

# Genetic Similarity Networks in populations and in metapopulations

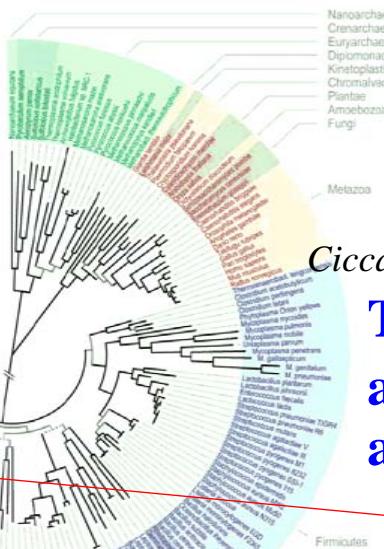
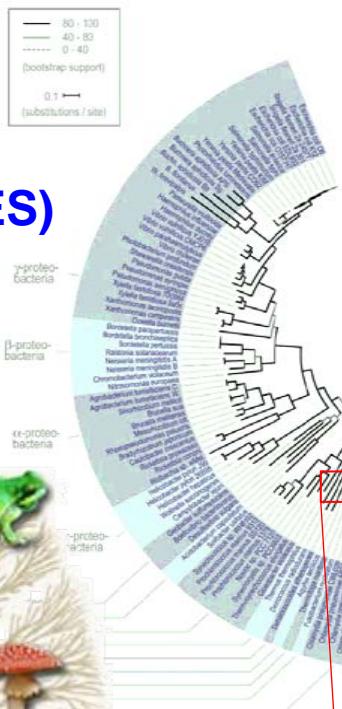
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3. **CCMAR**, CIMAR-Laboratório Associado, Universidade do Algarve, Faro, Portugal
4. **EEP/LEP**-Laboratoire Environnement Profond, IFREMER Centre de Brest, France

## NETWORKS (TREES) in EVOLUTION

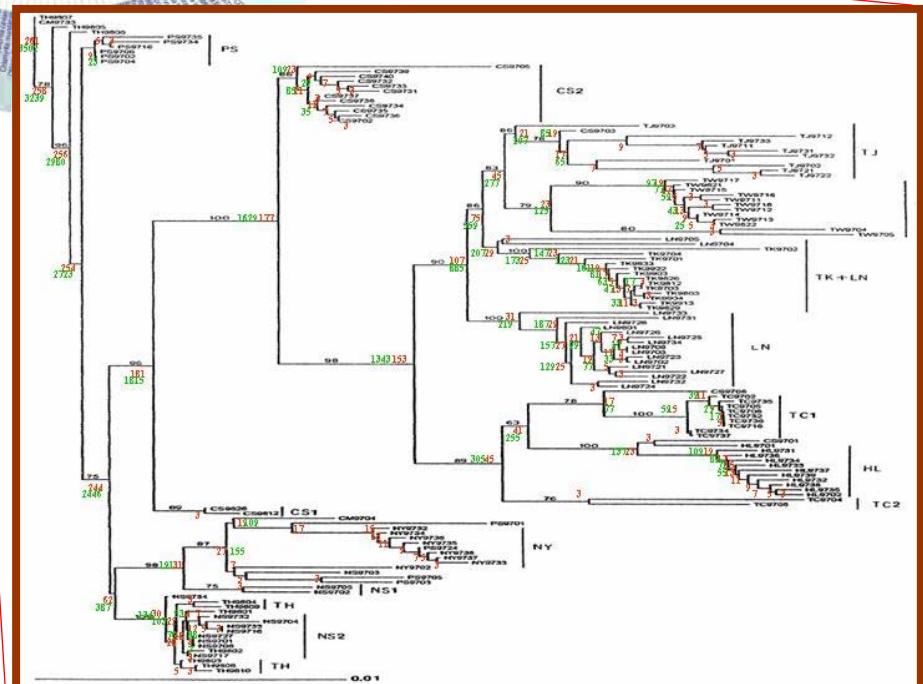


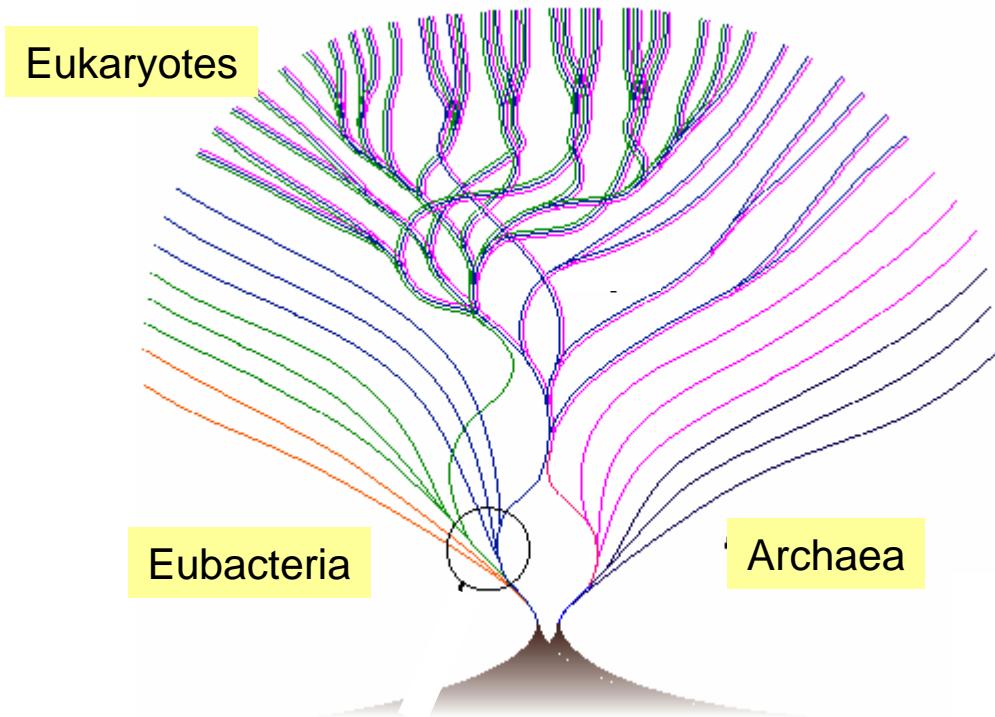
Tree of Life from [tolweb.org](http://tolweb.org)



Ciccarelli, F. D. et al. *Science* (2006)

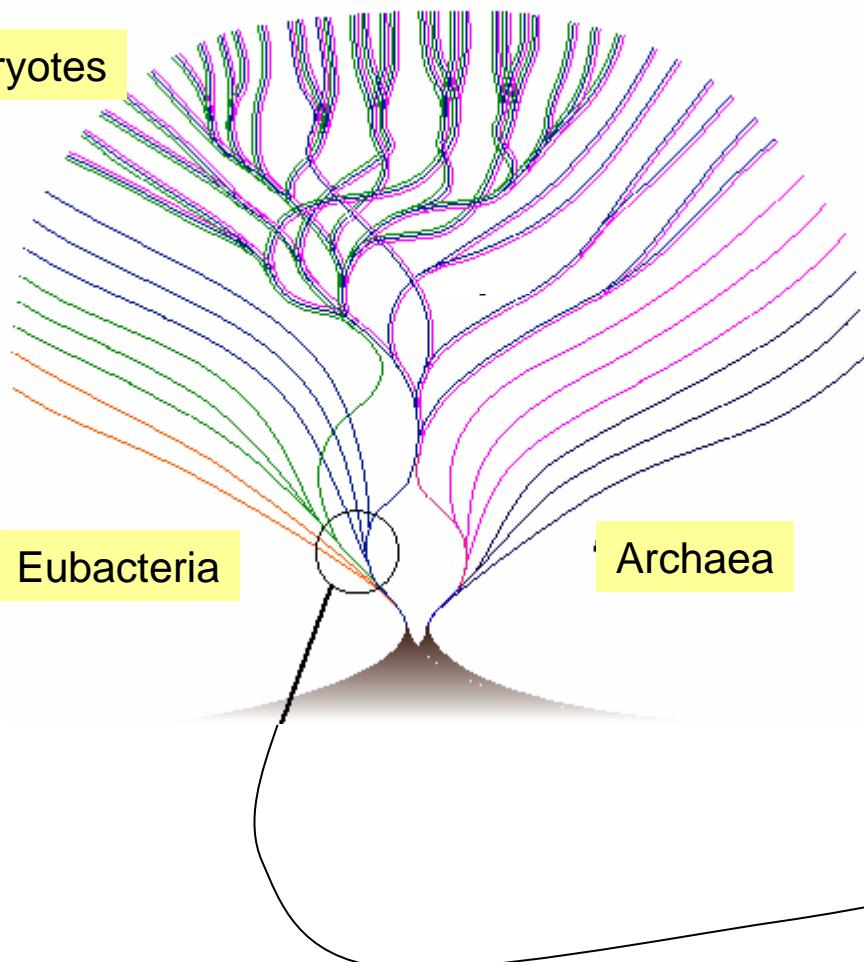
The “Tree of Life”  
and phylogenetic trees  
and networks





