Elisa Corteggiani Carpinelli

Citizenship: Italian ▪ **Date of birth:** 04 March 1982

Contact

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Key Skills

Enthusiastic scientist with great capability for design and management of scientific projects. Proficient or familiar with a vast array of laboratory techniques and with the fundamental data analysis tools. Skilled at scientific communication and teaching. Experienced in working in teams and in projects where a multidisciplinary approach is required.

Education

2007 to 2011	**PhD in Biochemistry and Biotechnology (grade: A)** University of Padua, Italy
2004 to 2006	**Master Degree in Molecular Biology (110/110 with distinction)** University of Padua, Italy
2001 to 2004	**Bachelor Degree in Molecular Biology (110/110 with distinction)** University of Padua, Italy
1996 to 2001	**High school diploma (100/100)** Liceo Classico F.A.Gualterio, Orvieto, Italy

Most relevant Post-graduate Schools, attended as student and/or as teacher

Teacher 2013	**XVII International School of Pure and Applied Biophysics (Venice)** Renewable energy and biofuels: a biophysical and biochemical approach
Student 2009	**School on Next generation sequencing: available technologies and applications (Padova)** Organized by the graduate school on Biochemistry and Biotechnology, teacher: Prof. Giorgio Valle
Student 2009	**School on Proteomics and Mass Spectrometry: a theoretical and practical course (Padova)** Organized by the graduate school on Biochemistry and Biophysics, teacher: Prof. Peter James
Student 2007	**XI International School of Pure and Applied Biophysics (Venice)** Advanced optical microscopy methods in biophysics

Post graduate Research

University of Padua, Padua, Italy — **Post Doctoral Fellowship**
Functional Genomics Research group (PI Prof. Giorgio Valle) — **May 2011 to May 2013**
Topics: functional genomics and mutagenesis of the microalgae *Nannochloropsis gaditana*
metagenomic analysis of water samples from an highly polluted area
Responsibilities: identification of scientific problems; design and realization of experiments; collaboration to various research projects of the group; realization of web facilities; education of undergraduate and master's students

University of Padua, Padua, Italy — **PhD program**
Functional Genomics Research group (PI Prof. Giorgio Valle) — **January 2009 to April 2011**
Topic: genomics and transcriptomics of the microalgae *Nannochloropsis gaditana*
Responsibilities: identification of a scientific problem of interest and elaboration of a scientific project; design of the experimental strategies to tackle the chosen scientific problem; realization of some of the experiments; coordination of the work of the other researchers involved in the project; setting up of innovative laboratory procedures; education of undergraduate and master's students

University of Padua, Padua, Italy — **PhD program**
Photosynthesis Research group (PI Prof. Giorgio Mario Giacometti) — **January 2007 to December 2008**
Topics: functional and regulatory aspects of the photosynthetic apparatus of high plants and cyanobacteria
peroxidase activities in the photosynthetic compartments
Responsibilities: design of the experimental strategies to tackle the assigned scientific problems; realization of the experiments; setting up of new laboratory procedures; troubleshooting; education of undergraduate and master students

Employments not in Academia

Various Private and Public Companies — **Short term contracts as Teacher**
Specialization courses about renewable energies for employees — **December 2013 to now**

Various elementary and high schools — **Short term contracts as Teacher**
Laboratories experiences for school children and refresh course for life science's teachers — **2007 to 2012**

Teaching Experience in Academia

University of Padua, Padua, Italy — **Teaching Assistant**
Laboratories of Molecular Biology — **Academic years** 2006-2007; 2007-2008; 2010-2011
Program: production of a library of *Lambda Phage* DNA; Plasmid DNA preparation from *E.coli*; genomic DNA extraction from human saliva; PCR amplification; agarose and polyacrylamide gel electrophoresis.

University of Padua, Padua, Italy — **Teaching Assistant**
Laboratories of Structural Biochemistry — **Academic years** 2008-2009; 2009-2010; 2011-2012
Program: growth and induction of E.coli strains transformed for the overexpression of a pH sensitive YFP; purification of the YFP by affinity chromatography; spectroscopic and electrophoretic analysis of the obtained fractions, fluorometric analysis of the purified proteins at different pH.

University of Padua, Padua, Italy — **Teaching Assistant**
Laboratories of Metabolic Biochemistry — **Academic year** 2011-2012
Program: measure of the photosynthetic activity of leaf disks in a simple experimental system in response to different lights; purification of mitochondria from yeast and measure of the ATP production of the purified mitochondria using a fluorometric assay.

