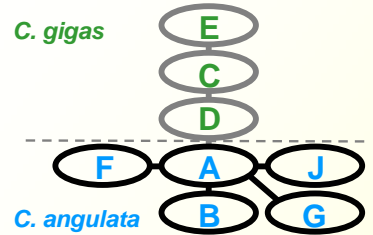


Phylogenetic tree obtained from sequence divergence of mitochondrial COI DNA



## 3. GENETIC VARIABILITY

The level of genetic variability of *C. gigas*, from samples collected in different parts of the world, appears to be lower than that of *C. angulata*, samples collected in Portugal, based on RFLP mitochondrial cytochrome oxidase C subunit I haplotypes (6). This difference could be related to the dissemination of *C. gigas* from Miyagi Prefecture to different regions in Japan and other places in the world where the Pacific oyster was introduced.



Minimum spanning tree of RFLP haplotypes (COI) from *C. angulata* and *C. gigas*

## 4. CYTOGENETICS ANALYSIS

Comparative analysis of restriction enzymes banding pattern revealed differences between all chromosomes of *C. angulata* and *C. gigas* with the exception of chromosome 10 (7).

	Apa I		Hae III	
	<i>C. angulata</i>	<i>C. gigas</i>	<i>C. angulata</i>	<i>C. gigas</i>
1				
2				
3				
4				
5				
6				
7				
8				
9				
10				

Haploid distribution of chromosomal bands in *C. angulata* and *C. gigas*, for the two restriction enzymes used (Apa I and Hae III)

## 6. CONCLUSIONS AND PERSPECTIVES

This study suggests that (1) *Crassostrea angulata* and *C. gigas* are genetically distinct although close related and (2) *C. angulata* has an Asian origin. The high genetic variability observed in *C. angulata* opens interesting perspectives for the development of conservation and breeding programs that can be useful for the expansion and diversification of the oyster culture industry.

## REFERENCES

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