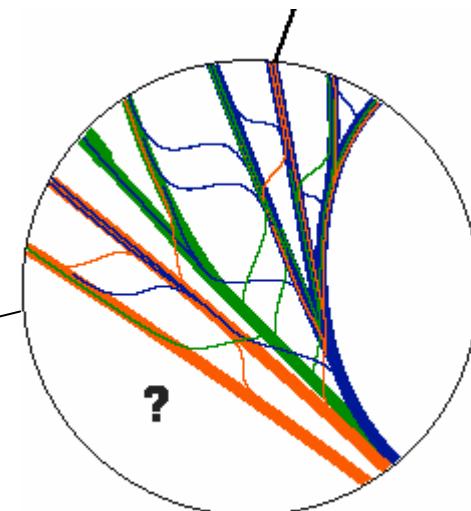
W. Martin, BioEssays 21.2, 1999

Eukaryotes



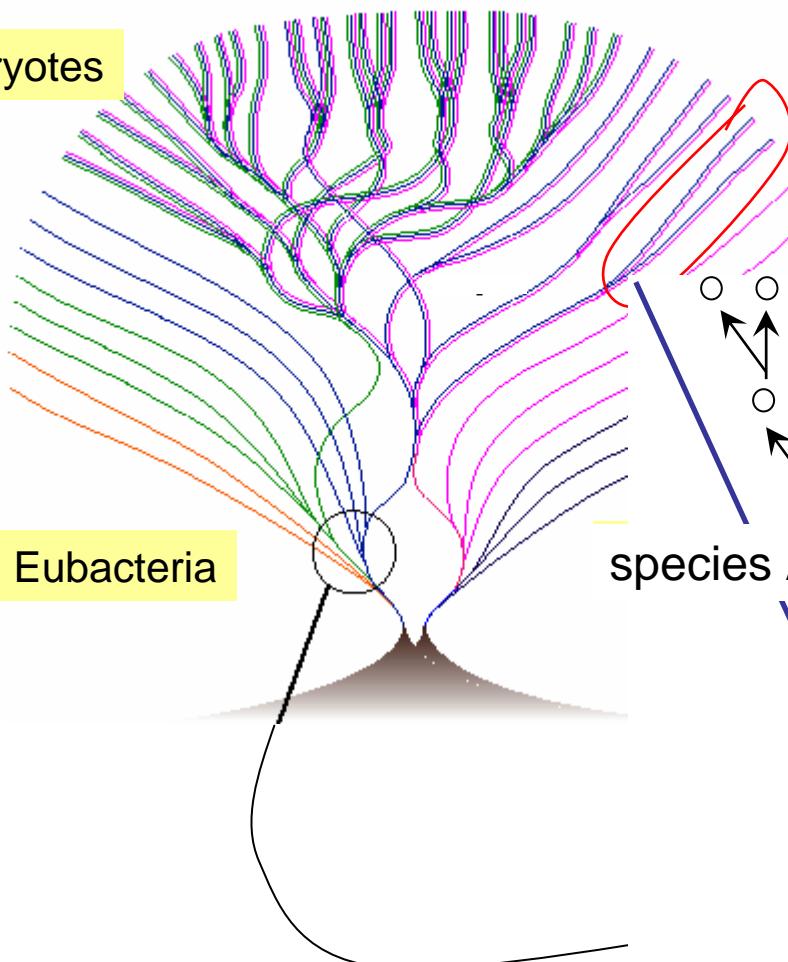
Archaea

Eubacteria



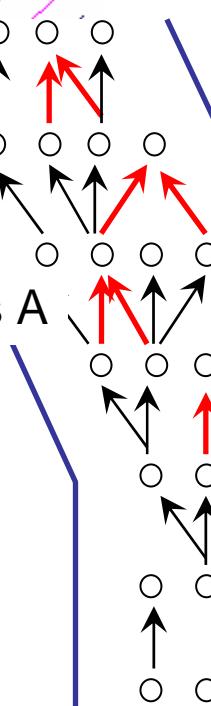
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Eukaryotes