University of Padua, Padua, Italy — **Teaching Assistant**
Laboratories of Biochemistry — **Academic year** 2012-2013
Program: introduction to absorbance spectroscopy, measure of the enzymatic kinetics of l-lactate dehydrogenase, mathematical formalisation of the data.

University of Padua, Padua, Italy — **Teaching Assistant**
Tutorials and Exercises of Metabolic Biochemistry — **Academic years** 2009-2010; 2010-2011; 2011-2012
Program: principles of bioenergetics; glycolysis, gluconeogenesis and pentose phosphate pathway; citric acid cycle; metabolic regulation; fatty acid metabolism; amino acid metabolism; hormonal regulation of mammalian metabolism; biotechnological applications of the metabolic manipulation of various microorganisms.

University of Padua, Padua, Italy — **Teaching Assistant**
Practical Laboratories of Genomics — **Academic years** 2010-2011; 2011-2012; 2012-2013
Programs of the three years:

- ✓ Library preparation of full-length transcripts using the In-Fusion Full Length library construction system, sequencing and bioinformatics analysis of the data;
- ✓ Introduction to PERL programming and realisation of a simple program for primer oligonucleotide design; experimental testing of the designed primers by PCR reaction and sequencing;
- ✓ Metagenomic analysis of a water sample: sampling, extraction of nucleic acids, library preparation, sequencing and data analysis

Technical skills

Molecular Biology	Purification of nucleic acids from various organisms (plants, algae and bacteria); design and production of recombinant constructs for genome mutagenesis and protein overexpression; transformation of bacteria, cyanobacteria yeast and algae; enzymatic manipulation of nucleic acids; agarose and polyacrylamide electrophoresis; pulsed field gel electrophoresis (PFGE).
Genomics and Transcriptomics	Genomic DNA library preparation using the *E.coli* host system; preparation of mate-paired libraries for SOLiD sequencing; preparation of libraries for Ion Proton sequencing; some experience with genome assembly; mRNA enrichment and ribodepletion of Total RNA samples; preparation of full length cDNA libraries; enzymatic manipulation of RNA for 5' end capturing.
Microscopy	*In vivo* Fluorescent and Confocal Microscopy
Biochemistry	Purification of active proteins and protein complexes from photosynthetic membranes; overexpression and purification of proteins in *E.coli* host system; native and denaturing protein electrophoresis, 2D gel electrophoresis; western blotting and immunodecoration; fplc and hplc for proteins and pigments analysis and purification; measures of oxygen evolution from photosynthetic samples; preparation of protein samples for analysis with mass-spectrometry.
Spectroscopy	Absorbance spectroscopy; pulsed amplitude modulated (PAM) fluorometry for analysis of photosynthetic activity; fluorescence spectroscopy.

Language skills

Italian (native language)	**English** (speak fluently; read and write with high proficiency)	**French** (basic knowledge)

Informatics skills

Basic knowledge of **Perl programming,** proficient usage of many available **biological databases** and **analysis tools**	Proficient usage of **spreadsheets** and **text editors,** good capabilities with **digital graphic software**	Proficient in the design and management of **web pages** and **blogs** and in the use of **socials**

Publications in international journals

- ✓ A deep survey of alternative splicing in grape reveals changes in the splicing machinery related to tissue, stress condition and genotype.
  Vitulo N, Forcato C, **Corteggiani Carpinelli E**, Telatin A, Campagna D, D'Angelo M, Zimbello R, Corso M, Vannozzi A, Bonghi C, Lucchin M and Valle G
  BMC Plant Biology. 14:99. doi:10.1186/1471-2229-14-99. Epub 2014 Apr 17.
- ✓ Chromosome scale genome assembly and transcriptome profiling of Nannochloropsis gaditana in nitrogen depletion.
  Corteggiani Carpinelli E, Telatin A, Vitulo N, Forcato C, D'Angelo M, Schiavon R, Vezzi A, Giacometti GM, Morosinotto T, Valle G.
  Mol. Plant (2014) 7 (2): 323-335. doi: 10.1093/mp/sst120. First published online: August 21, 2013
- ✓ Acclimation of Nannochloropsis gaditana to different illumination regimes: Effects on lipids accumulation.
  Simionato D, Sforza E, **Corteggiani Carpinelli E**, Bertucco A, Giacometti GM, Morosinotto T.
  Bioresour Technol. 2011 May;102(10):6026-32. doi: 10.1016/j.biortech.2011.02.100. Epub 2011 Mar 2.
- ✓ Going ultradeep to unravel the secret recipe of biofuel. **Elisa Corteggiani Carpinelli**
  LAP Pubblishing. 2011

