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Comune di Padova

Società Botanica Italiana

**ANNUAL MEETING OF THE
ITALIAN PHYCOLOGICAL
GROUP**

in conjunction with the

Annual General Meeting (AGM)

of the Federation of European Phycological Societies (FEPS)

By Isabella Moro, Katia Sciuto and Marion A. Wolf

Sala Rossini, Caffè Pedrocchi

November 14th - 15th 2014

Padova





Annual Meeting

Padova, 14th-15th November 2014

BY ISABELLA MORO, KATIA SCIUTO & MARION A. WOLF

**ORGANIZERS: ISABELLA MORO, KATIA SCIUTO, MARION A. WOLF, FRANCESCA DALLA
VECCHIA, MARA MARZOCCHI & RENATA TREVISAN**

Società Botanica Italiana
Annual Meeting of the Italian Phycological Group

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Federation of European Phycological Societies (FEPS)**

Sala Rossini, Caffè Pedrocchi
Padova, November 14th - 15th 2014

Friday, November 14th

8:30 Participant registration

9:00 Meeting Opening and Welcome Greetings

9:10 Invited talk

Cyanobacteria and cyanotoxins: recognition, research and risk management.
Prof. Geoffrey A. Codd, University of Stirling, UK

9:45 – 10:15 **Cyanobacteria**

Chair: Carlo Andreoli

9:45 Antarctic cyanobacteria biodiversity and mapping by remote sensing satellites:
preliminary data of a monitoring method of *in situ* populations.
Micheli C., Belmonte A., De Cecco L., Martini S., Marcelli M. & Borfecchia F.

10:00 Phototrophic biofilms from Indian Temples and application of a nanomaterial as a
remediation strategy.
Bruno L., Valentini F. & Adhikary S.P.

10:15 – 12:00 **Microalgae and toxins**

Chair: Rossella Pistocchi

10:15 Interactions between the toxic dinoflagellate *Ostreopsis* cf. *ovata* and the benthic
diatom *Tabularia* sp.
Pichierri S., Accoroni S., Romagnoli T., Righetti M., Guerrini F., Pistocchi R. &
Totti C.

10:30 Intraspecific variability in *Ostreopsis* cf. *ovata* revealed by AFLP and toxin
profiles.
Di Cioccio D., Italiano A., Procaccini G., Borra M., Biffali E., Rossi R., Soprano
V. & Zingone A.

10:45 – 11:15 **Coffee Break**

- 11:15 Assessing the harmful microalgae occurrence in a coastal mussel culture area, the Mar Piccolo in Taranto (Ionian Sea, Italy).
Caroppo C., Cerino F. & Cibic T.
- 11:30 Two ways of attachment to substrate of the toxic benthic dinoflagellate *Ostreopsis* cf. *ovata*.
Honsell G., Pezolesi L. & Pistocchi R.
- 11:45 Contribution by Simionati B. (BMR Genomics, Padova): Sanger and Next Generation Sequencing technologies for DNA Barcoding.
- 12:00 – 13:00 **Microalgae and adaptations**
Chair: Fabio Rindi
- 12:00 Identification of a metal-resistant "*Coccomyxa*" (Trebouxiophyceae) isolated from an extreme environment river in Sardinia (Italy).
Malavasi V., Tempesta S., Paoletti M. & Pasqualetti M.
- 12:15 Comparison of four methods for quantitative analysis of soil algae.
Zancan S., Zannoni M. & Trevisan R.
- 12:30 Polyphyletic nature of low pH adaptation in the genus *Klebsormidium* (Klebsormidiophyceae, Streptophyta).
Malavasi V., Ryšánek D., Škaloud P., Lukešová A., Hřčková K. & Rindi F.
- 12:45 *Tetraflagellochloris mauritanica* gen. et sp. nova (Chlorophyceae): motion and swimming patterns.
Barsanti L., Coltelli P., Evangelista V., Frassanito A.M. & Gualtieri P.
- 13:00- 14:30 **Lunch**
- 14:30 – 15:30 **Phytoplankton**
Chair: Mara Marzocchi
- 14.30 Who are the main planktonic primary producers in Mar Piccolo of Taranto?
Cibic T., Caroppo C., Karuza A., Di Poi E. & Del Negro P.
- 14:45 Phytoplankton distribution along the world from the TARA Oceans expedition.
Scalco E., Sarno D., Iudicone D., Tanaka A., Malviya S., Vincent F., Bowler C. & Zingone A.
- 15:00 Autotrophic communities in natural CO₂-dominated waters of the Aeolian Islands (Tyrrhenian Sea).
Cerino F., Fornasaro D., Karuza A., Ingrosso G., Kralj M., Comici C., Giani M., Cabrini M. & De Vittor C.
- 15:15 Exchange of indigenous and alien microalgae species from ballast waters, the BALMAS approach.
Bastianini M., Bernardi Aubry F., Finotto S., Penna A., Perini F., Cabrini M. & Pompei M.

15:30 – 16:30 Microalgae, systematics and molecular biology

Chair: Diana Sarno

- 15:30 Study of diatoms in sediments of an Alpine pond (Lake Welsperg, East Trentino, Val Canali, Parco Naturale Paneveggio - Pale di S. Martino).
Mattiazzo C., Ceschi Berrini C., Picarella M., Zannoni M. & Trevisan R.
- 15:45 Partial isolation of two *Scenedesmus acutus* genes homologous to *Chlamydomonas reinhardtii* ATP sulfurylase.
Zanlorenzi G., Sardella A., Marieschi M., Zanni C. & Torelli A.
- 16:00 Complete genome sequence of chloroplast and mitochondrial DNA of *Chlorella sorokiniana*.
Costelli C., Malavasi V., Orsini M., Cusano R., Concas A., Angius A. & Cao G.
- 16:15 Systematics and biodiversity of marine *Mastogloia* (Bacillariophyceae): revision of section Inaequales and phenetic methodologies applied to section Ellipticae.
Pennesi C., Poulin M., Romagnoli T. & Totti C.

16:30 – 17:00 Coffee Break

17:00 – 18:15 Macroalgae

Chair: Mario Cormaci

- 17:00 The phytobenthos of the Mar Piccolo of Taranto (Ionian Sea, Southern Italy): a novel of ninety years of disappearances, new arrivals and returns.
Petrocelli A., Portacci G. & Cecere E.
- 17:15 Updating of alien macroalgae in the Venice Lagoon, new introductions and cryptogenic species.
Sfriso A., Sfriso A.A., Marchini A. & Occhipinti-Ambrogi A.
- 17:30 First report of *Gelidium americanum* (Gelidiales, Rhodophyta) from the Mediterranean Sea.
Bottalico A., Boo G.H., Russo C., Boo S.M. & Perrone C.
- 17:45 The “Vatova algarium” project: a case study on biodiversity changes through historical samples in the molecular age.
Armeli Minicante S., Ceregato A., Manghisi A., Morabito M., Genovese G. & Sfriso A.
- 18:00 Phycological jokes...and more.
Furnari G.

18:15 – 19:00 Member Meeting

20:30 Social Dinner

Saturday, November 15th

9:00 Invited talk

Phytoplankton ecophysiology in an era of global changes.
Prof. John Beardall, Monash University, Victoria Australia

9:30 – 11:00 Microalgae, physiology and applications

Chair: Nicoletta Rascio

9:30 Effect of organic carbon sources on biomass production and photosynthesis of marine microalga *Nannochloropsis gaditana*.
Simionato D., La Rocca N. & Morosinotto T.

9:45 Selecting functional types of microalgae suitable for CO₂ sequestration and wastewater remediation.
Norici A., Ratti S. & Giordano M.

10:00 Effects of different nitrogen sources on C-fixation and N-assimilation in *Scenedesmus* sp.
Mazzotti M., Beardall J. & Pistocchi R.

10:15 Light and nutrient effects on ketocarotenoid synthesis in *Chodatodesmus australis*.
Simionato D., Segalla A., Morosinotto T. & La Rocca N.

10:30 Optical properties of diatom nanostructured biosilica: micro-optics from mother nature.
De Stefano M., Rea I., Coppola G., Dardano P., Di Caprio G., Ferrara M.A., De Stefano L., Congestri R., Antonucci A. & De Tommasi E.

10:45 Different FeSOD levels are associated with different Cr(VI) tolerance in two strains of *Scenedesmus acutus*.
Sardella A., Bertazzini M., Marieschi M., Zanni C., Forlani G. & Torelli A.

11:00 – 11:30 Coffee Break

11:30 – 13:00 Macroalgae and aquatic angiosperms

Chair: Ester Cecere

11:30 Marine benthic flora of the Mediterranean Sea: Chlorophyta.
Cormaci M., Furnari G. & Alongi G.

11:45 Macrophytes of the soft substrata of the Venice lagoon, abundance and distribution.
Sfriso A., Sfriso A.A. & Buosi A.

12:00 Ultrastructural study on the infection mechanism and host response of the marine oomycete *Eurychasma dicksonii* infecting brown seaweeds.
Tsirigoti A., Beakes G.W., Gachon C.M.M. & Katsaros C.

- 12:15 Distribution and genetic diversity of the coralline red algae *Lithophyllum byssoides* (Lamarck) Foslie and *L. stictaeforme* (Areschoug) Hauck along the Italian coasts.
Pezzolesi L., Hernandez-Kantun J., Falace A., Ponti M., Cerrano C. & Rindi F.
- 12:30 Growth rates of dominant macroalgae in areas potentially affected by anoxic crises: the Venice lagoon as a study case.
Sfriso A.A. & Gallo M.
- 12:45 Restoration of the habitat 1150* by transplantation of aquatic angiosperms in the northern basin of Venice lagoon: the Life “SeResto” project.
Buosi A., Facca C., Bonometto A., Boscolo R., Parravicini M., Pedrali C., Siega A., Volpe V. & Sfriso A.