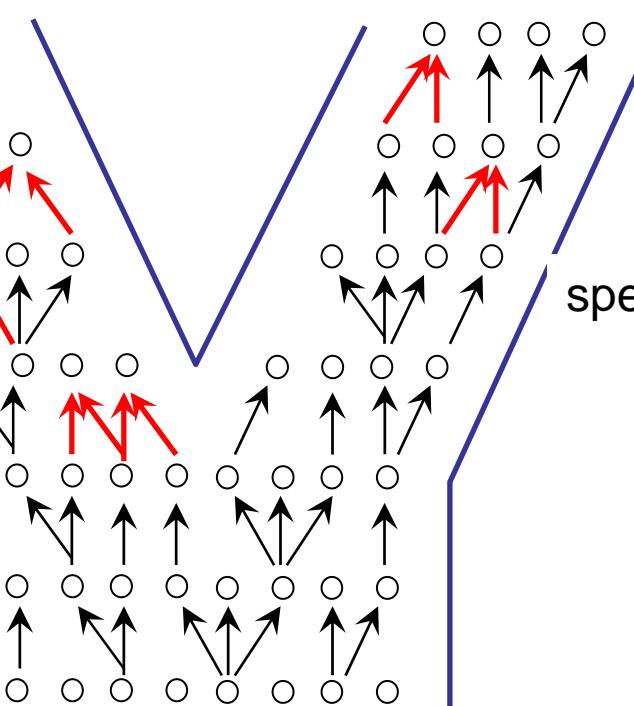


Eubacteria

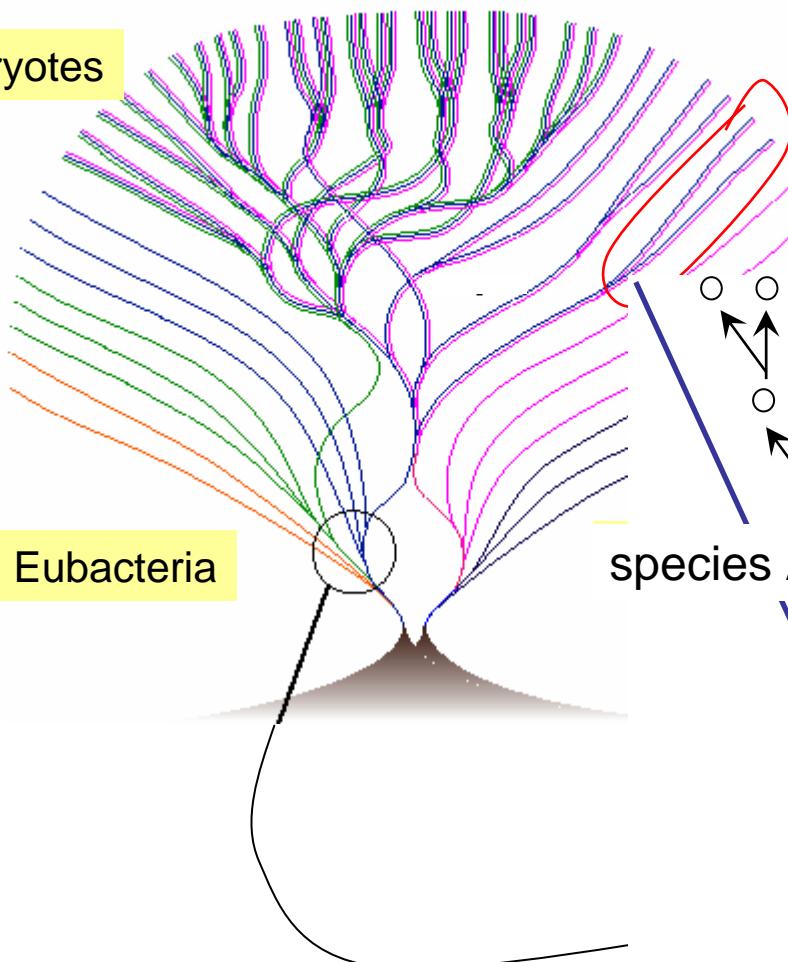
species A



species B

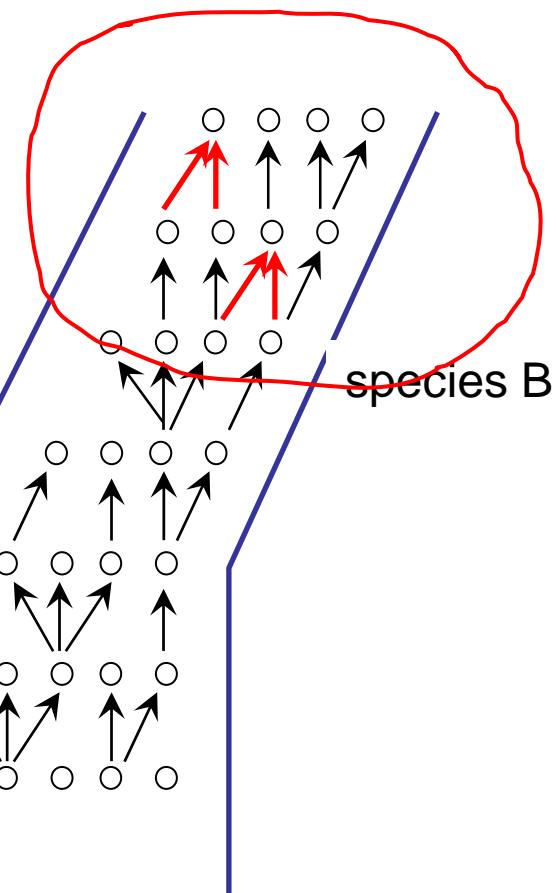


Eukaryotes

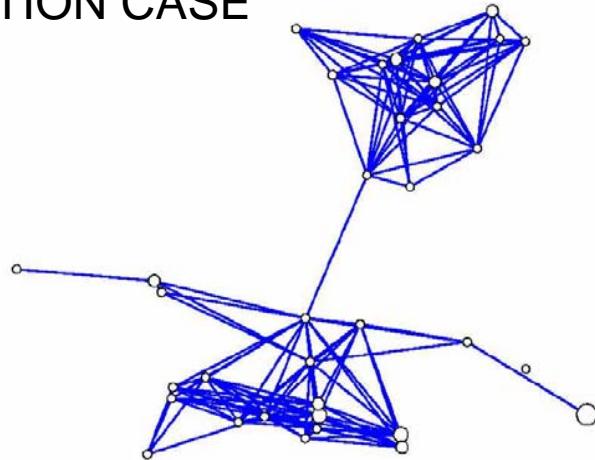


Eubacteria

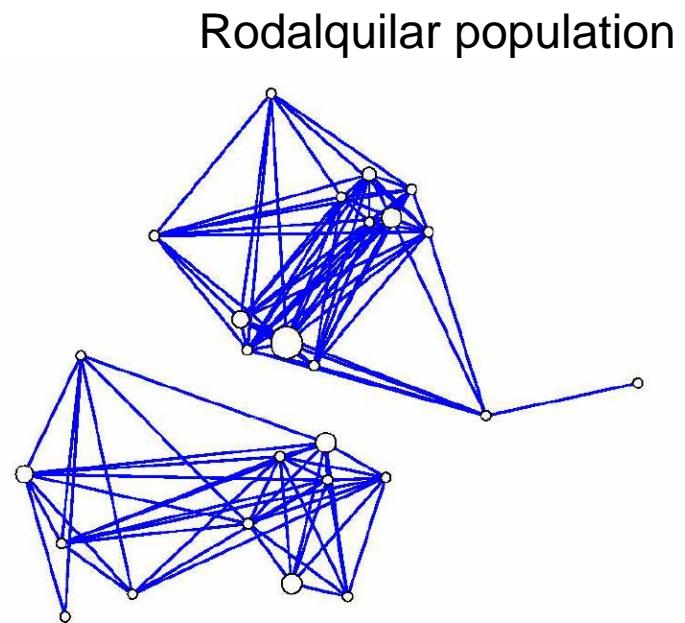
species A



## NETWORKS OF GENETIC SIMILARITY INTRAPULATION CASE



Roquetas population



Rodalquilar population

### THE AIM:

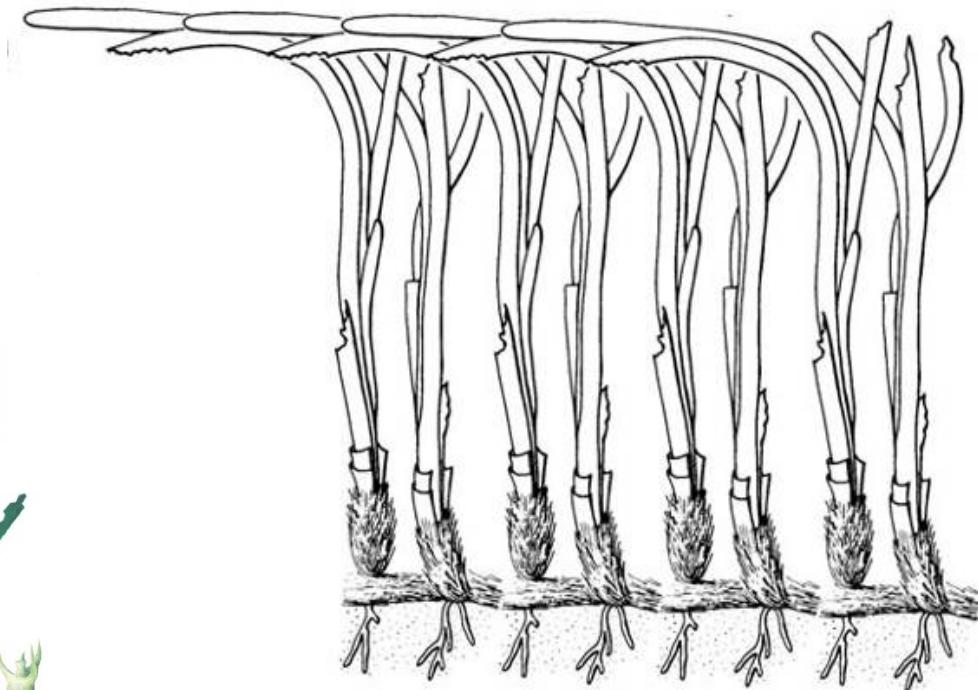
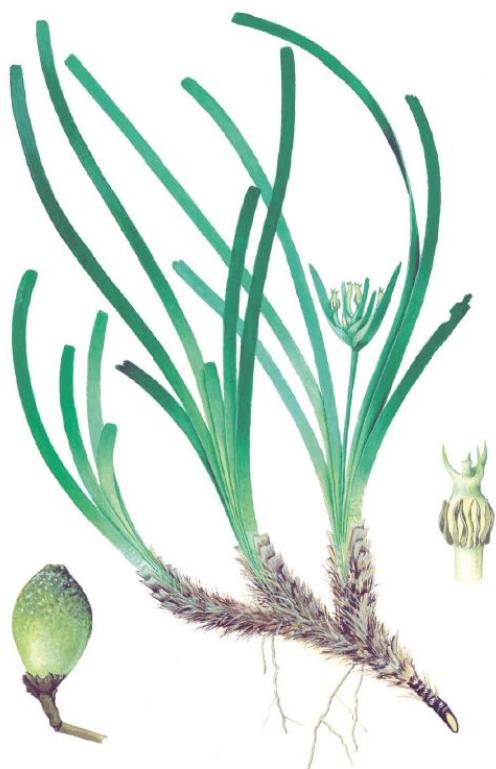
- To provide biologists with novel methods for analysis of population structure based on modern network theory advances
- To enrich the science of networks with a new case study with distinct properties



*Posidonia oceanica* meadows in Cabrera (Balearic islands)