Communication at Scientific Conferences in Italian Institutions

XVII School of Pure and Applied Biophysics, Venice, Italy — **Lecture**
Annual International School for PhD Students — **January 2013**
"Renewable energy and biofuels: a biophysical and biochemical approach"
Topic of the talk: Introduction to genomics and transcriptomics. Case study: the genome and transcriptome of the microalgae *N. gaditana*: what did we leant? Presentation of Bioinformatics tools to interrogate the genomic data.

Italian National Academy "Accademia dei Lincei", Rome, Italy — **Oral communication**
International Conference on renewable energy: — **November 2009**
"Biological processes as a possible source for renewable energy"
Topic of the talk: recent achievements on genomics and transcriptomics of the microalgae *N. gaditana*

Lectures and web

Collaboration with the "**Fenice Green Energy Park**" for **didactic laboratories** for school children about biofuels and for the setting up of a **photobioreactor** — **2013 to now**

Realization of **web pages and video-tutorials** for students and teachers (see http://elisacorteggiani.com/ section portfolio) — **Since 2008 and until now**

Cultural Association, Orvieto, Italy — **Communication at Public Conference**
Lectures for the 150 anniversary of "the origin of species" — **May 2009**
Topic of the lecture: what Darwin didn't know yet: evidences and elements that genetics and molecular biology added to Darwin's theory of evolution by natural selection.

Hall of Residence for University Students "Marianum", Padova, Italy — **Communication at Public Conference**
Lecture for the students of the residence — **January 2012**
Topic of the lecture: Let's talk about bioethics (the method used for the lecture and many of the contents were inspired by "Justice with Michel Sandel", and I added specific references to some topics of Bioethics)

"*F.A.Gualterio*" High School, Orvieto, Italy — **Invited Author for the School Journal**
Editorials about the scientific literature and the wonder for nature, with suggested readings — **School years** 2007-2008; 2008-2009

Going ultra deep to unravel the secret recipe of biofuel

Genomic, transcriptomic and biochemical analysis of the metabolism of the microalga *Nannochloropsis gaditana* in order to understand and increase its oil productivity

During the first two years of my PhD I was involved in various projects of biochemical characterization of the photosynthetic apparatus and of the proteins involved in its regulation. In this period I manifested a growing interest for some recent studies concerning the culturing of photosynthetic microorganisms to harness the energy of sunlight for powering human activities and I was therefore given the opportunity to contribute to a new project of the group concerning the production of biodiesel from microalgal biomass.

I started working at the culturing of various oleaginous microalgae, measuring their physiological parameters and their growth kinetics and setting up the protocols for nucleic acid and protein extractions. Some of the results of this work are reported in (Simionato et al. 2011). The project envisioned the realization of efficient production plants where microalgae were used as factories of substrates for biofuel production. The plants would have been the result of the collaboration between biologists and engineers. The work in this interdisciplinary team and the discussions that we shared during the periodical meetings represented for me an excellent scientific experience and contributed to enlarge my vision of the biotechnological task.

After attending a course for graduated students about next-generation sequencing, I had a proposal for my colleagues: I wanted to start a project of genome and transcriptome sequencing of a oleaginous microalga to pinpoint the genes responsible for the accumulation of oil inside the cell and to open up the perspective of genetic manipulation of the microorganism in order to boost its productivity. My supervisor agreed that the idea was interesting and gave me the chance to carry out the project on my own responsibility. In 2009 I started working on the sequencing of the genome and the transcriptome of the microalga *Nannochloropsis gaditana* in close collaboration with the group of Professor Giorgio Valle (Genomics Unit of the University of Padova) and of Doctor Tomas Morosinotto (Unity of Microalgal Biophysiology of the University of Padova).

After three years work, the results of my research were: the complete sequence of the genome of *Nannochloropsis gaditana* at chromosome level and the prediction and annotation of its genes (the data are deposited at the NCBI as bioproject 170989); the profile of the gene expression of *Nannochloropsis gaditana* in conditions of oil accumulation compared to conditions of standard growth (no oil) (the data are deposited at the NCBI as bioproject 231651); the elaboration of an interpretative model of the metabolic fluxes that lead to oil accumulation. My analyses of the genome and transcriptome of *N. gaditana* were accepted for publication on Molecular Plant in 2013 (Corteggiani Carpinelli et al. 2014) (pubmed id 23966634)

Moreover together with my colleagues of the Functional Genomics Unit of the University of Padova I worked at the release of a web resource of *Nannochloropsis* genome (www.nannochloropsis.org) and we also opened a blog (www.nannochloropsis.org/blog) to promote communication and collaboration among scientist involved in this field of investigation.

