

Curriculum Vitae

Nicola Vitulo

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1. Personal Information

Name and Surname: Nicola Vitulo
Place of birth: Rovereto, 23 September 1976
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2. Education

- In **1995** he obtained the high school qualification (Maturità Scientifica), at Istituto Statale “G. G. Trissino” in Valdagno (Vi).
- **21 March 2001** he obtained his degree in *Biological Science* at the department of Biology at the University of Padova. Thesis title: “Analysis of muscle transcripts containing repetitive sequences” (supervisor: Prof. G. Lanfranchi).
- **2002-2005** he was a PhD student in biotechnology at University of Padova. From 2002 to 2005 he worked in the laboratory directed by Prof. G. Valle (CRIBI, University of Padova). Title of the thesis: “*Bioinformatic analysis of the genome of Photobacterium profundum SS9*”. (Supervisor: Prof. G. Valle). **31/03/2005** he get the PhD.

3. Positions

- **01/04/2001-31/12/2002** he was a research grant holder at the genomic laboratory directed by Prof. G. Lanfranchi and G. Valle (CRIBI- University of Padova), within the research project B41 funded by Telethon Foundation.
- **01/01/2005-28/02/2006** he was a research grant holder at University of Padova, in the research laboratory of Prof. G. Valle.

Assegni di ricerca ai sensi dell’art. 51 comma 6 della Legge 27/09/1997 n. 449:

- **01/03/2006-30/04/2007:** Research fellow at University of Padova, in the research laboratory of Prof. G. Valle. Title of the Project: “Bioinformatic and post-genomic approaches to study molecular adaptation to high pressure and low temperature”
- **01/05/2007-29/02/2008:** Research fellow at University of Padova, in the research laboratory of Prof. G. Valle. Title of the Project: “Bioinformatic and post-genomic approaches to study molecular adaptation to high pressure and low temperature”

- **01/03/2008-28/02/2010:** Research fellow at University of Padova, in the research laboratory of Prof. G. Valle. Title of the Project: “Bioinformatic and post-genomic approaches to study molecular adaptation to high pressure and low temperature”
- **01/04/2010-31/03/2012:** Research fellow at University of Padova, in the research laboratory of Prof. G. Valle. Title of the Project: “Genomic analyses of food farming organisms by mean of bioinformatic approaches ”

Assegni di ricerca ai sensi dell’art. 22 e 24 della Legge 240/2010:

- **01/04/2012-31/03/2014:** Research fellow at University of Padova, in the research laboratory of Prof. G. Valle. Title of the Project: “Bioinformatic analysis of DNA methylation”.
- **01/04/2014-20/12/2015:** Research fellow at University of Padova, in the research laboratory of Prof. G. Valle. Title of the Project: “Development and application of innovative bioinformatics tools for the analysis of NGS data related to human disease”

Current Position

- **21/12/2015-today:** Researcher (fixed-term researcher, type b) at University of Verona, Department of Biotechnology.

4. Foreign Experience Activity

From July to December 2005 he has been a visiting research fellow at SCRIPPS Institution of Oceanography, University of San Diego, La Jolla, California, in the lab of Prof. Douglas Bartlett and Prof. Terry Gaasterland. During this period he worked on the comparison between the genome of *Photobacterium profundum* 3TCK, a mesophyle bacterium unable to grow at high hydrostatic pressure and the genome of *Photobacterium profundum* SS9 a psychrophiles and piezophiles bacterium isolated from an amphipod homogenate at a depth of 2500 in Sulu sea.

5. Teaching

5.1. Teaching

- Exercise teaching assistant in “*Bioinformatica IP*”, bachelor’s degree in Molecular Biology (academic year **2003-2004**)
- Exercise teaching assistant in “Bioinformatica”, bachelor’s degree in Biology (academic year **2003-2004**)
- Exercise teaching assistant in “Bioinformatica”, bachelor’s degree in Molecular Biology (academic year **2004-2005**)
- Teaching “*Bioinformatica*“ at Facoltà di Scienze MM.FF.NN, Università degli Studi di Verona, master degree in Agro-Industrial Biotechnologies, for a total of di 36 hours. (academic year **2005-2006**)
- Teaching “*Bioinformatica III*“ at Facoltà di Scienze MM.FF.NN, Università degli Studi di Padova, master degree in Molecular Biology, for a total of di 56 hours. (academic year **2005-2006**)
- Teaching “ *Bioinformatica III*“ at Facolta` di Scienze MM.FF.NN, Università` degli studi di Padova, master degree in Molecular Biology, for a total of 50 hours. (academic year **2006-2007**)
- Teaching “ *Bioinformatica III*“ at Facolta` di Scienze MM.FF.NN, Università` degli studi di Padova, master degree in Molecular Biology, for a total of 50 hours. (academic year **2007-2008**)