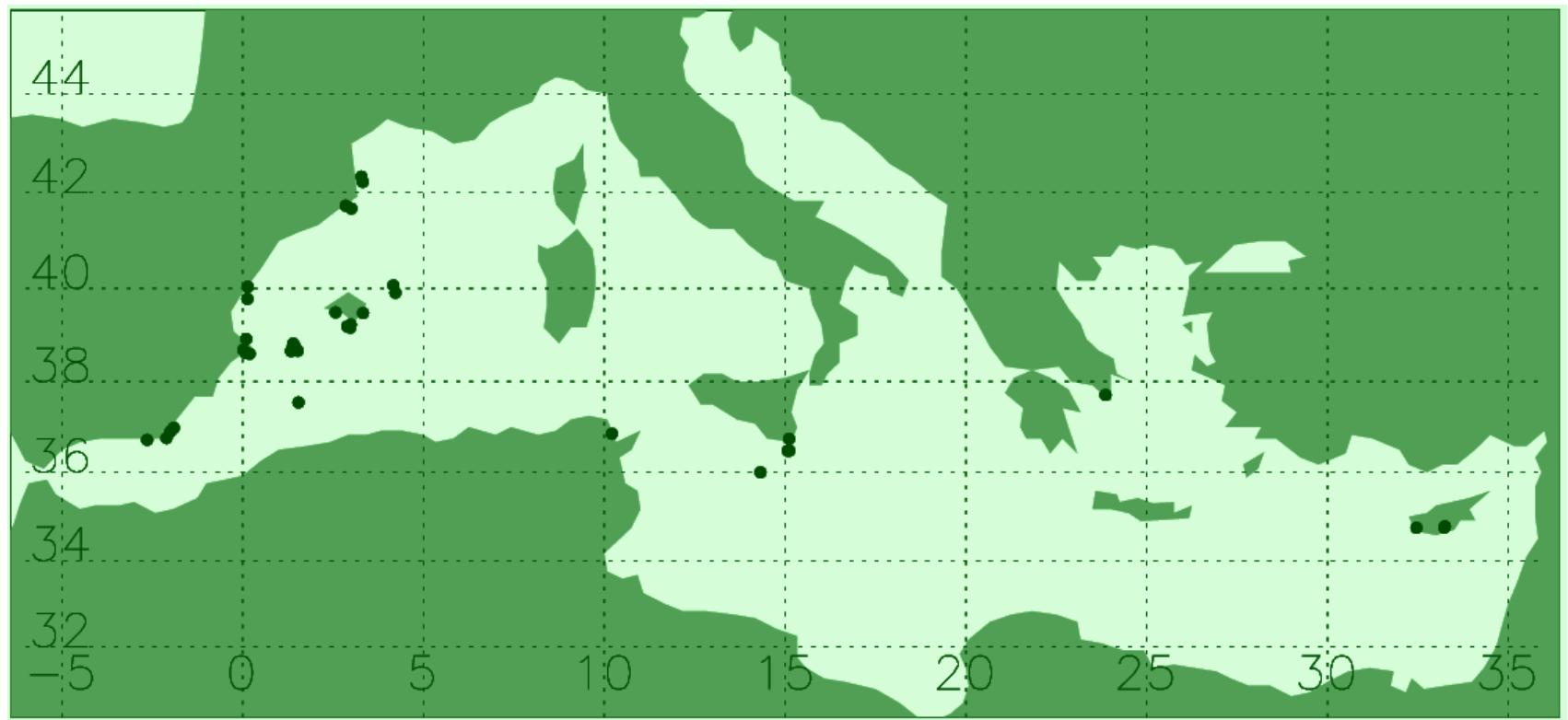
Posidonia oceanica meadows



Combined clonal + sexual modes of reproduction

## Constructing networks of genetic similarity in *Posidonia oceanica*

- **Sampling** the individuals: 40 ramets collected from 40 populations located in different places of the Mediterranean
- **Genotyping**: Characterization by 7 microsatellite loci.
- Network construction:
  - **Distance** definition: Distance matrix
  - Network construction by **thresholding** the distance matrix



The 40 sampling locations in the Mediterranean

## Constructing networks of genetic similarity in *Posidonia oceanica*

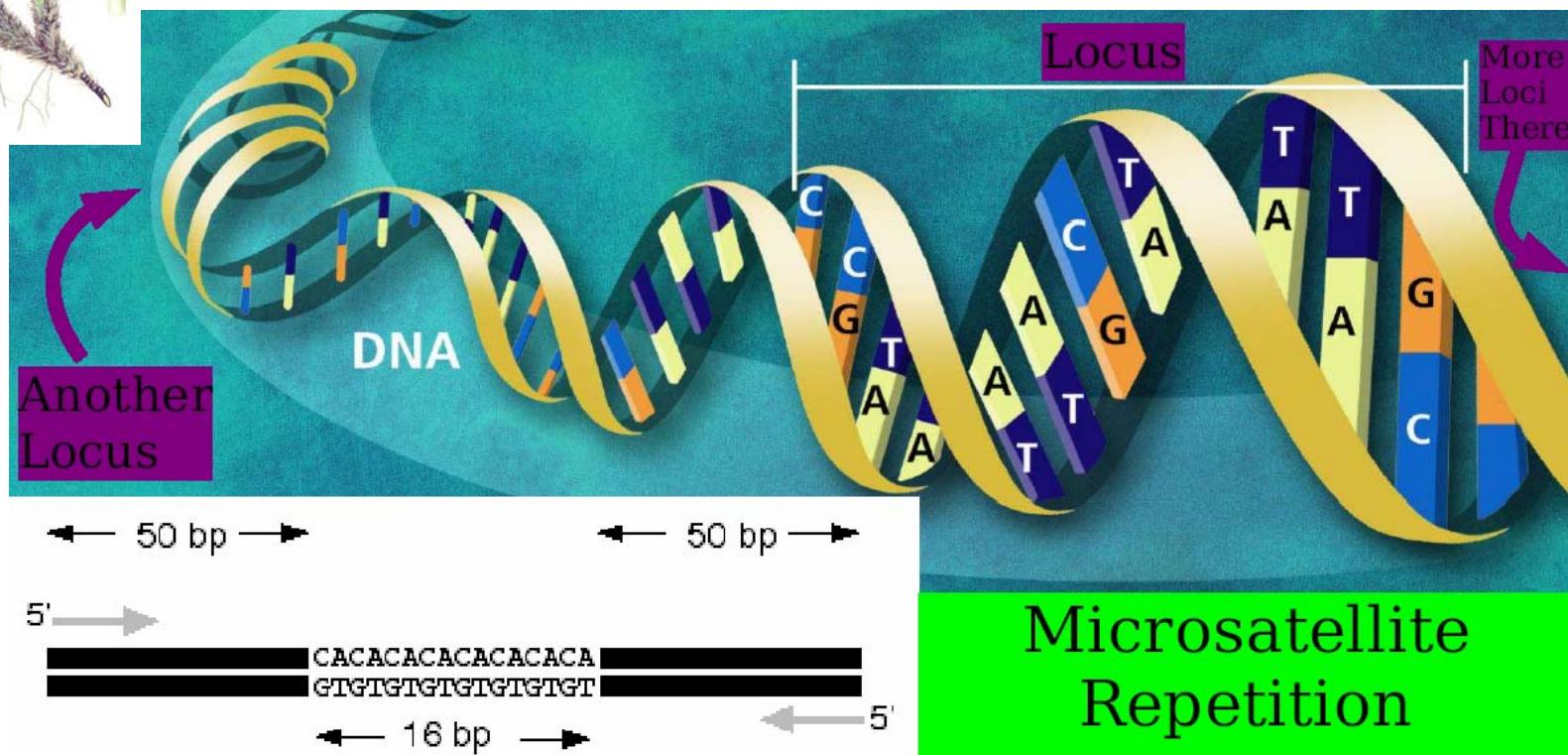
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Genetically characterizing the individuals:

**MICROSATELLITES**: hypervariable markers useful for intrapopulation studies

7 loci analyzed



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## DEFINING A DISTANCE BETWEEN INDIVIDUAL RAMETS OR GENETS

1	2	3	4	5	6	7	← Loci
(A <sub>1</sub> ,a <sub>1</sub> )	(A <sub>2</sub> ,a <sub>2</sub> )		...		(A <sub>i</sub> ,a <sub>i</sub> )		
134, 156	112, 170	140, 140	182, 204	90, 128	170, 172	130, 130	

(B <sub>1</sub> ,b <sub>1</sub> )	(B <sub>2</sub> ,b <sub>2</sub> )	...	(B <sub>i</sub> ,b <sub>i</sub> )
136, 156	112, 170	140, 140	182, 204