Introduction to the *Nannochloropsis'* metabolism discovery project

Various species of microalgae had been observed to convert efficiently the solar energy into triacylglycerols, which are optimal substrates for the production of oil-based diesel fuel. Despite some promising results obtained by cultivating the microalgae in photobioreactors, none of the currently available strains appeared to

be suitable for energetically convenient industrial production. A leap in productivity could be possibly obtained from the genetic improvement of the available oleaginous strains. In this respect, *Nannochloropsis* represented an attractive candidate, being a native oil producer; moreover it was later shown to be transformable with exogenous DNA, and some strains seem to be also capable of homologous recombination.

When cultured in normal growth conditions with sufficient nitrogen, *Nannochloropsis* cells had an oil content of about 30% of their dry weight. Various culturing conditions were observed to increase the average oil content per cell, however these conditions supported only slow growth rates of the cultures and therefore the overall productivity resulted decreased. Among these conditions there was nitrogen deprivation. Overcoming the trade-off between oil accumulation and biomass production was the first possibility that had to be tested in order to improve the productivity.

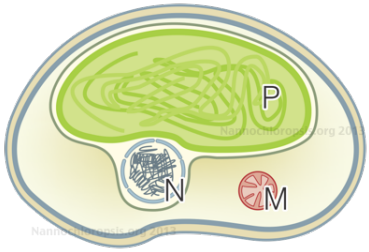

Figure 1 Schematic representation of *Nannochloropsis* single cell

Being *Nannochloropis* a poorly studied organism, the sequencing and annotation of the genome seemed the most rapid strategy to start delineating the metabolic pathways present in the cell and possibly involved in the accumulation of triacylglycerols. Moreover the genome sequence is a fundamental starting point for targeted genetic mutagenesis. Important information about the up-regulated and down-regulated pathways could be gained by comparing the abundance of the transcripts expressed when cells accumulated high amounts of triacylglycerol with the abundance of the transcripts expressed when cells showed only limited accumulation of triacylglycerols.

Results

Gene annotation

We obtained the sequence of the nuclear genome as well as of the genomes of the organelles of *Nannochloropsis gaditana* B-31. We assembled the 28.5 Mega bases of the nuclear genome in 58 large scaffolds, 21 of which accounted for complete chromosomes and we completely assembled the circular genomes of the organelles. We identified a total of 10646 genes and we attributed an annotation to 6311 of them. The analysis of the annotated genes using the “pathway tool” software yielded the metabolic map showed in Figure 2.

The analysis of the annotated genes and pathways revealed various traits, which are relevant for the genetic manipulation of *Nannochloropsis* with the final goal of improving its oil productivity in a production plant:

- We identified pathways leading to the synthesis of cellulose and sulphated fucans and pathways responsible for the remodelling of the cellulose. These indications casted a light on the molecular composition of the cell wall and also suggest possible targets of genetic modification. Indeed, one of the most energy consuming steps during oil extraction from *Nannochloropsis* is the breakage of the cell wall. Targeted genetic mutations of the genes assigned to these pathways might help weakening the cell wall and saving energy during oil extraction.
- We identified a group of genes that could be attributed to a pathway of biosynthesis of chrysolaminarines, which are very common storage sugars found in various neighbouring species of microalgae. The identification of a pathway of sugar storage is of particular interest, since its expression can be

studied to better understand the metabolic fluxes of carbon and energy in *Nannochloropsis* in different culturing conditions.

