

Genetic similarity networks: Weak and strong links In populations and in metapopulations

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The development of orolutionary theory in the framework of population genetics has indergone major progress with the arrival of molecular biology and molecular markers. Novel tools of analysis, free of nost of traditional theoretical assumptions, are needed for taking full advantage of the

modern genetic data sets. Here, we use recently in networks of genetic similarity (*Ro al. JRS Interface*, 2007) to an hierarchy and organization of th e.Universidade do Algarve Faro, Portugal de in diversity of a manno plant d oceanica, across its entire geo

> intrapopulation networks, in which nodes are genotypes, and interpopulation networks in which nodes are plant





2. NETWORK CONSTRUCTION: For each population, we construct networks in which the nodes are the individual ramets, linked if their genetic distance is smaller than a distance threshold. This is chosen as the mean simulated distance from parents and offspring



Populaton genetic substructure is clearly visualized # The networks are of the small/world type. Clustering is much higher than in random networks. This reveals strong correlations, implying not random mating, not easily detectable by oher means.



Ande size: betweeness centrality

1.DEFINING A DISTANCE BETWEEN INDIVIDUAL RAMETS: The fact that Posidonia is a diploid plant (i.e., its genome is organized in pairs of chromosomes) poses problems to use standard definitions of distance between individuals Here we introduce a distance defined as the sum of microsatellite repetition differences, comparing the pair of alleles at each locus in the way leading to the minimum value.



4. RESULTS: Intrapopulation genet networks

Betweenness-centrality and degree calculations allow to identify geographical regions acting as major hubs relaying gene flow

Sicily populations are the bridge for West/East gene flow. Balearic populations are central in the Western Mediterranean population structure





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