min<sub>1</sub>

$$\min_i = \min(|A_i - B_i| + |a_i - b_i|, |A_i - b_i| + |a_i - B_i|)$$

134, 156

136, 156

min

134, 156

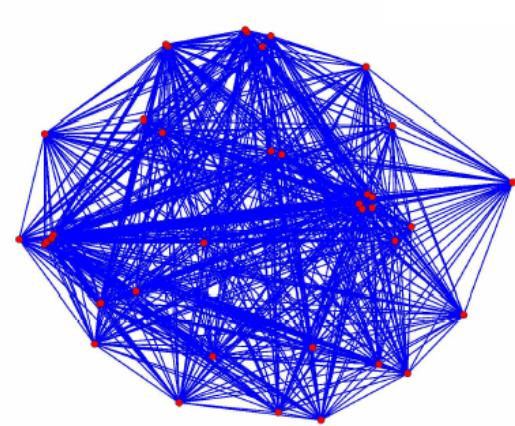
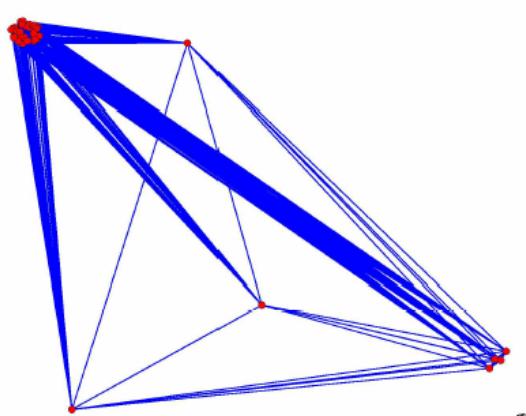
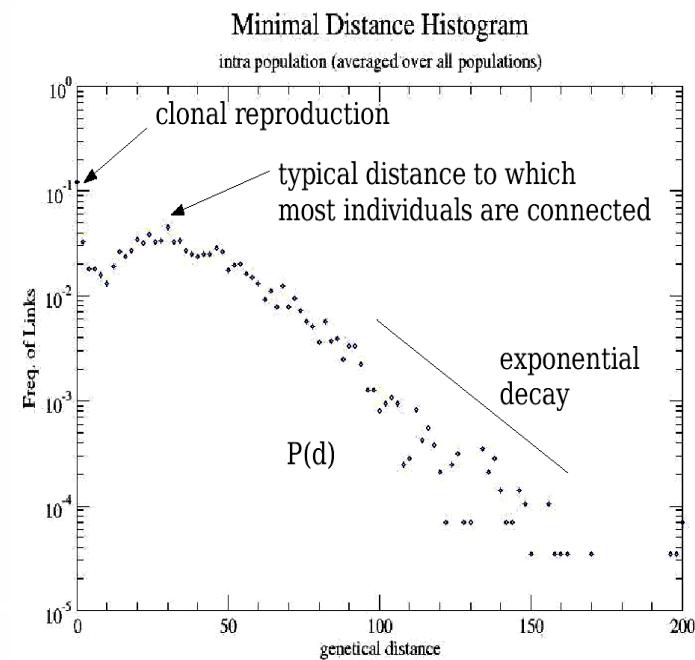
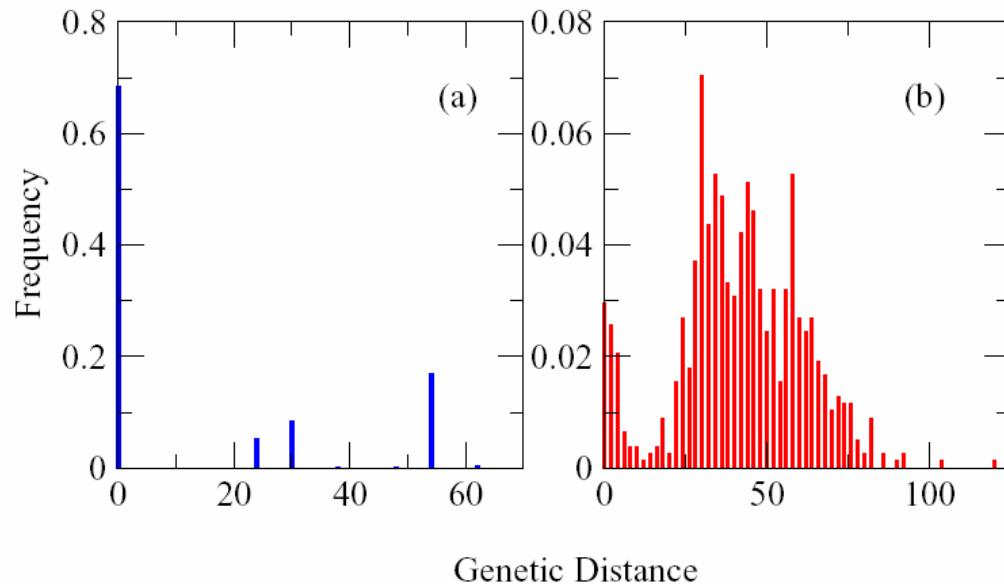
136, 156

$$2 + 0 = 2$$

$$20 + 22 = 42$$

$$\text{Dist}_g(\text{A}, \text{B}) = \sum_{i=1}^{\text{Num of Loci}} \min_i$$

## Intrapopulation Genetic Diversity Spectra (distance histograms)



## Constructing networks of genetic similarity in *Posidonia oceanica*

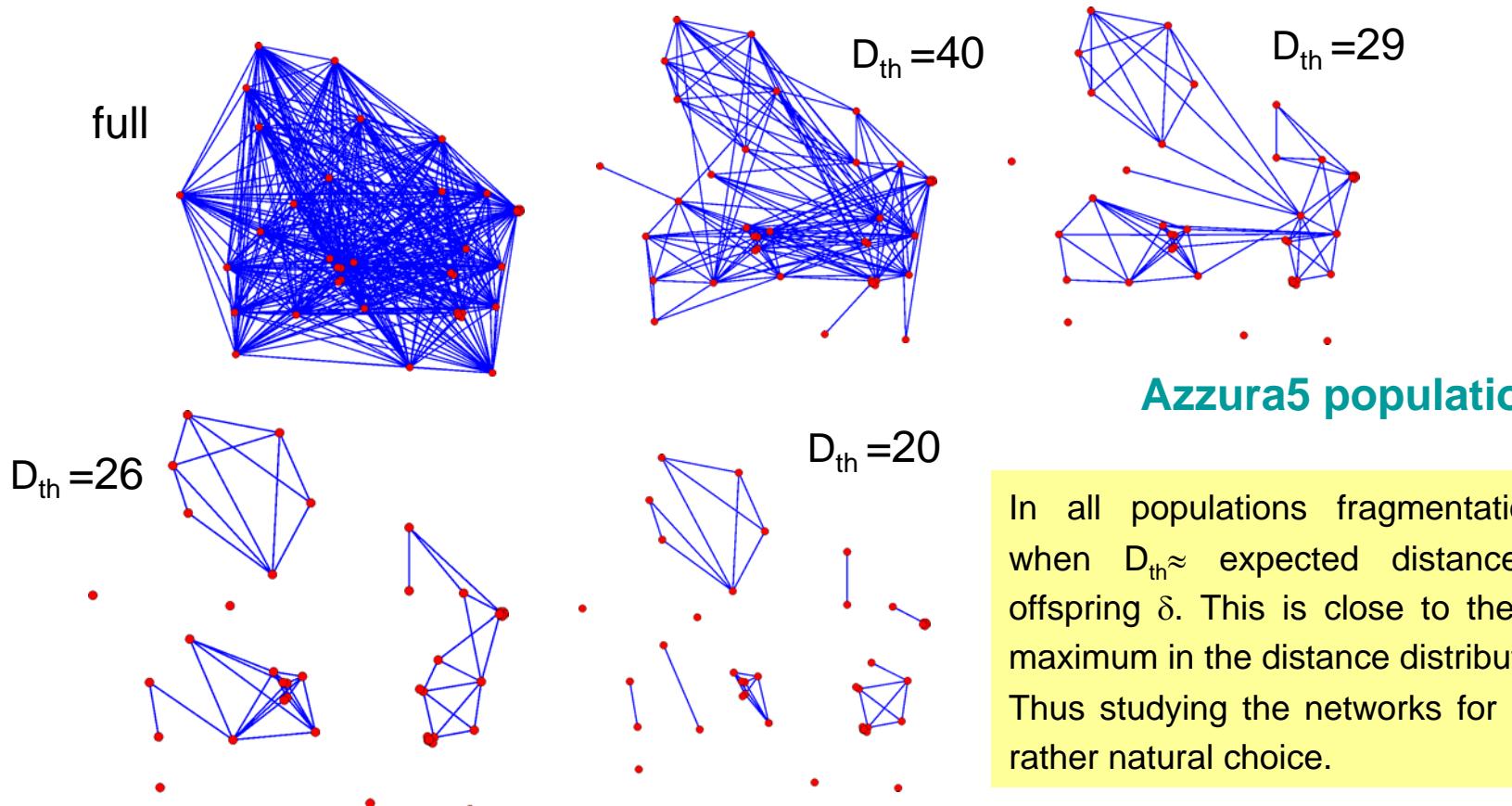
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## NETWORK GENERATION:

Links between ramets genetically closer than a threshold distance  $D_{th}$

Examples: Interactions in a stock market (Onnela et al, 2003)

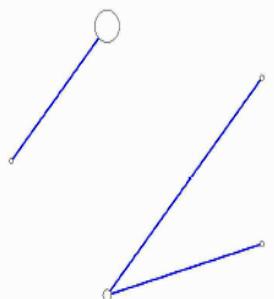
Functional networks in the human brain (Eguíluz et al, 2005).