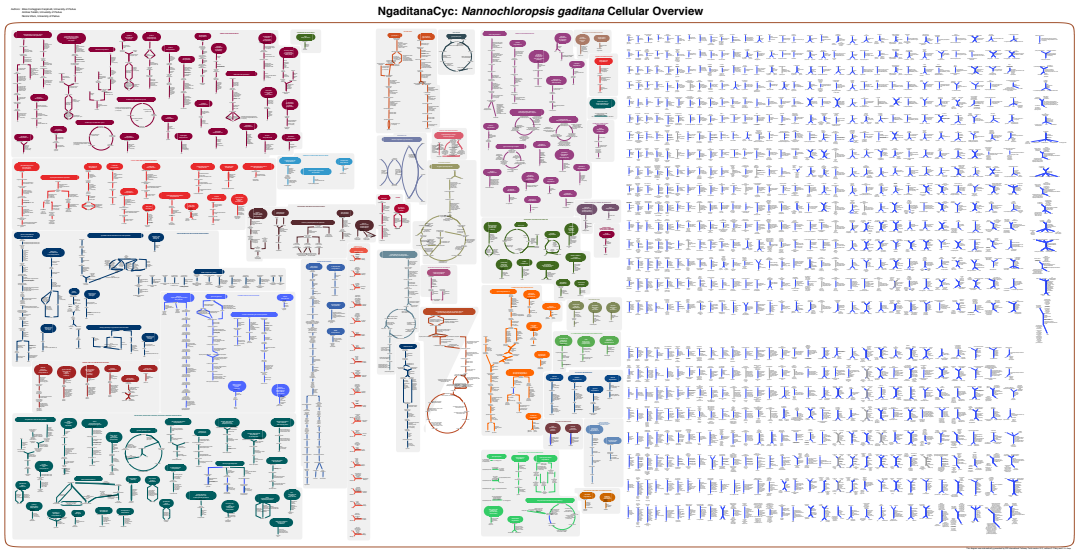

Figure 2 Map of the metabolic pathways identified in *Nannochloropsis gaditana* after genome sequencing and annotation

- A comparative analysis of the genes of *Nannochloropsis* in relation to the genes of various other algae of the red, brown and green groups has shown that *Nannochloropsis* has an expanded repertoire of some of the genes involved in triacylglycerol assembly. Most interestingly we found a high number of triacylglycerol lipases, many of them belonging to a gene family which seems to be exclusive to *Nannochloropsis*. Triacylglycerol lipases can affect lipid metabolism in many ways through triacylglycerol degradation and lipid remodeling. Further studies will be needed to enlighten the function of these genes are their rule in *Nannochloropsis* metabolism.
- We found genes essential for the RNA silencing process and we also found indication that miRNA might be expressed in *Nannochloropsis*. These findings open interesting perspectives for the genetic manipulation of *Nannochloropsis* using gene knock-down techniques based on the transient expression of siRNA.
- We found genes whose orthologous are annotated as blu-light sensors. Confocal microscopy analysis revealed the presence of red eye-spots in the cells located outside of the chloroplast that could be assigned as a blu-light sensing structure. If these attributions are correct, they open the perspective that a circadian regulation of growth and metabolic activity might be present in this microalga. Such a possibility would not be in contrast with some observations collected in outdoor cultivation plants and has important implication for the exploitation of this organism in production plants.

Triacylglycerol accumulation in nitrogen scarcity

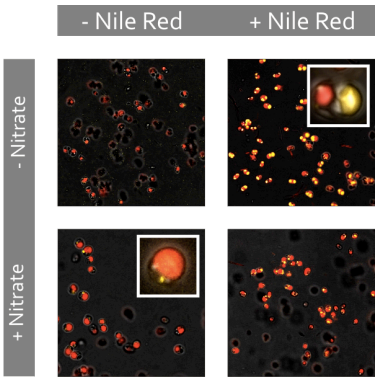

Figure 3 Confocal microscopy images of *Nannochloropsis* cells. In red the chlorophyll, in yellow the lipid droplets. From 11Corteggiani Carpinelli et al 2014

Upon treating *Nannochloropsis* cells with a substance that stains specifically the neutral lipids (Nile Red) we can observe that in nitrogen deprivation (-Nitrate) they accumulate big lipid droplets (yellow signal) usually not present in the cells grown in the presence of nitrogen (+Nitrate).
Comparison of the abundance of the transcripts in the cultures with sufficient nitrogen and poor lipid accumulation and in the cultures with scarce nitrogen and high lipid accumulation, offered the possibility to delineate the activation and the tuning down of various metabolic pathways and to hypothesize the balancing of the fluxes responsible for the accumulation of triacylglycerols inside the lipid droplets in nitrogen deprivation.