- Teaching “*Bioinformatica*” for FSE Regione Veneto n. 2120/1/4/1017/2008 Projects, code **CUP H75C08000210002** “*Tecnologie per la società dell'informazione*” at Facoltà d’Informatica dell’Università Ca’Foscari Venezia for a total of di 24 hours. (academic year **2009-2010**)
- Teaching “*Biostatistica computazionale e bioinformatica*” at Facoltà di Scienze Statistiche, Università degli studi di Padova, degree in Statistical Science, for a total of 26 hours. (academic year **2010-2011**)
- Teaching “*Biostatistica computazionale e bioinformatica*” at Facoltà di Scienze Statistiche, Università degli studi di Padova, degree in Statistical Science, for a total of 26 hours. (academic year **2011-2012**)
- Teaching “*Biostatistica computazionale e bioinformatica*” at Facoltà di Scienze Statistiche, Università degli studi di Padova, degree in Statistical Science, for a total of 26 hours. (academic year **2012-2013**)
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- Teaching “*Biostatistica computazionale e bioinformatica*” at Facoltà di Scienze Statistiche, Università degli studi di Padova, degree in Statistical Science, for a total of 26 hours. (academic year **2014-2015**)
- Teaching “*Biostatistica computazionale e bioinformatica*” at Facoltà di Scienze Statistiche, Università degli studi di Padova degree in Statistical Science, for a total of 24 hours. (academic year **2015-2016**)

5.2. Thesis co-supervisor

From 2007 to today he was co-tutor of 3 master thesis in Evolutionary Biology and 1 master thesis in Molecular Biology.

5.3. Advance teaching and workshop invited speaker

- 2005** Bioinformatic course, SIGA, Salsomaggiore Terme. Title presentation: “Microarray data integration and data mining”. 2-4 May 2005
- 2007** EC-US workshop “Cyber-infrastructure resources for genome-enabled research on microbial life and the marine environment”, 9-11 September 2007 at Arlington, VA, USA. His presentation was about web-services implementation and work-flow management system for metagenomic data integration.
- 2011** Workshop “RGASP 3” at Barcellona from 4 to 7 April 2011. His presentation was about alignment program PASS (Campagna *et al.* Bioinformatics, 2009) developed at CRIBI.
- Grape Research Coordination Network 3rd Annual Conference (June 2 - 5, 2011 – Lake Tahoe, California, USA). His presentation was about grape gene annotation.
- DAIS - Università Ca' Foscari di Venezia, January 31, 2011, seminar title: “*Introduzione alla biologia molecolare*”
- DAIS - Università Ca' Foscari di Venezia, February 2, 2011, seminar title: “*Introduzione alla biologia molecolare*”
- DAIS - Università Ca' Foscari di Venezia, March 30, 2011, seminar title: “*Sequenziamento di DNA mediante tecnologie di nuova generazione*”
- 2015** Workshop EPIGEN: Statistical Analysis of NGS Data. September 9-11, 2015 – Padua. He coordinated the third day workshop about genome re-sequencing and variant prioritization methods

6. Informatics Skills

- Excellent knowledge of Linux, Mac OS X and Windows operative systems.
- Excellent knowledge of Linux bash, Perl, Python, PHP
- Excellent knowledge of MySQL database management system
- Good knowledge of R statistical framework

7. Editorial and Reviewing Activity

- He is member of the Editorial board of ISRN Bioinformatics (<http://www.isrn.com/journals/bioinformatics/>)
- He acts as a referee for several scientific journals such as Bioinformatics, BMC Bioinformatics, BMC Genomics, PlosONE, Nucleic Acid Research.