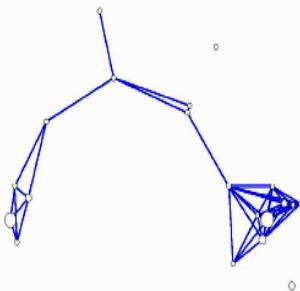
In all populations fragmentation occurs when  $D_{th} \approx$  expected distance parents-offspring  $\delta$ . This is close to the nonclonal maximum in the distance distribution. Thus studying the networks for  $D_{th} \approx \delta$  is a rather natural choice.

## GENET NETWORKS FOR $D_{th} \approx \delta$ (expected distance parent-offspring)

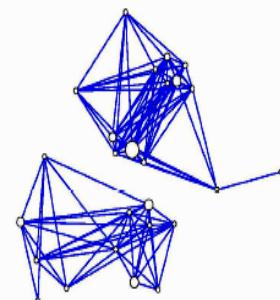
Es Castell (Cabrera)



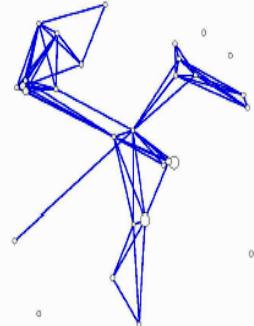
Cala Jonquet (Iberian Peninsula)



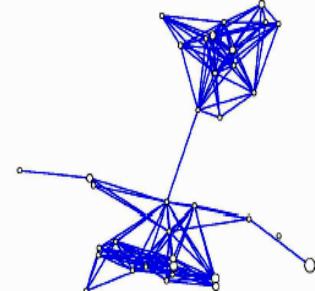
Rodalquilar (IP)



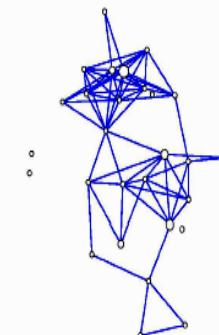
Azzura (Sicily)



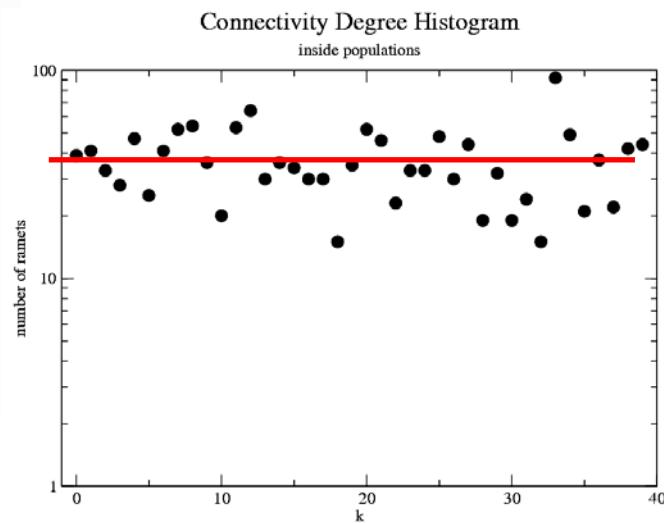
Roquetas (IP)



Cavalllets (Ibiza)



Groups, clustering, ... → population structure



	<i>G</i>	<i>S</i>	<i>C</i>	<i>L</i>	<i>Cr</i>	<i>Lx</i>	$\langle k \rangle$	$\rho$
Aqua Azzura 3	31	28	0.80	3.13	0.22	2.17	4.71	0.16
Aqua Azzura 5	29	25	0.78	2.43	0.26	2.01	4.76	0.17
Addaia	25	17	0.72	1.64	0.41	1.91	5.60	0.23
Amathous 3	18	11	0.77	1.45	0.33	1.86	4.67	0.27
Amathous 5	25	24	0.73	3.14	0.29	2.19	4.56	0.19
Agius Nicolaos	28	18	0.81	2.41	0.27	2.13	5.50	0.20
Calabardina	40	40	0.62	3.44	0.19	2.25	5.90	0.15
Cala Giverola	17	10	0.84	1.22	0.70	1.76	4.35	0.27
Cala Jonquet	20	18	0.79	2.95	0.37	1.89	4.60	0.24
Campomanes	22	12	0.66	1.77	0.25	2.18	4.00	0.19
Carboneras	16	16	0.78	1.75	0.75	1.49	8.50	0.57
El Arenal	32	27	0.76	2.74	0.27	2.11	5.25	0.17
Es Castell	05	03	0.00	1.33	0.00	1.33	1.20	0.30
Es Pujols	27	24	0.74	2.76	0.57	1.97	5.70	0.22
Es Cal des Oli	15	07	0.73	1.14	0.49	1.98	2.80	0.20
Ses Illetes	21	20	0.78	2.62	0.36	1.82	5.52	0.28
Cala Fornells	05	03	1.00	1.00	1.00	1.00	1.20	0.30
La Fossa Calpe	31	29	0.63	2.76	0.24	2.08	5.55	0.18
Las Rotes	34	21	0.75	1.98	0.20	2.25	4.65	0.14
Los Genoveces	14	13	0.86	1.45	0.86	1.34	7.71	0.59
Magaluf	26	18	0.64	1.88	0.39	2.11	4.46	0.18
Malta	29	24	0.67	2.19	0.33	1.89	5.24	0.19
Marzamemi	31	28	0.63	2.48	0.39	2.07	5.61	0.19
Es Port	05	05	0.90	1.10	0.90	1.10	3.60	0.90
Paphos	26	17	0.74	1.65	0.43	1.95	6.54	0.26
Playa Cavallers	28	24	0.63	2.45	0.30	1.97	4.86	0.18
Port Lligat	12	07	0.95	1.10	0.43	1.59	4.17	0.38
Porto Colom	21	16	0.83	1.42	0.75	1.55	7.62	0.38
Punta Fanals	26	26	0.70	2.06	0.48	1.83	7.54	0.30
Rodalquilar	27	14	0.84	1.32	0.37	1.75	8.22	0.32
Roquetas	35	34	0.79	2.47	0.33	1.86	8.74	0.26
C.Sta.Maria 13	20	19	0.73	2.37	0.43	1.79	5.50	0.29
C.Sta.Maria 7	22	16	0.66	1.74	0.61	1.82	4.91	0.23
Cala Torreta	21	10	0.75	1.84	0.13	2.37	3.33	0.17
Torre de la Sal	15	13	0.71	1.64	0.58	1.64	4.93	0.35
Tunis	34	30	0.77	2.80	0.28	2.15	5.41	0.16
Xilxes	12	05	0.47	1.80	0.08	2.37	1.50	0.14
$\langle x \rangle$	22.84	18.16	0.73	2.04	0.41	1.88	5.11	0.27
$\sigma$	8.54	8.82	0.16	0.65	0.23	0.32	1.77	0.15
$\min(x)$	5.00	3.00	0.00	1.00	0.00	1.00	1.20	0.14
$\max(x)$	40.00	40.00	1.00	3.44	1.00	2.37	8.74	0.90

Genet networks  
characteristics:

- Clustering larger  
than random

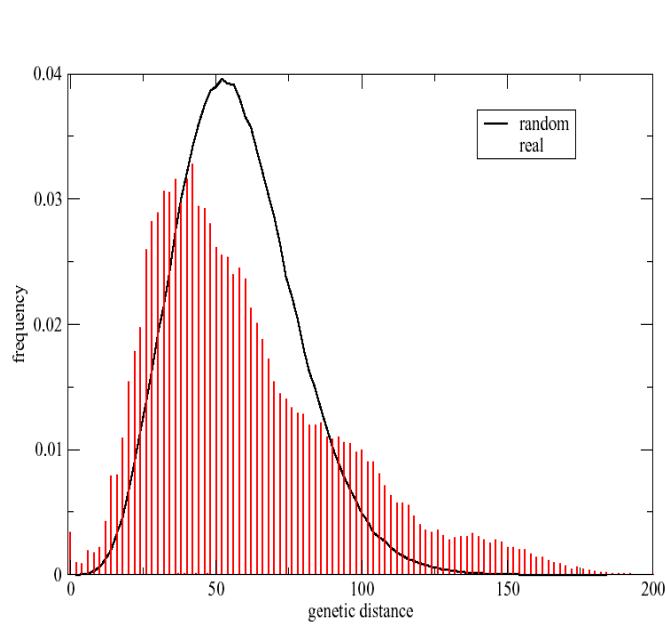
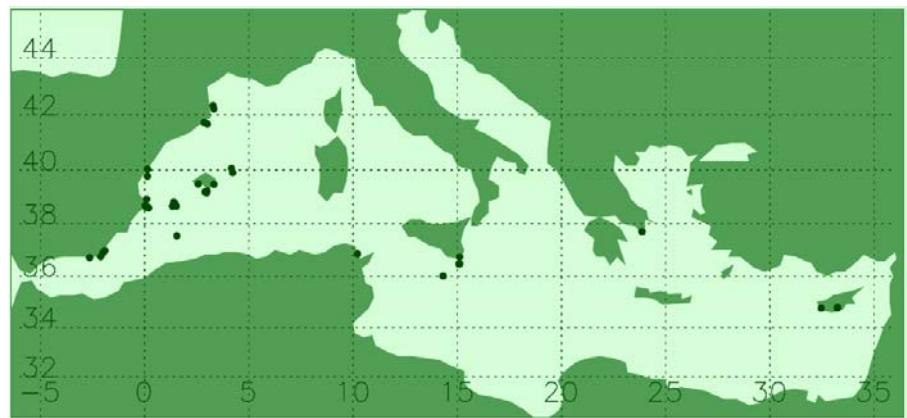
-Diameter of the  
same order