The analysis of the gene expression revealed that *Nannochloropsis* activated various mechanisms of nitrogen assimilation and redistribution in nitrogen scarcity and survived thanks to a partial reorganisation of its cellular metabolism.
Various genes whose function is related to controlled protein degradation were induced in nitrogen stress, together with genes coding for proteins involved in the formation of cytosolic sequestering vesicles, which are used for degradation and recycling of cellular components. The up-regulation of these degradative processes made aminoacids available for biosynthetic processes without the need of nitrogen input (which is normally needed for the synthesis of new aminoacids). In addition various degradative processes that release ammonium were also found over-expressed. The GS/GOGAT pathway (L-glutamine + 2-oxoglutarate + NADPH + H+ ⟷ 2 L-glutamate + NADP+) was activated in the nitrogen-deprived cells. The enzymes of this pathway are: glutamine synthetase (GS), which has a high affinity for NH_3 and catalyzes the incorporation of ammonia into glutamine; glutamate synthases and glutamine amidotransferase, which are able to transfer one amino group from glutamine to 2-oxoglutarate and release, as a result, two molecules of glutamic acid. The glutamic acid produced through this pathway is an available substrate for further incorporation of intracellular ammonia and represents also a source of amine groups for cellular biosynthetic processes. I therefore hypothesize that this glutamine–glutamate shuffle might act as a central intermediary of amine groups' exchange between degradative and biosynthetic pathways.

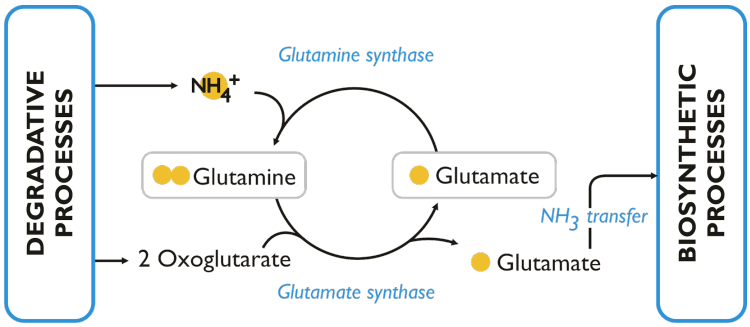

Figure 4 Schematic representation of the reorganization of the cellular metabolism in *Nannochloropsis* in nitrogen scarcity as deduced from RNA-Seq data. From (Corteggiani Carpinelli et al. 2014)

The genes predicted to function in the biosynthetic processes were still actively expressed at high levels for at least for 2-3 days after nitrogen deprivation with the exception of those responsible for protein biosynthesis of the organelles, which were instead severely tuned down even during early nitrogen deprivation.
In response to nitrogen deprivation, the cells reorganized their metabolism by degrading selectively unnecessary molecules and synthesizing new ones to allow survival even in the deficiency of a fundamental nutrient and the first activities that were tuned down were those that take place in the organelles.

The transcriptomic data showed that the genes involved in fatty acid and triacylglycerol biosynthesis were always abundant in the cells (both when nitrogen was available and when it was deficient) and that their expression was not correlated with the amount of oil accumulated in the cells. Also the expression of the genes involved in lipid degradation did not seem to change significantly. The general conclusion suggested by the experimental evidence was that *Nannochloropsis* constitutively synthesized lipids and that the metabolic reorganization that followed nitrogen deprivation increased the flux of substrates through the lipid biosynthetic pathways, which were in turn capable to sustain the increased metabolic flux.
Based on the available data I proposed a model of the metabolic response of *Nannochloropsis* to nitrogen deficiency that could justify an overproduction of fatty acids and as a consequence an accumulation of oil.

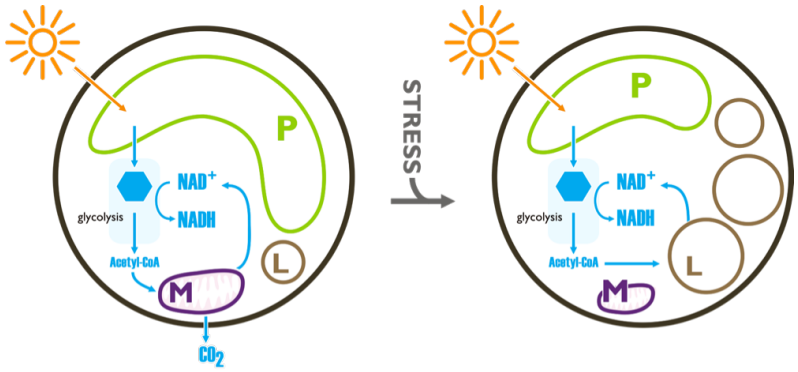

Figure 5 Potential Model of the flux trough the fatty acid synthesis pathways in nitrogen sufficient and nitrogen deficient culturing conditions based on transcriptomic data. P, plastid; M, mitochondrion; L, lipid droplet.