13:00 Closing Greetings

Annual Meeting
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Abstracts

Cyanobacteria and cyanotoxins: recognition, research and risk management

Geoffrey A. Codd

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School of the Environment, Flinders University, Adelaide, SA 5042,
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The tendency of aquatic cyanobacteria to produce colourful blooms, scums and mats under favourable growth conditions and in waterbodies used by man has undoubtedly been a major factor in their recognition throughout history and long before the development of the microscope. Examples range from the writings of the Roman Pliny the Elder in AD77, to William Shakespeare in 1596-8. The recognition of cyanobacteria today is aided by a rapidly developing range of techniques, from aircraft- and satellite-born optical sensors, to the polyphasic combination of microscopy and molecular biology. Whilst mass populations of cyanobacteria have adverse effects on waterbody biodiversity and the aesthetics and economics of water resources, their potent cyanotoxins act as major drivers in cyanobacterial research and the development of risk management measures to protect human and animal health. Several classes of cyanotoxins, including hepatotoxic tumour-promoters, neurotoxins, cytotoxins and skin irritants (microcystins, nodularins, cylindrospermopsins, anatoxins, saxitoxins, lipopolysaccharide endotoxins) have been purified and intensively researched over recent decades and efforts continue. However, several adverse actions of cyanobacterial cells and extracts on animal development and health, e.g. teratogenicity, neurotoxicity, endocrine disruption and immune dysfunction, which cannot be accounted for by the known cyanotoxins, indicate the production of further classes of bioactive compounds which may present health risks, e.g. retinoids. Cyanobacteria are also recognised as sources of neurotoxic, single amino acids including β -N-methylamino-L-alanine (BMAA) which can accumulate via aquatic food chains. The nature of an association of BMAA with human neurodegenerative disease is under intensive research. Risk management policies, from local, through national, to international level, are being developed and implemented to protect human and animal health from exposure to harmful levels of cyanobacterial cells and cyanotoxins. These range from the monitoring, analysis and reduction of cell populations and cyanotoxins in high-resource waterbodies, to cyanobacterial cell- and cyanotoxin removal in drinking water treatment processes. A current EU action, CYANOCOST (www.cyanocost.com) is contributing to these risk management needs by technology transfer and dissemination, via workshops and the production of handbooks.

Antarctic cyanobacteria biodiversity and mapping by remote sensing satellites: preliminary data of a monitoring method of *in situ* populations

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Cyanobacteria belong to an ancient group of oxygenic, photosynthetic organisms with a cosmopolitan distribution in many extreme environments, playing important roles in carbon and nitrogen cycles and modifying morphology, metabolism and light-harvesting systems. In particular Antarctic microbial ecosystems have stimulated interest by providing useful models of evolutionary ecology [1]. In fact the Antarctic ice sheet constitutes an exclusive and unique extreme natural environment for study of microorganisms which have been isolated from the global gene pool over timescales of evolutionary significance. In this context cyanobacteria should be considered sensible bio-indicators since they adapt their growth according to the very dynamic condition of the interface between land, ice and water. The polar marine ecosystems are particularly sensitive to climatic change and small temperature differences can have large effects on the extent and thickness of sea ice characterizing land-sea interface. Moreover the extensive mapping and characterization of cyanobacteria of polar habitats are of particular interest because in general they represent here the predominant species contributing a major component of the ecosystem photosynthetic biomass. In addition the strong abiotic stresses in these harsh environments during past evolutionary ages have shaped their particular resilience capability with the production of specific pigment and particular biochemical compounds potentially valuable for innovative biomedical applications and also for bio-energy innovative products.

In the framework of the Italian program for scientific research activities in Antarctica (PNRA) we investigated Antarctic cyanobacteria biodiversity by simultaneous sequencing of the nuclear ribosomal internal transcribed spacer (ITS flanked by partial 16S and 23S), and Chloroplast tRNA^{Leu} UAA intron (*TrnL*). We identified *Nostocales*, *Chroococcales* and *Oscillatoriales* species, collected in different habitats (soil, algal mats, lake sediments, ice-water) after their growth in cultures [2].

In this context we present preliminary data of an introduced method aim at monitoring the Antarctic ecosystem by remote sensing technique for mapping cyanobacteria *in situ* populations from space, using polar satellite sensors.

[1] Warwick F.V. (2000) Evolutionary Origins of Antarctic Microbiota: Invasion, Selection and Endemism. *Antarctic Science* 12: 374-385. <http://dx.doi.org/10.1016/j.cosust.2009.06.001>.

[2] Micheli C., Cianchi R., Paperi R., Belmonte A., Pushparaj B. (2014). Antarctic Cyanobacteria Biodiversity based on ITS and *TrnL* sequencing and its ecological implication. *Open Journal of Ecology* 4: 456-467. <http://dx.doi.org/10.4236/oje.2014.48039>

Phototrophic biofilms from Indian Temples and application of a nanomaterial as a remediation strategy

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In the State of Orissa (Eastern India) there are thousand Hindu temples that witness the past Indian religious art. The tropical climate of the region is characterized by an alternation of a dry and hot season with the rainy monsoon period. The exposed surfaces of these stone monuments made up by sandstone are extensively covered by phototrophic biofilms that cause aesthetic and structural problems to these valuable surfaces that need periodic restoration intervention. The phototrophic biofilms developing on these surfaces are mainly composed by cyanobacteria, and in particular, extremophile species that are able to thrive at the extended period of drought, high temperature and high radiation exposure thanks to the production of scytonemin and mycosporin-like pigments and different heat-shock proteins [1]. Moreover, the exopolysaccharides produced by these cyanobacteria are fundamental for the attachment to the substratum [2]. The biofilms appeared as black or brownish crusts during the dry season, in which cyanobacteria survive in a vegetative state, and as thick blue-green biofilms that are able to revive their metabolic activity soon after rewetting with the monsoon [3].

Studies were carried out on samples collected with non-invasive and non-destructive sampling techniques on different Indian monuments. The cyanobacteria present in the biofilms were characterized by light microscope, while the Confocal Laser Scanning Microscope (CLSM) allowed to investigate the architecture of the biofilms and the relationships between biofilm-forming microorganisms.

In order to develop an innovative non-invasive strategy for the remediation of these valuable sites a nanomaterial has been applied. Graphene Oxide (GO) is an oxygenated/functionalized carbon based nanostructured material [4] that has shown an antimicrobial activity toward *E. coli*. The GO was applied in this study on Indian biofilms and the effect was analyzed with CLSM and mini-PAM. The results obtained showed a reduction of the photosynthetic activity of the biofilms treated with GO, although the cellular mechanism of action remains unknown. The GO appeared as a promising tool to be applied as an environmentally sustainable nanomaterial for the restoration of Cultural Heritage.

[1] Adhikary S.P. (2000) *Indian J Microbiol* 40: 67–81

[2] Albertano P. (2012) In B. A. Whitton Editor, Chapter 11:p. 17-337

[3] Rossi F., Micheletti E., Bruno L., Adhikary S.P., Albertano P., De Philippis R. (2012) *Biofouling* 28: 215–224

[4] Xu Y. and Shi G. (2011) *J. Mater. Chem.* 21: 3311-3323

Interactions between the toxic dinoflagellate *Ostreopsis* cf. *ovata* and the benthic diatom *Tabularia* sp.

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The occurrence of benthic dinoflagellates belonging to the genus *Ostreopsis* has been recorded in both tropical and temperate regions. During the last decade, massive *O. cf. ovata* blooms have occurred in different coastal areas of the Mediterranean Sea typically during the late summer period. *O. cf. ovata* blooms have been related to human intoxication and to mass mortalities of benthic marine organisms due to the production of palytoxin-like compounds, including putative palytoxin and ovatoxin-a, b, c, d, e and f and mascarenotoxin-a and c.

Benthic diatoms are the most conspicuous fraction of microphytobenthos community of temperate regions, and even during intense *Ostreopsis* blooms they represent the bulk of microphytobenthos abundances. The production of secondary metabolites (allelochemicals) in order to compete with other co-occurring microalgae was reported in many planktonic dinoflagellates showing that many toxic microalgae may outcompete the co-occurring microalgal species. On the other hand, diatoms are also able to outcompete due to the high efficiency of nutrient utilization or to the production of metabolites which can inhibit the growth of other microalgae.

The aim of this study is to investigate the interactions between the bloom-forming dinoflagellate *Ostreopsis* cf. *ovata* and a benthic diatom (*Tabularia* sp.) common in the microphytobenthos community of the bloom area during summer.

We collected several microphytobenthos samples from Passetto station (Ancona) in order to isolate *O. cf. ovata* and *Tabularia* sp strains. We set up bi-algal cultures under controlled laboratory conditions with a initial cell density of 3×10^2 and 3×10^3 cells ml⁻¹ for *O. cf. ovata* and *Tabularia* sp respectively. Moreover we cultured *O. cf. ovata* in cell free medium where *Tabularia* was previously grown. In this experiment, we tested different cell density ratios (100:1 or 10:1) for *Tabularia* and *Ostreopsis* respectively.

The results show a decrease of *O. cf. ovata* growth ($\mu=0.125 \pm 0.055$) in co-cultures compared with the respective control ($\mu=0.220 \pm 0.053$), whereas no difference was observed between the growth of *Tabularia* sp. in co-culture respect to the control. Results of filtrate experiment show a decrease of *O. cf. ovata* growth when grown in *Tabularia* growth medium at cell density ratio of 100:1 ($\mu=0.097 \pm 0.001$) and 10:1 ($\mu=0.099 \pm 0.033$) respect to the control.

These preliminary results suggest that diatoms could exert a kind of control vs. *Ostreopsis* blooms. On the contrary, they seem not to be affected by *Ostreopsis* presence and abundance.