**SMALL WORLD**

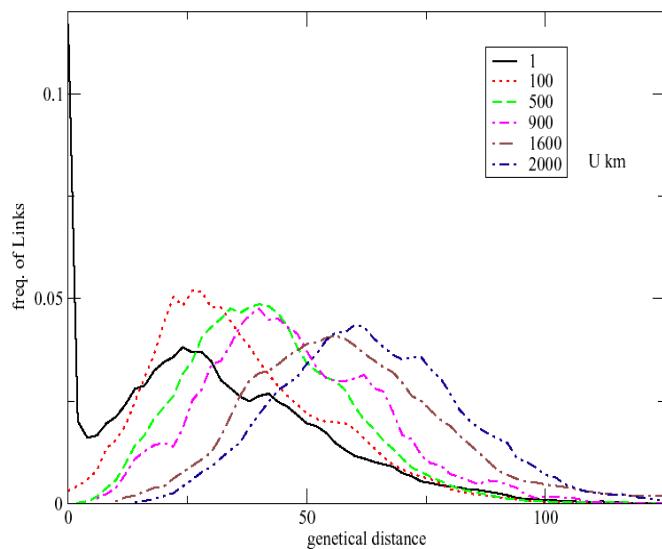
- High density of  
links

"distance networks"

## Genetic diversity spectrum across the whole Mediterranean

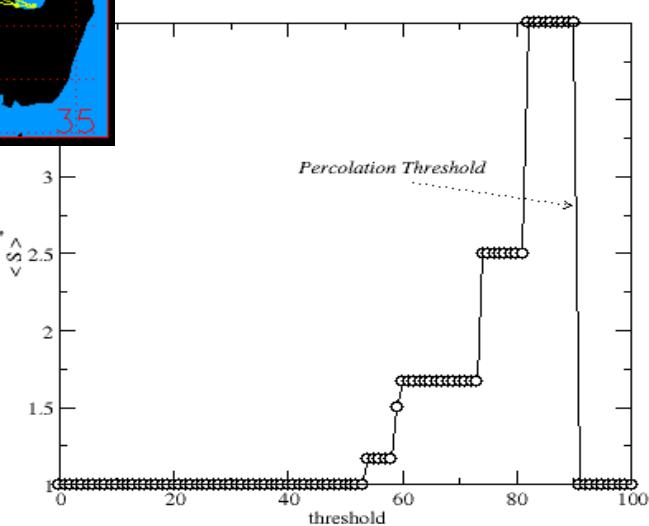
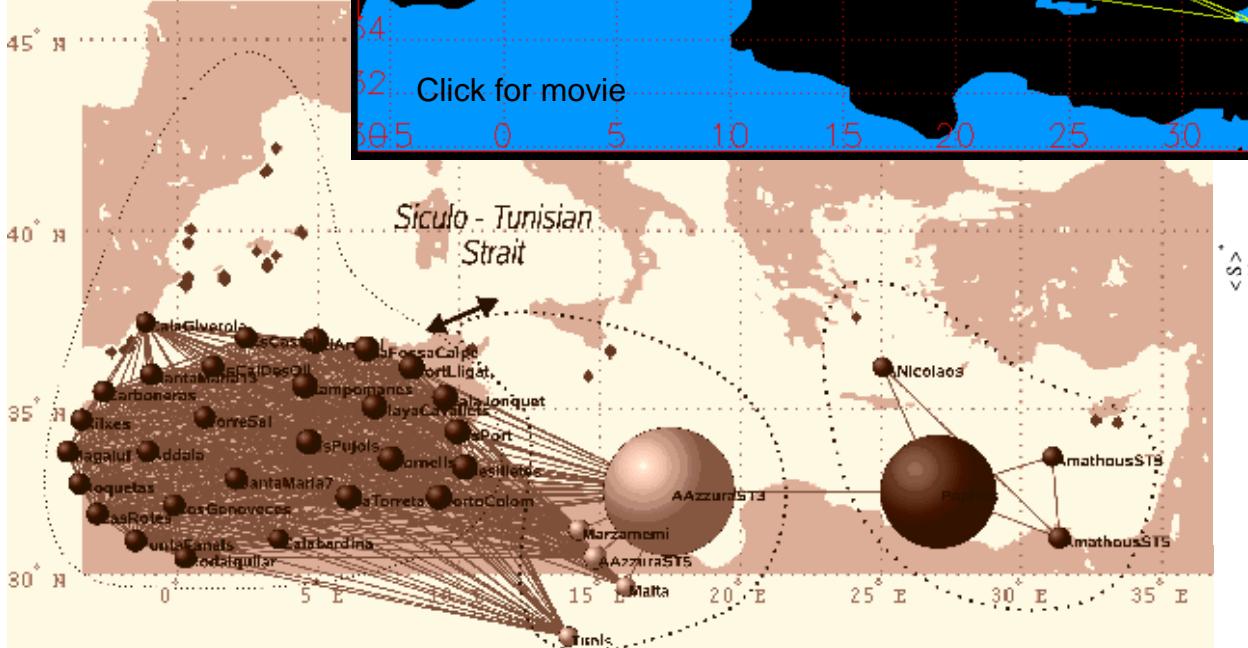
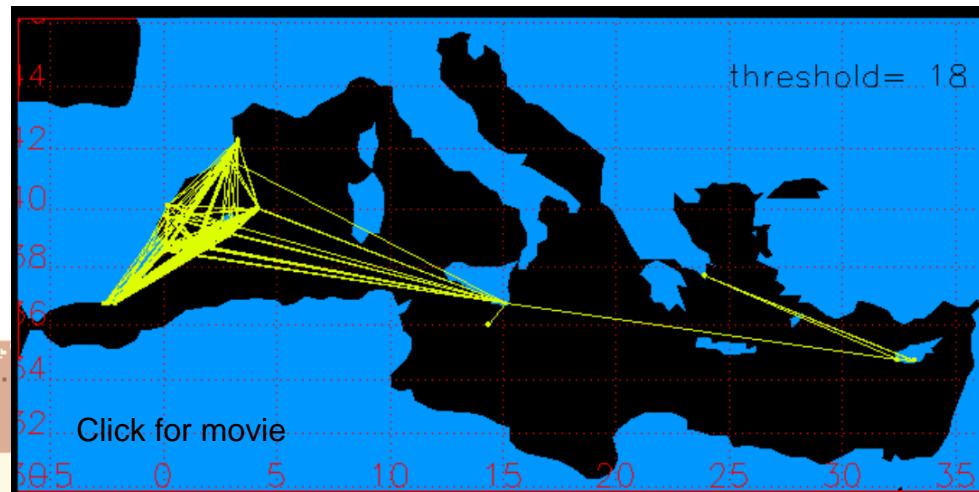


Histogram of Contributions from Links  
at geographical distance  $U - 100\text{km} < d < U$