8. Oral Presentation in Conferences

- 2002** Development of new bioinformatic tools for finishing and annotating bacterial genomes: application to the genomic sequence of *P. profundum*: a barophile/ psychrophile bacterium. BITS Pontignano (Siena) March 15-16 2002.
- 2006** A Global Gene Evolution Analysis on Vibrionaceae Family Using Phylogenetic Profile. BITS Bologna, April 28-29 2006.
- 2012** The First Sequencing Survey of Wheat Chromosome 5A Through NGS and Identification of Genes Controlling Useful Agronomic Traits. 19th EUCARPIA General Congress, , Budapest, Hungary 21-24 May 2012

9. Funded Research Projects

- 2016** “Journey to the cold and back : comparative genomics and transcriptomics in Antarctic and sub-Antarctic notothenioids” Programma Nazionale di Ricerca in Antartide. Bando PNRA 5 aprile 2016, n. 651. PNRA16_00226 – A1
- 2017** “Biocontrollo delle patologie della vite: strumenti e approcci bioinformatici innovativi per l’analisi della comunità microbica dell’uva (metagenomica) mediante l’utilizzo tecnologie di sequenziamento di nuova generazione (NiuGen)”, Regione Veneto, cod 1695-4- 2216-2016, assegni FSE.

10. Main Research Activity

Dr. Nicola Vitulo is a research assistant at the University of Verona, Department of Biotechnology. He works as computational biologist since 2002. During these years he had acquired a great expertise in the bioinformatics field developing skills in gene prediction and annotation, gene expression analysis, comparative genomics and data management.

The advent of the new sequencing technology (Next Generation Sequencing, NGS), capable of producing million of DNA sequences in a single run at a relative low cost, had a great impact on the ability to study genome complexity at genomic, transcriptomic and epigenetic level and provided interesting opportunities for the development of new bioinformatic resources for data analyses and management.

Dott. Vitulo had worked for many years in the genomic area developing a strong interest for many aspects of this field, especially focusing on the innovations and challenges introduced by the NGS technologies.

The main interests and research area are summarized below.

10.1. Sequence alignments

One of the typical tasks in a genomic project is the alignment of the sequenced reads on the reference genome. However, due to the huge amount of data that are produced by the next generation sequencer, fast and accurate software are needed. He contributes to the development of an alignment tool called PASS [12], able to fast align

on a reference genome the sequences codified both in a format called “colour space” (produced by SOLiD sequencer) and “base space”, that is the normal format produced by all the other sequencers. He also contributes to the development of an upgrade of the software (PASS-BIS) [18] for the alignment and management of reads produced by bisulphite experiments. Moreover in 2013 he was part of the RGASP consortium for the evaluation of the spliced alignment software [21].

10.2. Genome sequencing and gene prediction

He was involved in several important national and international genome sequencing projects as grapevine [9;24] tomato [17], wheat [16], the microalgae *N. gaditana* [20] (an important model organism for bio-fuel production) and the extremophile bacterium *Photobacterium profundum* SS9 (a model organism for adaptation at low temperature and high hydrostatic pressure). He contributed to these projects working on several different aspects spanning from the genome assembly to the gene prediction and annotation. In particular, gene prediction represents one of the most complex and important aspects of a genomic project as the identification of the coding genes allow a better understanding of the evolution and the biology of an organism. He supervised and worked on the construction of a bioinformatics platform for gene prediction and annotation that integrates the state-of-the-art methods for the identification of coding and non-coding sequences.

Briefly, the pipeline integrates several type of evidence: 1) ESTs and protein alignment on the reference genome, 2) RNA-seq transcript reconstruction both *denovo* and “genome guided” 3) *denovo* gene predictors trained with the dataset retrieved from the previous steps, 4) whole genome alignments. The final gene model derives from a weighted integration of all these evidence and includes also the alternative splicing isoforms. The platform performs also the gene functional annotation, integrating popular tools such as InterProScan.

The platform includes functionalities to predict non-coding RNAs as for example the long non-coding RNAs (lncRNA). A recent work based on this platform has been published here [24].

10.3. Transcriptomic and gene expression analysis

The transcriptome is the complete catalogue of the transcripts that are expressed in a cell in a specific moment. High-throughput technologies allow the quantification of each transcript in a cell or tissue at a very high resolution. The quantification and the comparison of the expression levels of these transcripts across different conditions is essential to interpret the functional elements of the genome, to understand organism development or disease molecular mechanisms, and to understand how organisms respond to environmental changes as for example under biotic or abiotic stresses.