Intraspecific variability in *Ostreopsis cf. ovata* revealed by AFLP and toxin profiles

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The widespread benthic dinoflagellate *Ostreopsis cf. ovata* produces considerable amounts of palytoxins, which are among the most potent non-proteic toxins found in marine environment. These substances cause diseases in humans and benthic fauna, thus representing a rising concern in coastal areas throughout the world. The Mediterranean-Atlantic populations of *Ostreopsis cf. ovata* appear to be rather homogeneous from the phylogenetic point of view, in spite of differences in physiological and ecological properties shown among sub-regions. The aim of our study was to assess and compare molecular diversity of Mediterranean *Ostreopsis cf. ovata* using population genetic markers and toxin profiles of Tyrrhenian Sea (Gulf of Naples and Gulf of Salerno) and Adriatic Sea (Ancona coasts) populations. Genetic diversity was investigated using amplified fragment length polymorphisms (AFLP) on 51 strains, while toxin profiles were obtained with liquid chromatography-mass spectrometry techniques (LC-MS/TOF) on a subset of 38 strains. Feasibility and reliability of the AFLP technique was confirmed by distinct fingerprints for a number of *O. cf. ovata* strains and by reproducible profiles from replicates of the same strain. A binary character matrix was compiled and a cluster analysis of the clones was performed to build a dendrogram for the evaluation of the relationships among strains. AFLP results based on the analysis of 85 loci demonstrated differentiation between the isolates from Ancona coasts and those from the Gulf of Naples, with a branch isolation of the Adriatic population. In the strains analysed, we detected ovatoxins, putative palytoxin and other PITX-like molecules not yet reported in the literature. Toxin profiles were generally comparable among the strains analysed, while some differences detected were independent from the geographic origin of the strains in most cases. These results confirm AFLP as a powerful technique for the identification of *Ostreopsis cf. ovata* populations at regional scale and support evidence for genetic and toxin diversity of this species in the Mediterranean Sea.

Assessing the harmful microalgae occurrence in a coastal mussel culture area, the Mar Piccolo in Taranto (Ionian Sea, Italy)

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Harmful algal blooms (HABs) have serious impacts on public health, aquatic organisms, aquaculture and tourism industries and marine coastal environments in many countries.

In the Mar Piccolo harmful algal blooms have been responsible for massive mussel kills since 1938 but in the last years the problem is worsening and recurrent summer anoxia crisis due to phytoplankton blooms are becoming more frequent. Particularly, in 2008 a heavy reduction (~35%) of the total commercial mussel harvest was detected in the Mar Piccolo with a valued loss of ~ € 13 millions. Furthermore, the lost of the seeds compromised the harvest of the following year. Responsible for the anoxia crisis was a massive bloom of diatoms (up to 3,000 cells x 10³ L⁻¹).

The aim of this work is to assess the occurrence of the harmful algal species and to discuss the development of tools for managing and mitigating the effects of HABs in one the most important farming sites in Italy, the Mar Piccolo of Taranto. Four sampling campaigns were carried out on a seasonal basis in the period 2013-2014 in six sampling sites.

Results evidenced the occurrence of potentially toxic diatoms (*Pseudo-nitzschia* cf. *galaxiae*, *P. delicatissima* group) and dinoflagellates (*Akashiwo sanguinea*, *Alexandrium minutum*, *Alexandrium* spp., *Dinophysis sacculus*, *D. caudata*, *Gonyaulax* spp.). As concerning *Pseudo-nitzschia* cf. *galaxiae*, it reached the highest values in April when it represented the most conspicuous component of the microphytoplankton community.

Previous knowledge and these more recent data will be useful to develop and implement plans for monitoring and management of HABs. These plans would include the integration of observation, forecast and communication into an action plan for rapid response to HABs. Initiatives are urgently needed to improve the communication with authorities responsible for environmental protection, economic development and public health for a sustainable mussel culture in the Mar Piccolo.

Two ways of attachment to substrate of the toxic benthic dinoflagellate *Ostreopsis* cf. *ovata*

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The toxic dinoflagellate *Ostreopsis* cf. *ovata* has been responsible of several benthic blooms along the Mediterranean coasts with severe consequences on benthic fauna and toxic aerosols. A prominent feature of this species is its ability to rapidly colonize different benthic substrates (macroalgae, pebbles, rocks, etc.) covering them with a continuous mucilage film embedding many cells. *Ostreopsis* mucilage has peculiar features, not observed in other dinoflagellates, and it is formed by a fibrillar network deriving by the aggregation of trichocysts and by an amorphous polysaccharidic matrix stainable by Alcian Blue. We present here some new observations on *Ostreopsis* mucilage in blooms occurred in different Mediterranean areas (Gulf of Trieste and coast of Sicily). SEM images confirm in all cases the role of trichocysts in *Ostreopsis* adhesion to substrate, but show the existence of two different ways of attachment, which can be predominant in different situations. The first one, already described, involves the convergence of many trichocysts at the ventral end of the cell, where they join together forming a single multi-threaded filament. This can be directly connected to the substrate allowing rotatory swimming movements of cells around the point of attachment, or the formation of a filamentous network connecting more cells. A second type of attachment involves the aggregation of trichocysts in several points along the girdle, forming short filaments which anchor firmly the cells to the substrate: in this case no movement is possible. Cells with this type of adhesion show by SEM a slimy, less definite surface aspect, suggesting the presence of more amorphous extracellular material. This appears to be confirmed by polysaccharide analyses, which indicate a higher production and release by strains with this type of attachment. Cells from blooms in the Gulf of Trieste show the first type of attachment, while cells from Sicily show both types. The different types of adhesion observed could reflect the ability of this species to colonize a wide variety of substrates.

Identification of a metal-resistant "*Coccomyxa*" (Trebouxiophyceae) isolated from an extreme environment river in Sardinia (Italy)

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In Sardinia, several decades of intense mining left high amounts of waste material and tailings that have caused serious ground and surface water pollution problems. The study area is located in the Arburese mining district (SW Sardinia, Italy), where lead and zinc sulfide ore deposits were mined until 1968 at Ingurtosu. The Montevecchio-Ingurtosu deposit consists of galena-sphalerite veins in a quartz gangue containing iron, calcium, and magnesium carbonate minerals. Different samples were collected along the river named Rio Irvi, during a floristic investigation in the autumn of the year 2011 and a coccoid green alga has been found and isolated. The study alga was isolated by reddish ferrous material scraped from the rock present in the river's edge in the station 2 located at 200 m s.l.m and characterized by a near neutral pH (6,85). The chemical analysis of sampling site showed that waters are strongly polluted by several heavy metals, in particular high levels of Cd (1.43 mg/l), Co (1,75 mg/l), Fe (227 mg/l), Mn (81 mg/l) and Zn (956 mg/l) are registered. After isolation and purification, stock cultures of axenic coccoid alga were established under controlled laboratory conditions (25°C, photoperiod of 12:12). The algae were maintained routinely in modified WARIS-H culture medium (McFadden and Melkonian, 1986) without soil extract under cool white light luminescent (80–100 $\mu\text{mol photons/ m}^{-2} \text{ s}^{-1}$). Molecular and morphological analyses were carried out to identify the green algal species. Phylogenetic analyses on 18S and 5.8S rDNA indicate that this strain belongs to the genus *Coccomyxa* and is included in *Elliptochloris* clade (*sensu* Pröschold *et al.* 2011) of the Trebouxiophyceae. The metal-resistant *Coccomyxa* isolated from this extreme environment is characterized by narrowly ellipsoidal slightly asymmetrical cells (3-5.4 x 6-8.5 μm), regularly curved, with rounded apices and without mucilaginous sheath. The cell shows a median depression and a smooth cell wall. The ultrastructural investigations (SEM-TEM) show the presence of a trilaminar cell wall, a very large parietal chloroplast (cup shaped) covering much of the cell wall, with starch granules inside the interthylakoidal spaces and without pyrenoid. One nucleus is visible in central part of the cell. Electron micrographs show that the microalga also contains in the cytoplasm several vacuoles filled with electron-dense material, which could correspond to lipid droplets. Propagation by two or four autospores released by apical splitting of the mother cell wall was observed. The microalga (strain SCCA 048) is maintained in culture flask (axenic conditions) at the University of Cagliari, Interdepartmental Center of Environmental Science and Engineering (CINSA), Sardinian Culture Collection of Algae (SCCA).

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Comparison of four methods for quantitative analysis of soil algae

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Dimension estimation of soil algae populations is essential for studying their role in soil communities. The main methods used to quantitatively analyze soil algae are overall four: *a*) pigments extraction and chlorophyll *a* quantification, *b*) observation and count of algae using a fluorescence microscope, *c*) the dilution plate count method and *d*) the so-called “Most Probable Number”. The latter two are referred to as indirect methods, because they provide the count of algae after their growth on a specific culture media.

The aim of this study is to compare these four different methods by applying each of them to the same soil samples.

The soil samples were collected from the top 2 cm layer of a grassland. On each sampling day, three samples were collected. Everyone of them was composed of 15 sub-samples, collected using a 2.5 cm diameter sterilized plastic tube.

The samples were mixed and cleaned from stones and plant and animal material, and then algal quantification using the four methods was performed.

Regardless of the method used, a density dominance of green algae (chlorophytes + xanthophytes + eustigmatophytes) was observed.

Indirect methods can select populations by using specific cultural terrains, which prevent or limit the growth of certain organisms. In this study we used a broad spectrum medium (BBM) and the BG11, specific for cyanobacteria. However, culturing allows the growth both of cells in the active phase and of inactive forms, which can also include organisms not able to live actively in the soil. Among the indirect techniques the method of the plates allowed a qualitative investigation besides the quantitative one. This method was the only one able to tell that green algae represent the utmost majority in our samples. The second indirect method, called Most Probable Number (MPN), made it possible to distinguish eukaryotic algae from cyanobacteria (thanks to the two different culture media), however MPN is designed to use liquid culture media, that are not always suited to soil algae.

Direct methods provide soil sample observation as such. The most used is the observation and count of algae with a fluorescence microscope, allowing the count only of the active cells at sampling time; it is however not suitable for samples with very low algal densities. Pigments extraction and chlorophyll *a* quantification, unlike the other three methods, allowed to obtain a biomass estimation but not a density one; nevertheless it is not suitable for soils with large amounts of plant organic matter.

In conclusion, in the context of a soil with relatively high algal concentrations (as derived from data reported in the literature), the use of any of the four methods we compared appears to give similar results. In order to obtain the greatest number of information, the parallel use of two methods seems to be advisable: one for the biomass estimation and the other one for the density estimation.

Polyphyletic nature of low pH adaptation in the genus *Klebsormidium* (Klebsormidiophyceae, Streptophyta)

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The capacity to adapt to low pH is widespread among algae. Some taxa are especially capable to thrive in low pH and are a recurrent presence in acidic habitats; some well-known examples are species of the chlorophycean genus *Chlamydomonas*, the Euglenophyte *Euglena*, the Chrysophyte *Ochromonas*, the diatom *Pinnularia* and red algae of the class Cyanidiophyceae. In general, these algae have been intensively studied, but their phylogenetic relationships with relatives occurring in non-acidic habitats are often unclear.