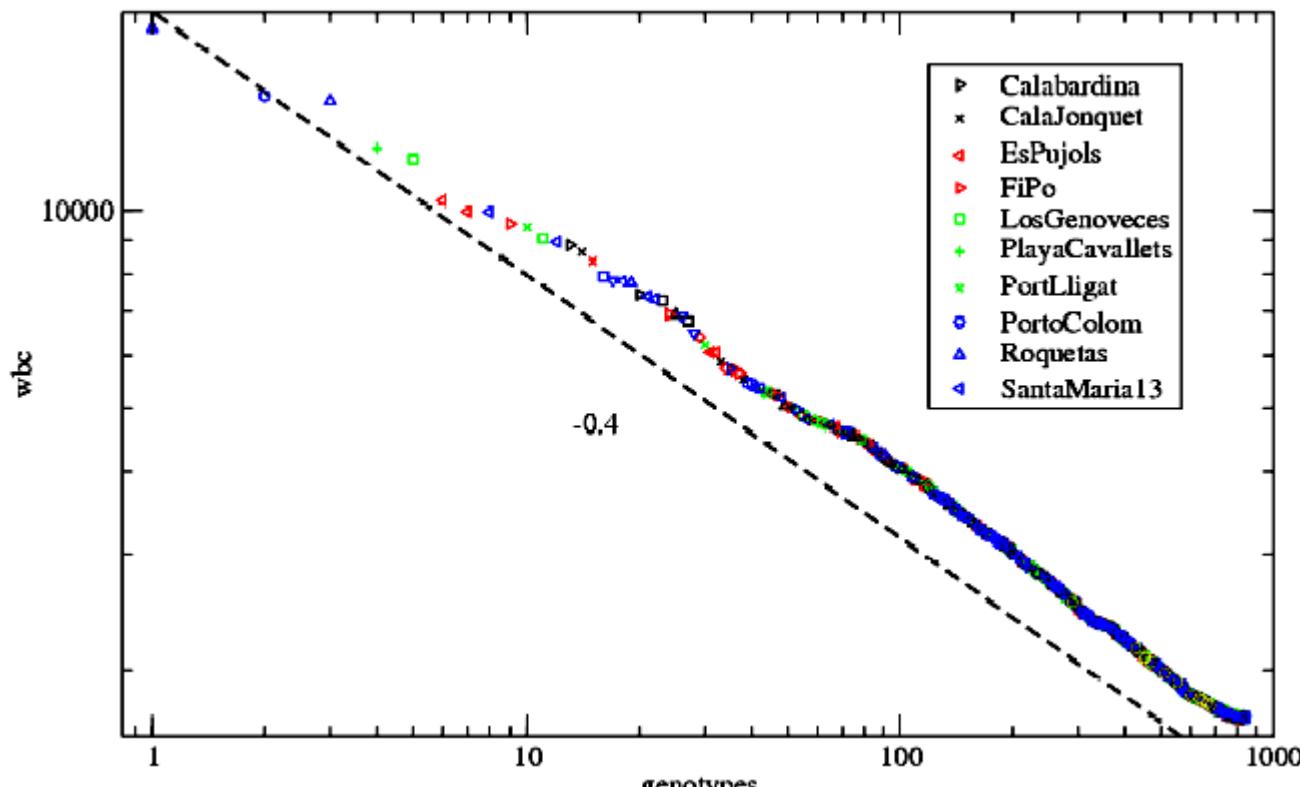


## NETWORKS OF GENETIC SIMILARITY

Interpopulation case (metapopulation)

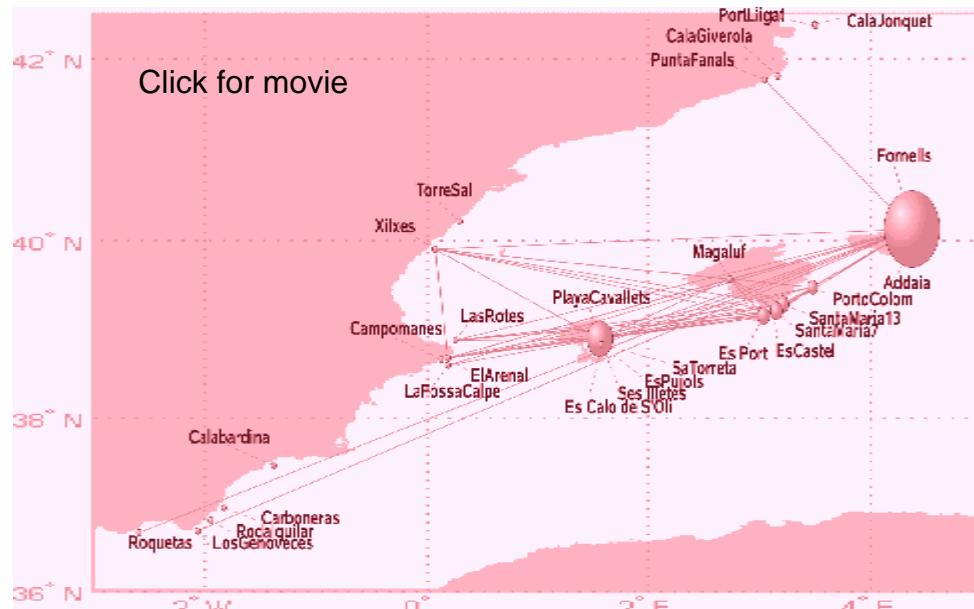


## Genotype betweenness



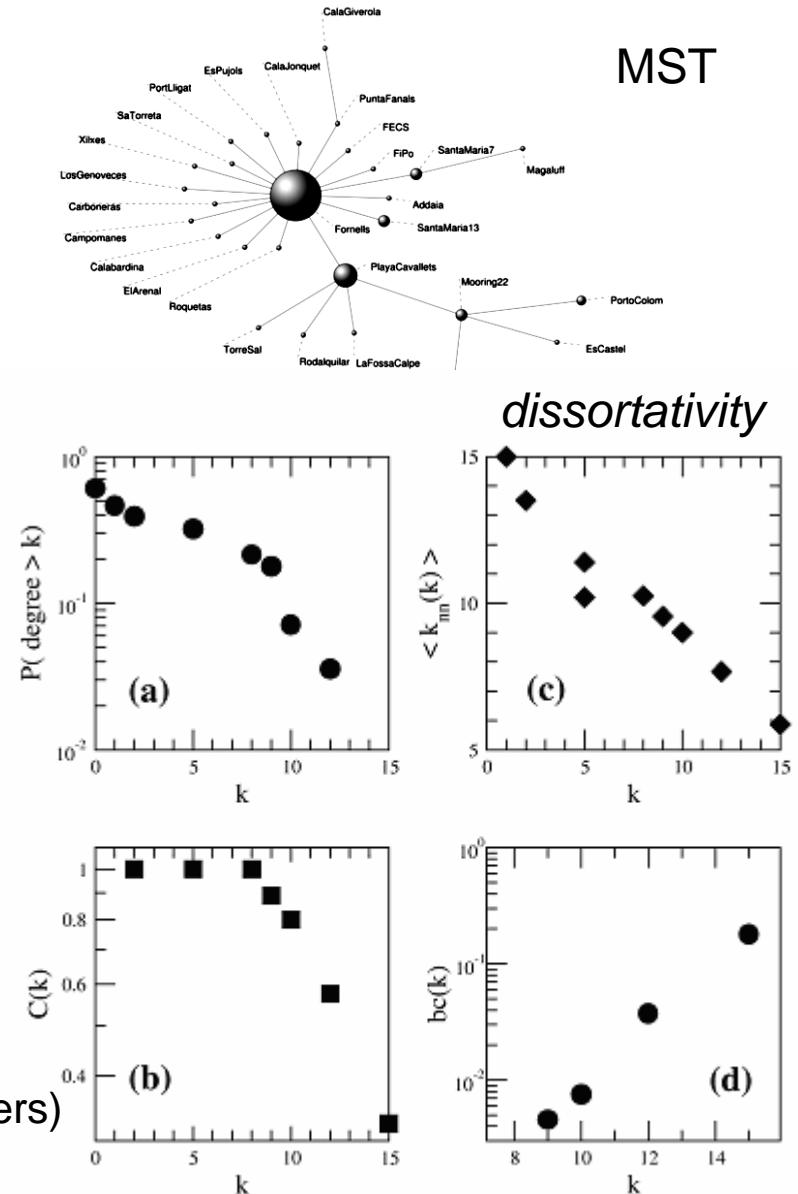
Genotype rank

Relevant to gene flow



**Population structure:** Nodes in the Balearic Islands have highest betweenness centrality and degree. “Star-like topology”

**Gene flow:** High clonality and large degree (Fornells and Es Port): net gene sources (exporters)



## SUMMARY

- Intraspecific genetic similarity networks provide powerful tools to summarize genetic information, and give insight into properties such as population structure. The methodology developed is useful for other species beyond Posidonia (Cymodocea is in progress).
- For the organism studied, intrapopulation networks are very dense small worlds. It would be interesting to relate network measures to ecosystem health
- Gene flow, central populations, gene sources, are conveniently revealed by network methods.

Rozenfeld et al., J. Roy. Soc. Interface 4, 1093 (2007)  
Rozenfeld et al., submitted (2008)  
Hernandez-Garcia et al., AIP Conf. Proc. 913, 78 (2007)  
Hernandez-Garcia et al., Physica D 214, 166 (2006)

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