Simionato et al. showed that despite the decrease of photosynthetic yield, photosynthesis is the only energy supply of the cells in nitrogen starvation. One of the most evident effects of nitrogen starvation that we noticed was the deescalation of the organelles. The model therefore states that the energy came into the system through the photosynthetic activity of the chloroplasts in both nitrogen sufficient and nitrogen depleted cultures, and produced glucose. After degradation of the glucose by glycolysis (the genes of this pathway were expressed at similar levels in both the two culturing conditions) the Acetyl-CoA and the reduced NAD(P)H were mainly reoxidised through the Krebs cycle and the mitochondrial respiration in nitrogen sufficient cultures. Only a small fraction of the Acetyl-CoA and of the reduced NAD(P)H entered the fatty acid biosynthetic pathway in this condition. During nitrogen starvation, due to the severe down-regulation of the mitochondrial genes, the reoxidation of the Acetyl-CoA and of the reduced NAD(P)H became less efficient and more substrates were available to enter the fatty acid biosynthetic pathway,

leading to the accumulation of oil into the lipid droplets. This interpretative model was tested experimentally using various inhibitors of the mitochondrial respiratory chain in nitrogen sufficient cultures and measuring the average amount of intracellular lipids of the growing cells. The results were encouraging but not conclusive because of the scarce uptake of the inhibitors by *Nannochloropsis* cells. According to this model the mitochondrial complex I subunits would be interesting targets for genetic modification aimed at increasing the lipid productivity of the cultures.

A web resource of *Nannochloropsis* to support research

While the production of data has become faster and cheaper, the necessity to fully analyze, organize and share them has become more pressing. I was deeply persuaded that the community of biochemists, biotechnologists and physiologist that worked with *Nannochloropsis* would have gained a lot of utility from the full access to the sequences of the genes and chromosomes, as well as to the metabolic and functional annotation and to the gene expression analysis in a format that could be accessible to anyone without the need of specific informatics skills.

Figure 6 Screenshot of the home page of the Nannochloropsis web platform

Thanks to the great resources of the bioinformatics group of the Functional Genomic Research Unit it was possible to developed a comprehensive bioinformatic platform for information retrieval and data analysis, which is available online at www.nannochloropsis.org. The platform integrates several resources: a quick search engine that, upon the input of a gene ID or function, returns the complete characterization of the gene, its sequence, and its genomic context; a query system that allows the user to obtain all the available information concerning a gene or a group of genes that correspond to the criteria used for the research (e.g. level of expression or enzymatic function); a genome browser displaying the annotation and the level of expression of each gene in different experiments; a blast search engine; a database of the metabolic pathways elaborate using the pathway tools framework and a scientific blog.

Three months after the platform was made available on the web, it had more than 1000 unique visitors per month and the number of pageviews has been steadily growing since then.

My personal view of this scientific experience

The *Nannochloropsis* project has represented the most complete and autonomous research experience of my early carrier as research scientist. It has allowed me to cultivate my scientific interest for metabolic biochemistry, it was the first scientific project that I had the possibility to conceive and it has been a nice teamwork experience thanks to many excellent colleagues and students. All the work was characterized by a lively curiosity, a motivational commitment and a lot of creativity.

Metagenomics

One of the first applications of the next generation sequencing technologies to sparkle my interest was metagenomics. Throughout immeasurable time, microorganisms have evolved and accumulated remarkable physiological and functional heterogeneity, and now constitute the major reserve for genetic diversity on earth. Cultivation-independent assessment of microbial genomes offers a major resource for observing the pallet of the different metabolic strategies; furthermore, this material is a major asset in the search for new enzymes for various industrial processes. Currently, there is a global political drive to promote industrial biotechnology as a central feature of the sustainable economic future of modern industrialized societies. This requires the development of novel enzymes, processes, products and applications. Metagenomics might represent an important resource for finding new molecules with diverse functions.