Klebsormidium is a genus of filamentous green algae widely distributed in freshwater and terrestrial environments, well known to include some strains living in extremely acidic conditions. In this study, we investigated the phylogenetic position of eighteen strains of *Klebsormidium* from low pH habitats using *rbcL* and ITS rDNA sequence data in a concatenated dataset. The strains were collected from several sites in Europe (Czech Republic, Germany, Italy) and U.S.A. (Ohio), mainly in areas affected directly or indirectly by carbon mining activities.

In the molecular phylogeny, low-pH strains of *Klebsormidium* formed a polyphyletic assemblage. They were representative of sixteen lineages and corresponded morphologically to six species (*K. crenulatum*, *K. elegans*, *K. flaccidum*, *K. fluitans*, *K. nitens*, *K. scopulinum*), with the exception of four strains for which an unambiguous identification was not possible.

Most of the strains belonged to lineages not covered in previous molecular studies, as shown by the fact that only three had sequences identical to records already available in GenBank. *K. scopulinum* from Ohio was recovered in the same clade with the only acidophilic *Klebsormidium* sequenced so far, *K. acidophilum*. Low pH strains morphologically referable to *K. flaccidum* and *K. nitens* were polyphyletic, in agreement with results for non-acidophilic strains of the same morphospecies.

In conclusion, the genus *Klebsormidium* is a group of morphologically and physiologically dynamic algae in which the capacity of adaptation to low pH conditions has been developed multiple times independently. We postulate that extreme acidophilic populations probably originate from populations of various species growing locally when strongly acidic habitats become available. Based on the present evidence, acid-adapted lineages of *Klebsormidium* appear to have mostly a restricted geographical distribution, with the only exception of a lineage containing strains from Czech Republic, New Zealand and Ohio.

***Tetraflagellochloris mauritanica* gen. et sp. nova (Chlorophyceae): motion and swimming patterns.**

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Tetraflagellochloris mauritanica L. Barsanti et A. Barsanti, gen. et sp. nov. is a tetraflagellate green alga isolated from soil samples of a saline dry basin near F'derick, Mauritania. Morphological, ultrastructural and molecular-sequence data from the 18S rRNA gene and ITS2 were used to assess the phylogenetic position of the green algae. This alga can grow as individual cells or form non-coenobial colonies of up to 12 individuals. *Tetraflagellochloris* propels its ellipsoidal cell body, which has typical diameter of 10 μm , using two pair of flagella, whose lengths are about 50 μm for the long and 30 μm for the short.

Biflagellate green algae such as *Chlamydomonas* display synchronous beating with identical frequencies and phases to elicit breaststroke swimming (BS).

We report here the unique alternative mode of synchronization found in eukaryotic aquatic microorganism, that *Tetraflagellochloris mauritanica* uses, in which flagella display synchronous beating with identical frequencies but locked anti-phases to elicit a sort of crawl swimming (CS).

The cells of *Tetraflagellochloris*, either single or in a group, show not only the type of permanent flagellar out of phase synchronization, but also a complex swimming motion pattern, consisting of alternating short and rapid swimming period and longer resting period, and backward swimming with a ciliary beating that proceeds in fits and starts.

Who are the main planktonic primary producers in Mar Piccolo of Taranto?

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The Mar Piccolo is a semi-enclosed basin in the Ionian Sea. It is liable to pollution since it receives a considerable amount of sewage and industrial waste. In order to comprehend the influence of anthropogenic contamination on the dynamics of planktonic primary producers in the water column, four sampling campaigns were carried out on a seasonal basis in the period between June 2013 and April 2014. Sampling was performed in six sampling sites characterized by different levels of contamination. The abundance and biomass of planktonic phototrophs were investigated at surface and bottom depths and associated with physical-chemical features of the water column in order to detect their seasonal dynamics. The lowest abundance of all planktonic photoautotrophs was detected in February 2014 whereas the dynamics among different size-classes widely varied for the rest of the study period. In June 2013 autotrophic nanoplankton reached its maximum abundance with respect to all campaigns and their distribution was generally characterized by a decreasing surface-bottom gradient. In October the picophytoplankton peaked to 10^9 cells L⁻¹, thus reaching their maximum abundance in the entire area and largely prevailing over the nanoplanktonic fraction, with higher abundances detected in the inner inlet. The condition encountered in April favoured the proliferation of larger phototrophs, in particular micro-sized and partly nano-sized. In that survey microphytoplankton reached abundances up to 285-folds those observed during other campaigns with higher abundances towards the inner part of the Mar Piccolo.

Phytoplankton distribution along the world from the TARA Oceans expedition

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Productivity of the ocean relies on phytoplankton activity. Yet our knowledge of the biodiversity patterns of this important component of ocean life is still poor. The Tara Oceans project, an interdisciplinary study based on a 3-years research cruise across the world's seas, aims at studying the marine ecosystem at the global scale, with a unique sampling program that includes optical and genomic methods to describe marine organisms (viruses, bacteria, archaea, protists, and metazoans) in their physical and chemical environment. In this framework, our goal was to increase knowledge of marine phytoplankton diversity and distribution in the south-west Indian (3 stations), south Atlantic (7 stations), and Antarctic Ocean (3 stations) based on bottle and net samples (5-20 μm and 20-180 μm size-fractions). Using light microscopy, we estimated the total phytoplankton abundance and the relative abundance (RA) of microphytoplankton species. Net samples were also examined by scanning electron microscopy.

The study area showed very different oceanographic characteristics, spanning from relatively high nutrient concentrations at two coastal stations near Cape Town, one of them characterized by an upwelling event, to oligotrophic waters in the south-west Atlantic Ocean, and including polar waters in the Antarctic Ocean.

A total number of 353 taxa were identified, including 182 Dinophyta, 139 Bacillariophyta, 18 coccolithophores and 14 other taxa. Phytoplankton abundance was generally low ($1 \cdot 10^3$ - $3.5 \cdot 10^4$ cells $\cdot\text{L}^{-1}$), with the exception of the upwelling station ($1.9 \cdot 10^6$ cells $\cdot\text{L}^{-1}$). Diatoms were generally the most represented group, followed by small undetermined flagellates and coccolithophores. Microphytoplankton was dominated by diatoms at the Indian, south-east Atlantic and Antarctic Ocean stations (RA>40%), while dinoflagellates, mainly represented by *Tripos* spp. or *Gonyaulax* spp., had the higher RA at the south-west Atlantic stations. Undetermined flagellates dominated only at one of the Antarctic stations where *Phaeocystis* sp. contributed than 90% of the total population. Among diatoms, *Fragilariopsis doliolus* characterized the phytoplankton assemblage at the coastal station near Cape Town (RA > 50%) while *F. kerguelensis* reached more than 90% of the microphytoplankton at the Antarctic stations. A tiny araphid diatoms, *Nanoneis longta*, never reported after its description, was exclusively observed in Indian and Atlantic Ocean stations around the African coasts. Hierarchical clustering showed three main groups, one including the stations near the African coasts, another those from south-west Atlantic Ocean and a third one including the Antarctic stations. Microphytoplankton data proved to be very useful to intercalibrate and validate the 18s rDNA data (V9 tag) obtained from HTS DNA-metabarcoding analyses.

Autotrophic communities in natural CO₂-dominated waters of the Aeolian Islands (Tyrrhenian Sea)

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Part of the CO₂ released into the atmosphere as result of human activity is absorbed by the oceans, leading to a decrease of the surface ocean pH. An important, short-term approach for mitigating potential global climate change is expected to be the carbon capture and storage (CCS). This technology involves the capture of CO₂ emitted from large point sources and its injection into deep geological reservoirs. However, possible CO₂ leakage from these CCS sites could represent a threat to marine ecosystem, also if the significance and magnitude of the biological, ecological and biogeochemical responses of marine microorganisms and communities are not still well known. Currently, most of information derives from perturbation experiments carried out in the laboratory and in mesocosms and not from observations in areas naturally enriched with CO₂. The natural CO₂ gas seeps in the relatively shallow waters around the Aeolian Islands (southern Tyrrhenian Sea) give an excellent opportunity to study the impact of CO₂ on the ecosystem as a large-scale real-world analogue of what might occur at a leaking offshore CCS site. In the framework of the European projects ECO2 and Eurofleets, five cruises were carried out in 2011 (27 July-1 August), 2012 (2-11 June and 19-31 October), 2013 (21-31 May), and 2014 (7 -25 May). Samples were collected in the water column: i) along a transect offshore Panarea in 2011 to investigate the impact of gas seeps on large spatial scale and the existence of eventual gradients; ii) in two stations near the Basiluzzo Island during all cruises in order to define seasonal variations; iii) along another transect in 2012 and 2014 in the coastal area of Panarea limiting the investigations on small spatial scale. Here, in addition to CO₂ leakages, gas emissions characterized by H₂S smell were detected as well. Both prokaryotic and eukaryotic autotrophic communities were analyzed in terms of abundance and biomass with the purpose to relate biological parameters to high quality measurements of the carbonate system and of other environmental parameters. The proportion between prokaryotes and eukaryotes widely varied in the entire study area with the exception of June 2012 when the net dominance of eukaryotic community was observed. The eukaryotic community resulted dominated by undetermined nanoflagellates in terms of abundance, whilst dinoflagellates were the main taxonomic group in terms of biodiversity, in all cruises and in all stations. In Panarea offshore area, higher abundances were recorded at deeper layers compared to the surface, while waters at the Basiluzzo Island and coastal Panarea transect did not show particular difference either among the stations or the sampled depths.

Exchange of indigenous and alien microalgae species from ballast waters, the BALMAS approach

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The Adriatic Sea is a unique and highly sensitive ecosystem. The economic development and social existence of its coastal states depend heavily on a clean and preserved Adriatic Sea. However, the Adriatic Sea is also a seaway used mainly by international shipping transporting goods to and from Europe (as hinterland), with intense local shipping as well. Of increasing concern is the introduction of harmful aquatic organisms and pathogens (HAOP) via ships' ballast waters (BW). The general BALMAS (Ballast Water Management System for Adriatic Sea Protection) objective is to establish a common cross-border system, which will link all researchers, experts and responsible national authorities from Adriatic countries in order to avoid unwanted risks to the environment from the transfer of HAOP. This will be achieved through control and management of ships' ballast waters and sediments.

