Project no. 043251

EDEN

ECOLOGICAL DIVERSITY AND EVOLUTIONARY NETWORKS

Instrument: Specific Targeted Project (STREP)

Thematic Priority: Integrating and strengthening the European Research Area
NEST Pathfinder initiative Tackling Complexity in Science

D1.3 (D14). **Web-based database containing network phylogenies and genetic diversity networks**

Due date of deliverable: Month 33
Actual submission date: Month 33

Start date of project: 1 January 2007   Duration: 36 months

Organisation name of lead contractor for this deliverable: CCMAR
Contributor: IMEDEA-UIB

Project co-funded by the European Commission within the Sixth Framework Programme (2002-2006)		
Dissemination Level		
PU	Public	PU
PP	Restricted to other programme participants (including the Commission Services)	
RE	Restricted to a group specified by the consortium (including the Commission Services)	
CO	Confidential, only for members of the consortium (including the Commission Services)	

NOTE: This is a short description of deliverable D1.3 . The deliverable itself is in
`http://ifisc.uib-csic.es/EDEN/fichaOutput.php?idOutput=17`
and in `http://ifisc.uib-csic.es/eden/Data/`

D1.3 (D14)
Web-based database containing network phylogenies and genetic diversity networks

The EDEN project has developed novel methodologies to characterize genetic relationships among biological individuals and species by using network methods. This deliverable consists in a series of data files, accessible via the EDEN web, containing results of analysis of two seagrass species, *Posidonia oceanica* and *Cymodocea nodosa*.

The entry URL for the database is http://ifisc.uib-csic.es/eden/Data/

Details of the methodology used to obtain each file and of the meaning and interpretation of the different concepts (such as Genetic Diversity Spectrum, GDS, percolation thresholds, etc.) are described in deliverables D4.1 (http://ifisc.uib-csic.es/EDEN/fichaOutput.php?idOutput=14),
D4.2 (http://ifisc.uib-csic.es/EDEN/fichaOutput.php?idOutput=18) and in the references cited there. In fact, the following two references contain enough material to understand all the concepts and files presented here:

Spectrum of genetic diversity and networks of clonal organisms. *A.F. Rozenfeld, S. Arnaud-Haond, E. Hernandez-Garcia, V.M. Eguiluz, M.A. Matias, E. Serrao, C.M. Duarte.* Journal of the Royal Society Interface 4, 1093-1102 (2007) . http://dx.doi.org/10.1098/rsif.2007.0230

Network analysis identifies weak and strong links in a metapopulation system. *A.F. Rozenfeld, S. Arnaud-Haond, E. Hernández-García, V.M. Eguíluz, E.A. Serrão and C.M. Duarte.* Proceedings of the National Academy of Sciences of the USA (PNAS) 105, 18824-18829 (2008). http://dx.doi.org/10.1073/pnas.0805571105

Data files are organized in two main directories, corresponding to each of the two species:

Posidonia oceanica: http://ifisc.uib-csic.es/eden/Data/Posidonia

Microsatellite data analyzed are from
Arnaud-Haond et al. (2007) Vicariance patterns in the Mediterranean sea: East-West cleavage and low dispersal in the endemic seagrass *Posidonia oceanica*. *Journal of Biogeography*, 34, 963-976.
doi: 10.1111/j.1365-2699.2006.01671.x
The dataset itself is available on the EDEN web
(http://ifisc.uib-csic.es/EDEN/fichaOutput.php?idOutput=70), and is also included in the data compilation conforming deliverable D1.2 (http://ifisc.uib-csic.es/EDEN/fichaOutput.php?idOutput=12).

Data in this web database are organized in intrapopulation results (**IntraPops** folder) and interpopulation networks and data (**InterPops** folder). The **interpopulation** folder contains representations of the Posidonia network across the whole Mediterranean and in the Spanish coast area (as EPS figures and as .paj files, the native format of the network analyzer program pajek, http://vlado.fmf.uni-lj.si/pub/networks/pajek/). The **intrapopulation** folder contains two subdirectories: **GDS** contains postscript files with the Genetic Diversity Spectrum from all populations analyzed. The vertical red line marks the genetic distance used as threshold to construct the intrapopulation networks. It is chosen as the one-generation outcrossing distance, which approximately corresponds to the peak in the GDS of each population and is also very closely related to the percolation point. The folder **NetsAtOutcrossing** contains a file in pajek format .net for each population, showing the corresponding network of genetic similarity where nodes are sampled genets, i.e. the different multi-locus genotypes found at the meadow, and the links are established among genets at a genetic distance smaller than the threshold distance.

Cymodocea nodosa: http://ifisc.uib-csic.es/eden/Data/Cymodocea

Microsatellite data analyzed are from
F. Alberto et al. (2008) Genetic differentiation and secondary contact zone in the seagrass Cymodocea nodosa across the Mediterranean–Atlantic transition region. Journal of Biogeography 35, 1279 – 1294 (2008). doi:10.1111/j.1365-2699.2007.01876.x
The dataset itself is available in the EDEN web
(http://ifisc.uib-csic.es/EDEN/fichaOutput.php?idOutput=69), and is also included in the data compilation conforming deliverable D1.2 (http://ifisc.uib-csic.es/EDEN/fichaOutput.php?idOutput=12).

Data in this web database are organized in intrapopulation results (**IntraPops** folder) and interpopulation networks and data (**InterPops** folder). The **interpopulation** folder contains representations of the Cymodocea network across its whole samplingrange (as PNG and SVG). The full GDS and the Minimum Spanning Tree (MST) are also presented. The file percolation.eps shows the percolation analysis that has been used to define the network threshold. The **intrapopulation** folder contains three subdirectories: **GDS** contains postscript files with the Genetic Diversity Spectrum from all populations analyzed. The folder **NetsAtOutcrossing** contains a file PNG and another SVG for each population, showing the corresponding network of genetic similarity where nodes are sampled genets, i.e. the different multi-locus genotypes found at the meadow, and the links are established among genets at a genetic distance smaller than the threshold distance (threshold obtained from the percolation analysis).Finally, the folder **percolation** contains an EPS figure for each population, showing the percolation analysis used to define the network threshold.