During my Post-Doc at CRIBI in the group of Genomics, while collaborating on various projects of the group (including the realization of a metabolic pathways database of *Vitis vinifera*) I was given the possibility to design and realize a metagenomic experiment together with my colleague Andrea Telatin. The experiment had to fulfill the task of testing the performances of the Ion Proton sequencer on amplicons, whole metagenomes and ribosomal RNA fragments. We identified an interesting ecosystem, the Canale Scaricatore in Padova. This river crosses for a short trait an industrial area and collects various pollutants. We collected various water samples from the polluted area and we set up an innovative protocol to extract both total DNA and RNA at the same time in order to allow a more significant comparison of the sequencing data. I also prepared the sequencing libraries and we worked together on the analysis of the sequencing data testing various available software tools. The sequences produced by this first run of Ion Proton resulted too short and too few to support significant conclusions. Nevertheless we noticed the presence of various bacteria capable to degrade toluene and benzene derivatives and we focused our attention on the search of their genomic sequences in order to gain some information about possible enzymes of interest.

Despite the poor biological conclusions that we were able to reach using the available data, this scientific experience was of great interest for the two of us. Indeed we were very happy to try ourselves at this new task and to earn some technical instruments useful for metagenomic analysis, which we both hope to use again in the future.

Photosynthesis

I carried out the research project for my Second Level Degree in the research unit of Photosynthesis of Professor James Barber at Imperial College in London.

During my stay in the laboratory I focused my efforts in the purification of functional Photosystem II (PSII) complexes from various cultures of Synechocystis PCC 6803 in which the PSII was present in relatively small amounts (i.e. from cultures grown in iron depletion and from strains with mutations effecting PSII subunits).

The result of my efforts was the successful purification of functional and relatively pure PSII complexes from the iron-depleted cultures and from the mutant cultures of Synechocystis. The analysis of the particles of PSII obtained from the iron depleted cultures revealed that the Photosystem II did not undergo structural or functional changes upon iron deprivation differently from PSI, which in iron scarcity was surrounded by an extra antenna giving rise to a PSI-antenna supercomplex. According to the evidence that we produced the absence of iron was affecting only the amount of Photosystem but not its structural or functional characteristics.

It is during this experience in the laboratory of James Barber that I acquired much of my knowledge about photosynthesis and the lot of my abilities as scientist. The beginning of my interest for renewable energies and for artificial photosynthesis also dates back to that period and to the interesting discussions with the scientists with whom I came in touch.

During the first two years of my PhD training a continued working on photosynthesis, this time in the laboratory of Professor Giorgio Giacometti at University of Padova. My work in Padova was mainly focused on the regulative aspects of the photosynthetic process and I was involved in various projects of the group. The most of my research was concentrated on the study of peroxidase activities in the thylakoid lumen.

Teaching

During my PhD and Post-Doc I had an intense activity as Teaching Assistant in molecular biology, biochemistry and genomics and I was also given the responsibility of tutoring some Undergraduate Students during their Graduation Projects. Despite teaching in Academia is not strictly a research experience I found it relevant to include a short paragraph about this activity in my report. My research interests indeed have both shaped and been shaped by my experiences as teacher, especially in the design of the laboratory activities.

The activity as teacher has been often the occasion for me for great experimentations, both for the scientific topics that I chose to examine and for the abilities that I had the chance to test and improve.

When I organized my first laboratory class of metabolic biochemistry I decided to include a simple experience about photosynthesis, which I was very confident to carry out with enthusiasm and competence, and a second experience about the measuring of the ATP production of isolated mitochondria, which I had never done before but I had been willing to observe for a long time. Choosing the topics for the tutorials and exercises of metabolic biochemistry I allowed myself to study something about diets and human metabolism during one academic year and about the industrial applications of various strains of bacteria during another. I once agreed to organize a laboratory experience of metagenomics for the students of the course of genomics in order to enjoy also myself for the first time working on a project in this interesting field. To my delight both the students and me were able to learn a lot from that laboratory experience.

Working in the didactic laboratories gave me the opportunity to collaborate with many different colleagues and to have various roles. Being responsible of conceiving and organizing in various occasions the didactic laboratories was a good training for learning how to manage a project and how to coordinate the work of a group of people.

Teaching was a great opportunity to improve my communication skills and was also the occasion for testing various instruments. It is during my laboratory classes indeed that I decided to exploit the potential of web pages and blogs for science communication for the first time. In Figure 7 I show the screenshot of a blog that I've used for a few years with the students of metabolic biochemistry and that other teachers often visit. I have recently tested the video-tutorials as useful tools to integrate the lectures and I am still studying and practising to improve my capability of producing good quality videos as well as useful illustrations.

Figure 7 Screenshot of my blog about metabolic biochemistry, used by students and by other teachers