Ballast water transferred by vessels has been widely recognized as a prominent vector of HAOP species, which are, according to the United Nations, one of the four greatest pressures on the world's oceans and seas, causing global environmental changes and also posing a threat to human health, property and resources. The BWM Convention (2004) set global standards on ballast water management (BWM) requirements, while recognizing that regional and local circumstances must be considered for its effective implementation. The volume of BW discharged into Adriatic Sea ports is above 10 million tons per year and due to a foreseeable growth in traffic could soon increase considerably. The presence of HAOP in ballast waters discharged into Adriatic ports has been proven, and their negative impacts have already been recorded. Adriatic countries have recognized that the BW issue is very critical and complex, and that key barriers to a viable solution are a lack of data (e.g. the presence and invasiveness of HAOP in Adriatic ports, BW uptake and discharge activities, sediment disposal, chemical pollution with BW) and a scarce knowledge (e.g. port baselines and monitoring, BW sampling for compliance control, risk assessment, how to deal with non-compliant vessels, early warning systems, effectiveness of BWM systems and measures). This data and knowledge will enable Adriatic countries to implement BWM Convention requirements through a common BWM plan, and provide support to responsible authorities for faster and effective decision making with a decision support system (DSS).

A strategic common cross-border approach was recognized to be crucial because of the shared, specific, vulnerable, economically important, semi-enclosed environment, in which control over HAOP as well as international shipping cannot be limited by political borders. This work will report about the first results regarding microalgal aspects of the project.

Study of Diatoms in sediments of an Alpine pond (Lake Welsperg, East Trentino, Val Canali, Parco Naturale Paneveggio - Pale di S. Martino)

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Lake Welsperg is an artificial pond for ornamental purposes (Tomasi, 2004). It's at an altitude of about 1,020 m a.s.l., close by Villa Welsperg (where nowadays there is the administrative office and the visitor center of Ente Parco Paneveggio-Pale di S. Martino). In particular, this pond lies between two peaty fields: one at north near Villa Welsperg and the other at south near Palù Grant. Its extension is about 5,000 sq. m and it has a maximum depth of about 3 m. Lake Welsperg is located in Val Canali, it is fed by Rio Brentella coming out from the fields located south of Villa Welsperg and it is a tributary of Torrente Canali which flows into Torrente Cison and the latter then into River Brenta.

Lake Welsperg usually freezes 4 months a year (personnel communication from P.G. Partel). In 1853 the Welsperg's family built Villa Welsperg; in 1932 the pond was created for fish breeding. In 1953 Lake Welsperg was enlarged by the construction of a dam on the south-west side. In 2006 the Ente Parco set the natural appearance and the ecological functions of Lake Welsperg. In 2009 the pond was emptied and sediment cores were taken on 8 December by a manual Hiller core. Three cores, respectively 20 cm (A), 15 cm (B) and 27 cm long, were collected. Then the sediments were treated in order to get diatom frustules. After cleaning, permanent slides were prepared; the following species were found: *Achnanthes* sp., *Amphora pediculus*, *Aneumastus tusculus*, *Brachysira neoexilis*, *Brachysira* cf. *vitrea*, *Cyclotella distinguenda*, *Cyclotella radiosa*, *Cymbella affinis*, *Cymbella helvetica*, *Denticula tenuis*, *Encyonopsis* sp., *Eucocconeis flexella*, *Fragilaria leptostauron*, *Fragilaria pinnata*, *Gomphonema* sp., *Nitzschia recta*, *Sellaphora pupula*, *Staurosira microstriata*, *Stephanodiscus alpinus*.

The main chemical and chemical physics parameters of water samples collected on 27 June 2014 were measured: air temperature 18.7 °C; water temperature 17.2 °C; pH 8.82; SO₄ 115.00 mg/l; N-NO₃ 303 µg/l; N-NH₄ 34 µg/l; Ca 45.60 mg/l; TP 4 µg/l; TN 0.54 mg/l; conductivity 308 µS/cm; maximum transparency. It follows that Lake Welsperg is oligotrophic, very rich in calcium and sulphates, probably because of basin lithology.

The lake bottom is fully covered by *Chara vulgaris* (Ettl et al., 1997; Bazzichelli et al., 2009). On surface it's possible to recognize floating flocculates of *Spirogyra* sp. On 27 June 2014 five cobblestones were collected in order to recognize diatoms and benthic algae; among these we found: *Chroococcus* sp. (cyanophyceae); *Ankistrodesmus falcatus*, *Cosmarium* sp., *Monoraphidium contortum*, *Oedogonium* sp., *Scenedesmus* sp. (green algae); *Cocconeis placentula*, *Cyclotella bodanica*, *Encyonopsis subminuta*, *Epithemia goeppertiana*, *Fragilaria acus*, *Fragilaria ulna* var. *ulna*, *Gomphonema pumilum*, *Navicula cryptotenella*, *Navicula radiosa*, *Nitzschia angustata*, *Denticula tenuis* and *Fragilaria leptostauron* (diatoms).

Partial isolation of two *Scenedesmus acutus* genes homologous to *Chlamydomonas reinhardtii* ATP sulfurylase

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In the freshwater green alga *Scenedesmus acutus*, sulfur starvation induces a transient increase of Cr(VI) tolerance, both in the wild type and in a Cr-tolerant strain, associated to an increased capacity of sulfur uptake and assimilation leading to an increase in cysteine synthesis during the recovery in standard medium (Gorbi et al 2007). Despite being chromium tolerance not related to the induction of phytochelatins, the tolerance to this metal seems strictly connected to sulfur metabolism (Pereira et al., 2008; Schiavon et al., 2008). It is well known that sulfur starvation induces a huge variation in gene expression in *Chlamydomonas reinhardtii* (Zhang et al 2004) as well as in other algae and in land plants (Bochenek et al., 2013). Among the genes overexpressed there are plasma membrane high affinity sulfate transporters and many enzymes of the sulfate assimilation pathway. Once sulfate entered the cell, it is activated by the enzyme ATP sulfurylase which catalyze the first reaction of the reductive/assimilation pathway. In order to verify if differences in ATP sulfurylase expression is involved in the observed transient increase in Cr-tolerance, as well in the differential sensitivity shown by the two *S. acutus* strains, we tried to clone fragments of ATP sulfurylase genes. Primers designed on the sequence of *C. reinhardtii* and used both on genomic DNA and cDNA from 24h S-starved algae allowed the cloning of two isoforms homologous to *C. reinhardtii* ATS1 and ATS2. The cloned fragments share high sequence homology but differ for some specific aminoacid residues nearby the active site suggesting a different substrate affinity of the two isoforms. Moreover preliminary results show a different expression of the two enzymes, being ATS1 likely expressed in a constitutive manner while ATS2 is induced by sulfur starvation.

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Complete genome sequence of chloroplast and mitochondrial DNA of *Chlorella sorokiniana*

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The last few decades have seen a rising interest in genome characterization and, as a result, a growing number of algae chloroplast, mitochondrial and nuclear genome have been sequenced to better understand their evolution. Within the Chlorophyta clade *sensu* Lewis & McCourt (2004), the Trebouxiophyceae group consists mainly of unicellular and colonial green algae, which are found mostly in subaerial habitats and as phycobionts in lichens. This group includes the Chlorellaceae family (Brunnthal, 1915) which is characterized by the well-known genus *Chlorella* Beijerinck. One member of this genus is *Chlorella sorokiniana* which is a non-motile unicellular alga which can grow phototrophically by exploiting wastewaters and flue gases as costless sources of inorganic nutrients and carbon dioxide, respectively. When cultivated under specific operating conditions, this strain is capable to accumulate significant amounts of fatty acids to be viably exploited for the production of biofuels (Lizzul *et al.*, 2014). These characteristics make this strain, as well as most of the species belonging to the *Chlorella* genus, particularly promising in the biotechnological, environmental and energy sectors (Concas *et al.*, 2010, 2014). In this study, the complete sequence of chloroplast (cp) and mitochondrial (mt) genome of the *C. sorokiniana* strain (SAG 111-8k) have been obtained. The cpDNA (Orsini *et al.*, 2014a) consists of circular chromosomes of 109,811 bp, which encode a total of 109 genes, including 74 proteins, 3 rRNAs and 31 tRNAs. The mtDNA (Orsini *et al.*, 2014b) consists of circular chromosomes of 52,528 bp and encodes a total of 31 protein coding genes, 3 rRNAs and 26 tRNAs.

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Systematics and biodiversity of marine *Mastogloia* (Bacillariophyceae): revision of section *Inaequales* and phenetic methodologies applied to section *Ellipticae*

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Mastogloia Thwaites ex Smith is the diatom genus widespread throughout the world and it includes more than 410 epilithic and epiphytic species. In 1933, Hustedt introduced 11 sections based on very general morphological characters to discriminate between species, with only one section representing freshwater habitat. Nevertheless, the systematics of this genus is still under review: recently we revised the Hustedt's section *Sulcatae* and part of section *Ellipticae*. In this study, we present the last part of the revision of the section *Ellipticae* which has been completed with phenetic analysis, and the revision of the section *Inaequales*, including three new species.

The relationships between 33 taxa of *Mastogloia*, section *Ellipticae* were investigated using cluster analysis in order to test morphological characters used in diatom systematics and to assess how well the current classification reflects the morphological correlation among all the taxa and the possible relationships in this group. In our phenogram, based on the variability of 21 morphological characters, *M. subaspera* Hustedt, *M. ovulum* Hustedt, *M. barbadensis* (Greville) Cleve and *M. emarginata* Hustedt, which were closely related in Hustedt's key classification, appear to be more distant and less correlated with each other. This difference is probably attributable to many new morphological details obtained through electron microscopy.

The morphological revision of the section *Inaequales* lead to highlight their main characters: (i) a partectal ring distant from the valve margin and attached to it with a small siliceous flange, and (ii) different sized and shaped of partecta, with the larger ones at specific locations. Moreover, new taxa for the science *Mastogloia caulis* Pennesi & Totti, *M. tottii* Pennesi & Poulin and *M. enzi* Pennesi are presented.

The biogeography of species of the section *Inaequales* is also reported: *M. cuneata* (Meister) Simonsen, *M. manokwariensis* Cholnoky and *M. pusilla* Grunow are ubiquitous and show worldwide distribution, while most species are frequently reported in the Indonesian Archipelago (Indian Ocean, South China Sea, North Pacific Ocean), in the Caribbean and Bermuda Archipelagos (Atlantic Ocean) and in the Mediterranean Sea.

The phytobenthos of the Mar Piccolo of Taranto (Ionian Sea, Southern Italy): a novel of ninety years of disappearances, new arrivals and returns

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Long-term studies allow to evaluate all the significant changes which an ecosystem encounters with time. In this respect, the Mar Piccolo of Taranto represents a good example for the studies on the phytobenthos. Indeed: in the Twenties the first researches were carried out; up to the Seventies they were occasionally performed; in the Eighties they became continuous and are still ongoing as such. Therefore, the presence of historical series of data gives the chance of assessing both qualitative and quantitative modifications, which occurred against the phytobenthic communities of the basin in almost a ninety-year period, showing that they are strongly linked to anthropogenic activities.

In the Twenties up to the Fifties, the Mar Piccolo was depicted as a basin with limpid and clean seawater where *Cystoseira* spp., *Halimeda tuna*, *Flabellia petiolata* and many other seaweed species, typical of healthy environments, commonly lived. Most of them also sexually reproduced. Among the phanerogams, *Cymodocea nodosa* formed a luxuriant meadow. At that time, mussel farming, Navy dockyard and sewages pollution were already present, but their pressure was low.

In the Sixties and the Seventies, since the pressure of these polluting activities became stronger, less resistant species disappeared, such as most of brown macroalgae, in particular *Cystoseira* spp. In that period, the Mar Piccolo bottom was mainly colonized by rhizophytic green algae, such as *Caulerpa prolifera*. *Cymodocea nodosa* meadow dropped to sparse and scarce spots.

In those years a considerable rise of the Taranto population occurred, leading to the expansion of the town, and so, all of 14 not preventively cleansed sewages began to discharge in the Mar Piccolo. Therefore, in the Eighties and the Nineties, phytobenthic populations shifted towards assemblages typical of eutrophic environments characterized by unattached Ulvales and Gracilariales, vegetatively reproducing, which reached high biomasses, especially in spring and summer. *Cymodocea nodosa* almost disappeared, except some rare tuft.

Moreover, in those years, another type of pollution came out in the basin, the biological pollution due to the introduction of alien species. Indeed, in 1986, two red macroalgae, native from the Atlantic Ocean, were recorded, representing the first report for the Mediterranean, that is *Agardhiella subulata* and *Solieria filiformis*. In a short time, they became the dominant summer species in the unattached community of the Mar Piccolo up to the end of the Nineties. In 1998, the Pacific brown seaweed *Undaria pinnatifida* was found attached onto the docks of the old town.

In 2000, the increase of importation of extra-Mediterranean mussels to satisfy the local market caused the rise, up to 13, of the number of alien seaweeds in the Mar Piccolo. They came from different areas and showed different behaviours. In the same period, the progressive closing of waste-water plants began and the Navy dockyard activities were moved to the Mar Grande basin. Consequently, seaweed and phanerogam assemblages in the Mar Piccolo changed again. Concerning seaweeds, in the last years, several species present in the Twenties reappeared and sexually reproduced, such as *Padina pavonica*, *Peyssonnelia* spp. With respect to phanerogams, *Cymodocea nodosa* not only considerably widened its distribution in the basin, but also began to sexually reproduce, sprouting flowers and fruits. Moreover, in the last years, *Ruppia cirrhosa* appeared and formed a luxuriant meadow.

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Updating of alien macroalgae in the Venice Lagoon, new introductions and cryptogenic species

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The number of alien macroalgae in the Venice Lagoon is steadily increasing and some of them have colonized large areas of the basin. An accurate revision of the literature, despite the exclusion of many cryptogenic species, has increased the number of the verified species to 28 (5 Chlorophyceae, 6 Phaeophyceae, 17 Rhodophyceae) accounting for the 55% of the Italian non-indigenous species (NIS), whereas some other taxa require a confirmation. Out of these, 3 taxa considered invasive worldwide (*Gracilaria vermiculophylla*, *Sargassum muticum*, *Undaria pinnatifida*) and other 3 (*Agardhiella subulata*, *Solieria filiformis*, *Hypnea flexicaulis*), invasive only in the Venice lagoon and in some transitional systems of the Northern Adriatic Sea (Po Delta lagoons and Pialassa della Baiona pond, in the Veneto and Emilia-Romagna Regions), appear among the dominant species. The most abundant taxa are the Rhodophyta *Gracilaria vermiculophylla* (the black *Gracilaria*), a free-floating species reported only since 2008 (Sfriso *et al.*, 2010), and *Agardhiella subulata* recorded in the lagoon since 2003 (Curiel *et al.*, 2005). Other two species, *Sargassum muticum* and *Undaria pinnatifida*, whose introduction dates back to the first years of the '90s, show pronounced seasonal fluctuations. In particular, *G. vermiculophylla* shows the most rapid expansion and, at present, has mainly colonized the most confined and eutrophic areas of the lagoon. In the spring of this year this species, together with *A. subulata*, has almost completely replaced the laminar Ulvaceae in the area of Campalto, northward to the trans-lagoon bridge, thus avoiding the quick biomass collapse and the anoxic crisis occurred in July 2013, due to the dominance of *Ulva laetevirens* and *Ulva rigida*. In comparison to Ulvaceae, which fluctuate on the whole water column triggering a rapid biomass collapse, these Rhodophyta, whose biomass ranges from 3 to 5 kg fwt m⁻² (*G. vermiculophylla* accounts for ca. 90% of the total biomass), do not hamper water circulation due to their slower growth and decaying.

Gracilaria vermiculophylla is an example of an invasive NIS that has replaced a native thionitrophilous species having a negative impact on the environment. Moreover, should its biomass be used in the food and cosmetic industries, it might have an important commercial value.

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First report of *Gelidium americanum* (Gelidiales, Rhodophyta) from the Mediterranean Sea

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A species of *Gelidium*, morphologically very similar to *G. pusillum*, was collected from Apulia (Southern Italy). Molecular sequencing data (*rbcL* and *cox1*) revealed it to be *Gelidium americanum*, known from the tropical and subtropical western Atlantic.

At first described as *Pterocladia americana*, the species was later transferred to *Gelidium* on the base of cystocarp features.

Morphological and anatomical observations performed on the Mediterranean specimens of *G. americanum* are presented along with comparisons with published data on the species.

G. americanum was found fully established on rocks and shells in three different localities on both Adriatic and Ionian coasts. Therefore it is very likely that the species is not a recent introduction; it may have entered the Mediterranean by natural pathways through the Strait of Gibraltar and it reasonably occurs in other Mediterranean areas, but has not yet been recorded due to the misidentification with other common congeners. The alternative scenario that it has been introduced as a consequence of human activities, seems to be less likely.

The “Vatova algarium” project: a case study on biodiversity changes through historical samples in the molecular age.

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The first studies on the flora and algal associations in Venice lagoon date back to the XVIII century, and were conducted by Olivi (1749). In the XIX-XX centuries, they were followed by the classic works of Naccari (1828), Zanardini (1847) De Toni & Levi (1885-1888), De Toni (1889-1924), Vatova & Schiffner (1937), Sighel (1938), Vatova (1940) and Pignatti (1962).

At the Museum of Natural History in Venice, together with the *Algarium Zanardini*, which is undoubtedly the most valuable collection of species mainly from the Adriatic Sea, there are the algal collections made by Vatova in the 30s.

Recently, a new collection of Vatova was found in the library of ISMAR-CNR in Venice. The collection is entitled “*Distribuzione e polimorfismo di Gracilaria confervoides nella laguna di Venezia*” and includes more than a thousand of samples collected between 1942 and 1950. The results of this study had never been published.

The aim of our project is to review the newly found collection by an integrated approach of both classic taxonomic methods and DNA barcoding techniques, using protocols designed for ancient DNA.

The information recorded on the historical algarium grants the possibility to monitor changes that have occurred over time where specimens were collected, but also a taxonomic revision of the identified species and, last but not least, the revaluation of museum records in the framework of the molecular age.

Phycological jokes...and more

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Hoping to induce listeners to smile, a series of original jokes are presented. They are mainly based on algal names but also on different topics.

Because they'll be most probably little intelligible to people not speaking Italian, the author begs foreign colleagues' pardon.

Phytoplankton ecophysiology in an era of global change

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The world is currently undergoing changes in climate, the rates of which are unprecedented in global history. Algae are responsible for around half of Earth's annual primary production and are the basis of most aquatic food chains. Understanding the effects of global climate change on these organisms is thus of paramount importance to our ability to make informed decisions about the future of marine ecosystems, production and the global carbon cycle.

Using published information from the literature and new data from my laboratory I will discuss how elevated CO₂ and temperature are likely to impact on primary productivity and physiological performance of microalgae. I will also discuss how changes in CO₂ can lead to alterations in elemental and macromolecular composition of these organisms, including toxin production. I will also present data showing how changes in climate-driven factors (CO₂, temperature, pH) may also interact with other stressors, such as nutrient limitation, increased UVB flux and interactions with other organisms such as viruses.

Effect of organic carbon sources on biomass production and photosynthesis of marine microalga *Nannochloropsis gaditana*

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Microalgae are receiving increased attention as possible feedstock for biofuels production. In particular, their reserves are considered a promising source of oil which can be converted into biodiesel. Algae generally exploit light and carbon dioxide to sustain the entire metabolism (photoautotrophy) but in some cases they are able to use in addition organic carbon sources to implement the biomass production (mixotrophy) in terms of cells growth and lipids accumulation. Mixotrophy, thus, can be exploited to support algal growth over night or in dark-zones which characterizes the environment inside a photobioreactor, the algae large scale cultivation system for biodiesel production. The algae belonging to the genus *Nannochloropsis* are now considered as model organisms for this kind of studies because they have fast growth rate and good lipid productivity under many different conditions of nutrients availability and illumination. In order to optimize the productivity of algae, the growth of *N. gaditana* was performed in both minimal F/2 medium and rich F/2 medium (nitrogen, phosphorous, iron excess). In this way, it has been possible to test the effective influence of organic carbon sources (sucrose and glycerol) on algae metabolism. During the growth curves cell number, photosynthetic parameters, pigment content, lipid accumulation and ultrastructure analyses through electron microscopy were considered. Results show how *Nannochloropsis* is able to exploit both glycerol and sucrose to support biomass production even if photosynthesis is negatively affected by the former. Then, lipid accumulation seems to be stimulated by mixotrophy when *Nannochloropsis* suffers also of nutrient limitation. From TEM it appears clear the formation of lipid droplets inside cells next to the appearance of some other reserve structures probably related to the major carbon availability.

Selecting functional types of microalgae suitable for CO₂ sequestration and wastewater remediation

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The use of microalgae to sequester CO₂ is often not taking in due consideration the physiological ability of organisms to cope and thrive with the high CO₂ concentrations present in flue gases. We wanted to select which functional type of alga was the most suited for growth in the presence of high CO₂ levels and to assess the overall physiological responses occurring under these conditions. *Dunaliella salina*, *Thalassiosira pseudonana*, *Phaeodactylum tricornutum*, *Botryococcus braunii* were chosen because different both with respect to their mode of acquiring CO₂ and for their use of nutrients. The tolerance of high pCO₂ and its effect on biomass composition were investigated.

To further steer and engineer CO₂ sequestration systems using microalgae, the effect of other flue gas compounds on algal growth must be considered. Moreover, the opportunity to make flue gas-fed algal cultivation more sustainable thanks to the exploitation and remediation of wastewater may require fundamental research. Preliminary data are shown also in this respect.

Effects of different nitrogen sources on C-fixation and N-assimilation in *Scenedesmus* sp.

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The microalgal biomass applications strongly depend on the composition of the culture medium and, after carbon, nitrogen is quantitatively the most important element contributing to the dry matter amount and composition. The aim of this study was to investigate the physiological responses of an Australian isolate of the freshwater algae *Scenedesmus* sp. grown with two different nitrogen sources, nitrate and ammonium, under four different conditions: (N) with 28 mg/l of N-NO₃⁻, (A) with 28 mg/l of N-NH₄⁺, (AA) with 28 mg/l of N-NH₄⁺ and air bubbling as carbon source, and (DA) with 56 mg/l of N-NH₄⁺. From previous studies it was well known that, even if ammonium represents the most energetically efficient nitrogen source, nitrate is the most common used source allowing to reach the highest biomass. Our results confirmed the highest growth of the cultures under nitrate which reached a double number of cells at the end of the exponential phase compared with those supplemented with ammonium. The dissolved inorganic carbon (DIC) uptake was also measured and a faster consumption of all the three sources (HCO₃⁻, CO₃²⁻, CO₂) of carbon was observed in the condition with ammonium. Measurements of the intra- and extracellular pH were parallelly performed in order to verify the effect of the ammonium on the pH rise, due to the release of protons with the ammonium uptake. Results showed that both internal and external pH were lower in the culture with the highest growth, so that a change in pH value doesn't seem to be the cause for the lower growth in the presence of ammonium. In relation to the supply of different nitrogen sources, at different concentrations and in the absence or presence of air as inorganic carbon source, our findings suggest that the algae grown under ammonium, have a faster uptake of the nitrogen source, and consequently a faster depletion of cellular carbon skeletons.

Light and nutrient effects on ketocarotenoid synthesis in *Chodatodesmus australis*.

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During a scientific expedition in Antarctica, in the austral summer 1990, Prof. C. Andreoli collected a coccoid microalga from a transitory pond near the Gondwana Station, Terra Nova Bay, Victoria Land (Antarctica). This organism was recently characterized by a polyphasic approach and resulted to be a new species of Chlorophyceae, named *Chodatodesmus australis* and belonging to the new genus *Chodatodesmus* (family Scenedesmaceae) (Sciuto et al., 2014). Physiological analysis, recently, showed the ability of this Antarctic isolate to grow at different temperatures (from 4°C to 25°C), with an optimum growth rate at about 20°C. At all growth temperatures, the microalga resulted also able to synthesize antioxidant ketocarotenoids as part of a photoprotective mechanism activated to avoid the risk of photooxidative damage by excess of light. The synthesis of these compounds, identified by mass spectrometry as cantaxanthin, astaxanthin, ketolutein and their esters, was accompanied by the production of large amounts of lipids. The fact that this microorganism belongs to Scenedesmaceae, a family which is receiving increasing attentions in biotechnology, in addition to the commercial high-value of microalgal lipids and ketocarotenoids, strongly addressed our attention on this isolate. In the present study, by the mean of a multicultivator system (PSI, MC1000), we tested the effects of different light regimes and nitrogen availability on biomass and ketocarotenoid production by *C. australis*. The instrument, a small photobioreactor with eight culture slots (80 ml), each illuminated by a set of led light individually adjustable between 10 to 900 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$, allows the verification of a wide range of light intensities in a single experiment. Each slot is also equipped by an optical density detector, that measures every hour the turbidity (750 nm) of the culture, simplifying the monitor of microalga growth curve. In all the considered conditions, morphology, ultrastructure, lipid accumulation, chlorophyll and carotenoid content and photosynthetic activity, have been determined and correlated with the growth rate and biomass production.

Sciuto et al., 2014 J. Phycol. (submitted)

Optical properties of diatom nanostructured biosilica: micro-optics from mother nature

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Some natural structures show three-dimensional morphologies of symmetry and complexity well far beyond than those fabricated by best technologies available. This is the case of diatoms, unicellular microalgae, which protoplasm is enclosed in a nanoporous microshell, made of hydrogenated amorphous silica, called frustule. We have studied optical properties of *Arachnoidiscus* genus single valve in visible and ultraviolet range. We found photonic effects due to diffraction by ordered pattern of pores and slits, accordingly to an elaborated theoretical model. For the first time, we experimentally revealed spatial separation of focused light in different spots, which could be basis of a micro-spectrometer. Moreover, deep knowledge and characterization of such intricate structures could be of great inspiration for photonic devices of next generation.

Different FeSOD levels are associated with different Cr(VI) tolerance in two strains of *Scenedesmus acutus*

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Despite being chromium tolerance not related to the induction of phytochelatins, the tolerance to this metal seems strictly connected to sulfur metabolism (Pereira et al., 2008; Schiavon et al., 2008). In the freshwater green alga *Scenedesmus acutus* sulfur starvation induces a transient increase of Cr(VI) tolerance both in the wild type and in a Cr-tolerant strain (Gorbi et al 2007). This transient increase is lost after 2-day recovery in standard medium. Studies based on microarray analysis showed that in *Chlamydomonas reinhardtii* sulfur starvation induces the expression of numerous genes, among which plasma membrane sulfate transporters, many enzymes of the sulfate assimilation pathway and enzymes involved in the antioxidative response, such as superoxide dismutase (SOD), GPX, FSD and SHMT (Zhang et al 2004). In order to verify if differences in SOD expression are involved in the observed transient increase in Cr-tolerance, as well in the differential sensitivity shown by the two *S. acutus* strains, we analysed SOD protein levels after different time of Cr(VI) exposure. No changes was observed in MnSOD or in Cu/ZnSOD following Cr treatment. On the contrary, immunoassays showed in the Cr-tolerant strain treated with Cr(VI) 1mg/l significantly higher levels of FeSOD than in the wild type. A 3-day sulfur starvation enhances FeSOD levels in both strains, though remaining significantly higher in the Cr-tolerant strain. At the present, it is not clear if the enhancement of FeSOD levels could be directly involved in the transient tolerance induced by S-starvation. Nonetheless, these results suggest the existence of a different threshold of oxidative stress perception that may induce a prompter response of the Cr-tolerant strain to Cr exposure.

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Marine benthic flora of the Mediterranean Sea: Chlorophyta

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After a brief introduction on general characteristics, classification, geographic distribution and ecology of Chlorophyta (green algae), an identification key to macroalgal genera, species and infraspecific *taxa* of that Phylum occurring in the Mediterranean Sea is given. Following a taxonomic-nomenclatural revision of macroalgal *taxa* to date recorded from that Sea, 183 *taxa* at specific and infraspecific level are accepted, 122 are considered as *taxa inquirenda* and 26 are considered as *taxa excludenda*. Moreover, six new nomenclatural changes are proposed. The systematic arrangement adopted, derives from the most recent works based on molecular analyses. Of each *taxon* a brief description, preceded by iconographic references as well by references reporting its distribution in the Mediterranean Sea, is given. Moreover, the treatment of most *taxa* is enriched with notes supporting either synonymies indicated, or taxonomic choices followed or the reasons for considering the *taxon* as *inquirendum* or *excludendum*. The paper is completed by a glossary of 120 entries, an index of all *taxa* quoted in the text and 95 plates illustrating all *taxa* at specific and infraspecific level (*taxa inquirenda* excluded) described in the text.

Macrophytes of the soft substrata of the Venice lagoon, abundance and distribution.

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In late spring and autumn 2011 the flora spread in the soft substrata of the Venice lagoon was investigated in 118 stations in order to assess the ecological status applying the Macrophyte Quality Index (MaQI). Globally, 137 taxa were recorded (56 Chlorophyceae, 65 Rhodophyceae, 11 Phaeophyceae, 1 Xanthophyceae and 4 aquatic angiosperms i.e. *Cymodocea nodosa*, *Ruppia cirrhosa*, *Zostera marina* and *Nanozostera noltii*. Among them, 4 species were new records for the Venice lagoon: *Acrochaete inflata* (Ercegovic) Gallardo *et al.*, *Cladophora battersii* Hoek, *Cladophora socialis* Kützing; *Gayliella mazoyerae* T.O. Cho, Fredericq *et* Hommersand and one species also for the Mediterranean Sea: *Uronema marinum* Womersley (Sfriso *et al.*, 2014). One species, i.e. *Lophosiphonia obscura* (C.Agardh) Falkenberg was the first record after Pignatti (1962), whereas *Ceramium polyceras* (Kützing) Zanardini and *Pyropia elongata* (Kyllin) Neefus & J. Brodie, previously reported by other names are the result of molecular analyses and nomenclatural revisions. Some species, already reported in the past, were only recorded in close fishing ponds: *Lamprothamnion papulosum* (Wallroth) J. Groves, *Valonia aegagropila* C. Agardh and *Polysiphonia spinosa* (C. Agardh) J. Agardh.

The most common taxa, which were recorded in a number of stations ≥ 50 integrating the records of the two seasons, were 4 Chlorophyceae: *Ulva laetevirens* Areschoug (70), *Achrochaete viridis* (Reinke) Nielsen (66), *Ulva rigida* C. Agardh (61) and *Chaetomorpha ligustica* (Kützing) Kützing (50); 4 Rhodophyceae: *Gracilaria gracilis* (Stackhouse) Steentoft *et al.* (66), *Chondria capillaris* (Hudson) M. J. Wynne (66), *Hypnea flexicaulis* Yamagishi & Masuda (59), *Agardhiella subulata* (C. Agardh) Kraft *et* M. J. Wynne (57); 1 Xanthophyceae: *Vaucheria submarina* (Lyngbye) Berkeley (52). Among them, surprisingly, *H. flexicaulis* and *A. subulata* are just two non-indigenous species (NIS) of recent introduction. In addition to the finding of these two NIS and *Uronema marinum*, other 7 alien taxa were found in a smaller number of stations.

The check-list recorded in this survey in the soft substrata of the Venice lagoon reports the highest number of species in comparison to the previous study of Curiel *et al.* (2006) that, sampling 90 stations in spring and autumn in the early 2000s, recorded 103 taxa.

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Ultrastructural study on the infection mechanism and host response of the marine oomycete *Eurychasma dicksonii* infecting brown seaweeds

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In recent years, global seaweed production in aquaculture systems has increased exponentially. Marine oomycetes are relatively little studied despite the fact that are frequent parasites of algae. The oomycete *Eurychasma dicksonii* is one of the most common and widespread marine pathogens and attacks a broad spectrum of more than 45 brown algal species. The present study investigated the mechanism used by the pathogen to attach on the host cell wall and force its way into algal cells. Detailed ultrastructural examination of early stages of infection revealed a needle-like structure which develops within the attached spore and extends along its axis. Parallel to the formation of this structure, the basal part of the spore cell wall (adhesorium-like) is particularly modified in order to guide this needle-like tool to penetrate the host cell wall. The unique injection mechanism is shared with *Haptoglossa* species which suggests that this is an important characteristic of early diverging oomycetes. Furthermore, the encystment and adhesion mechanism of *E. dicksonii* shows significant similarities with other oomycetes, some of which are plant pathogens. In addition to the above, the application of special staining and immunofluorescence techniques showed the deposition of β -1, 3 glucans on the host cell wall at the pathogen penetration site, a strategy similar to physical responses previously described in infected plant cell walls. It is assumed that the host response in terms of callose-like deposition is an ancient response to infection.

Distribution and genetic diversity of the coralline red algae *Lithophyllum byssoides* (Lamarck) Foslie and *L. stictaeforme* (Areschoug) Hauck along the Italian coasts

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Coralline red algae (Rhodophyta, orders Corallinales and Sporolithales) represent a universal component of hard-bottom coastal communities and play a key role in many ecological processes. Some species act as bioconstructors, providing a wealth of habitats for many algal and animal species. In the Mediterranean these bioconstructions are widespread and occur both in the littoral zone (trottoirs of *Lithophyllum byssoides*) and in the sublittoral zone (coralligenous bottoms, where coralline algae are the main constituents). A good knowledge of their distribution and population structure is essential for their conservation, but at present molecular data assessing taxonomic identity and genetic variation in Mediterranean corallines are very limited. We investigated two important bioconstructor corallines, *Lithophyllum byssoides* and *L. stictaeforme* (Corallinales, Corallinaceae), using sequences of the plastid *psbA* gene and mitochondrial *cox2,3* spacer, markers widely used for discrimination between closely related species and phylogeographic studies in red algae.

Samples of *L. byssoides* and *L. stictaeforme* were obtained from 15 sites along the Italian shores. In the *psbA* phylogeny, Mediterranean populations of *L. byssoides* formed a well-supported clade sister to Atlantic populations. The samples from the Italian shores were unexpectedly diverse, with several haplotypes exclusively associated with individual sites. Several clades corresponding to well-defined biogeographical units were recognized, in particular for the Ligurian Sea, Campania coastline and the Adriatic Sea. In the *psbA* phylogeny, *L. stictaeforme* formed a well-supported monophyletic group, belonging to a larger clade which included also samples of other species of *Lithophyllum* from Atlantic Europe and the Mediterranean. Italian samples of *L. stictaeforme* were subdivided in several clades; whereas some clades had widespread geographical distributions, others were circumscribed to individual sites or areas (e.g., the northern Adriatic, southwestern Sardinia). The *cox2,3* analyses yielded results in agreement with the *psbA* results, producing overall similar geographical patterns.

Our results show an unexpectedly high genetic variation in both *L. byssoides* and *L. stictaeforme* and suggest that in these species geographic distributions reflect molecular phylogenetic patterns better than morphological data. In *L. byssoides*, populations from different areas represent distinct genetic units, which appear to have limited dispersal and require special attention in terms of conservation efforts.

Growth rates of dominant macroalgae in areas potentially affected by anoxic crises: the Venice lagoon as a study case.

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The last year an hypo-anoxic event occurred in the Venice lagoon in July near the Airport "Marco Polo", mainly due to *Ulva* biomass degradation (Bastianini *et al.*, 2013). This resulted in showy fish die-offs and foul smell. This year, a monitoring activity was performed in two stations (away from each other 3.6 km), on the sides of the bridge watershed that connects Venice with mainland, to assess macroalgal growth rates of four of the most common seaweeds: *Ulva rigida*, *Gracilaria gracilis*, *Gracilariopsis longissima* and *Gracilaria vermiculophylla* and variations in the main physico-chemical parameters of water and sediment. These species were grown in grid cages of 25x25x25cm, with mesh size of 1 cm, and weighted weekly restoring every time 200g for cage, accounting for a biomass of ca. 3.2 kg m⁻², similar to that recorded in field. A visual census at the beginning of May reported a predominance of *Ulva* at Tresse in front of the industrial area of "Porto Marghera" and a predominance of the alien species *G. vermiculophylla* at San Giuliano near the airport. This species recorded in the lagoon in 2008 (Sfriso *et al.*, 2010) in 2014 completely replaced the Ulvaceae avoiding anoxic crises. The data collected from May to September highlighted significant differences between the stations and a different algal growth behaviour for the monitored species. The reactive phosphorus in the water column was 8 times higher at S. Giuliano than at Tresse, the reactive silicates were 49% higher and salinity was lower with 19.8 psu against the 23.3 psu at Tresse. This seemed to confirm the influence of freshwater coming from the near Osellino river at S. Giuliano. In May-June all macroalgae showed a luxuriant growth: *G. vermiculophylla* predominated at San Giuliano showing the highest growth rate (1.32 % d⁻¹) whereas *U. rigida* displayed the highest growth rate at Tresse (5.34 % d⁻¹). In July-August all macroalgae were affected by pulsing growth conditions due to alternation of weather conditions. In the whole period Gracilariaceae displayed a more uniform growth pattern with a maximum in July (7.0% day⁻¹), *Ulva* instead fluctuated weekly between growth and decline (from 17.8 to -6.0 % day⁻¹) increasing the risk of anoxic crises. As a result, the replacing of laminar Ulvaceae by Gracilariaceae seems to limit in the short term the occurrence of other anoxic events at S. Giuliano where slower and more stable growth rates were found; at Tresse instead the high instability and growth rates can be cause of concern.

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Restoration of the habitat 1150* by transplantation of aquatic angiosperms in the northern basin of Venice lagoon: the Life “SeResto” project.

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Pristine coastal lagoon conditions are characterized by wide meadows of aquatic angiosperms and their reduction or disappearance is a symptom of environmental deterioration. Their presence plays a crucial role in the environment preservation, both from the abiotic and biotic point of view. Angiosperms consolidate bottoms, prevent erosion, support benthic and fish communities, favouring the bird presence. Over the past few decades, the aquatic angiosperms have receded significantly in the lagoon of Venice, in particular in the central and northern basins, as a consequence of many anthropogenic activities (Sfriso et al., 2007). At present most of the pressures that affected the northern lagoon have decreased and there are the conditions for an angiosperm recolonization. To favour the angiosperm recolonization which, in the northern basin, is delayed or hampered by many natural barriers (tidal lands and islands) the European Commission has funded the Life nature project “SeResto” (LIFE12 NAT/IT/000331) aiming at restoring and consolidating the priority habitat 1150* in the northern part of Venice lagoon, by the transplantation of small sod-bearing aquatic angiosperms. These submerged plants contributing to the biodiversity enrichment and safeguarding the bottom erosion may accelerate the achievement of the good ecological status as required by the WFD (2000/60/EC). For this purpose, in spring 2014, 9 sods (diameter ca. 30 cm) of different angiosperms, i.e. *Nanozostera noltii*, *Zostera marina*, *Cymodocea nodosa* and *Ruppia cirrhosa* have been transplanted in 17 areas of the northern lagoon selecting the plants in relation to the area hydrodynamics, sediment grain-size and water depth. In addition, the plant spreading was enhanced by the dissemination of hundreds of rhizomes with the collaboration of amateur fishermen and hunters. During the next spring, other 18 stations will be transplanted and the angiosperm recruitment will be recorded till April 2018 by determining their expansion, the environmental parameters related to their growth and spreading. Moreover, indices, based on macrophytes, macrobenthic and fish fauna will be applied to assess the ecological status improvement. Preliminary results are encouraging in great part of the selected areas but, as expected, some difficulties have been recorded in areas with high water turbidity and growth of thionitrophilous macroalgae, favoured by the unexpected weather conditions of this year. These areas will be further transplanted until the rooting of the selected species.

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