He was involved in several transcriptome projects on a wide range of organisms that go from plants to animals [27,26,24,23,22,20,19,15,14,10] and he contributed to both the development of bioinformatic pipelines for data analysis and to the results interpretation. In particular, he developed a bioinformatic platform for the analysis of RNA-seq data. Briefly, the platform performs several steps: 1) reads alignment on the reference genome, 2) transcript quantification, 3) identification of the differentially expressed genes, 4) gene ontology and pathway gene enrichment analysis for data interpretation. Currently he is using the platform and providing a bioinformatics support to several RNA-seq projects in collaboration with other groups. Among the other, he is involved in projects concerning 1) human muscle differentiation, 2) presinilin knock-out mice to study Alzheimer disease, 3) ck2b knock-out mice to study immune system development 4) lizard tail regeneration 5) the algae *N. gaditana* to study the response to different light conditions.

Moreover he developed also a platform for the analysis of microRNA expression (miRNA-seq). miRNAs are small non coding transcripts that play a very important role in regulating gene expression. Currently he is involved in a project to study miRNA regulation during glucocorticoid treatment in children with inflammatory bowel disease.

10.4. Comparative genomic and evolution

- He developed a method to study bacterial genome evolution based on a modified version of the phylogenetic profile based on the idea that proteins involved in the same metabolic pathway or structural complex tend to evolve together. He applied this method to study the *Vibrionaceae* family evolution [7].
- He was involved in a project to produce a robust phylogenetic framework to accurately reconstruct evolution at the genome level. This method was applied to infer and study the relationships among the acanthomorph teleost model fishes [13].

- He performed a phylogenetic analysis to study the evolution of the cell cycle-associated Mob domain-containing proteins in eukaryotes [8].
- Within the genome sequencing project of the wheat chromosome 5A, he was involved in the analysis of the gene content in order to identify and reconstruct a virtual gene order (genome zipper) of the wheat genes based on the syntenic region in *Brachypodium*, sorghum and oryza [16].

10.5. Alternative splicing in plants

He worked on a new version of Grape gene prediction, extending it to include alternative spliced isoforms [24]. The analysis was based on 124 RNAseq SOLiD libraries from leaf, root and berry, from different grape genotypes under different physiological and stress conditions. He described for the first time the alternative splicing in grapevine and studied the correlation of alternative splicing with tissues as well as genotypes. Moreover he studied the expression of splicing factor genes and identified differences between genotypes that can be relevant in the response to selective pressure.

10.6. Genome and exome resequencing

Re-sequencing is used to determine the genomic variations of a sample in relation to a common reference sequence. The generated sequences are aligned to the reference genome and searched for SNPs and CNVs as well as genomic rearrangements and indels. He acquired expertise and skills in tools for variant calling, variants annotation and data mining and interpretation. In particular within the strategic project “Bioinfogen” funded by University of Padova, he is currently involved in the development of a web platform for variant prioritization called Queryor. A preliminary version of the platform is available at <http://queryor.cribi.unipd.it/cgi-bin/queryor/login.pl>. Moreover he is involved in several projects in collaboration with Istituto Nazionale dei Tumori di Milano, Fondazione IRCCS for the analysis of exome sequencing data to study genome variability in patients affected by ovary and thyroid cancer.

11. Scientific Activity Parameters

Parameters	
Number of publications	41
Total number of citations	3618
H-index contemporary	16

* Parameters from *Scopus* (last update 21/06/2017).

12. Publications

1. Vitulo N, Dalla Valle L, Skobo T, Valle G, Alibardi L. Transcriptome analysis of the regenerating tail vs. the scarring limb in lizard reveals pathways leading to successful vs. unsuccessful organ regeneration in amniotes. *Developmental Dynamics*. 2017;246: 116–134. doi:10.1002/dvdy.24474
2. Vitulo N, Dalla Valle L, Skobo T, Valle G, Alibardi L. Downregulation of lizard immuno-genes in the regenerating tail and myogenes in the scarring limb suggests that tail regeneration occurs in an immuno-privileged organ. *Protoplasma*. 2017; 1–15. doi:10.1007/s00709-017-1107-y
3. Vannozzi A, Donnini S, Vigani G, Corso M, Valle G, Vitulo N, et al. Transcriptional characterization of a widely-used grapevine rootstock genotype under different iron-limited conditions. *Frontiers in Plant Science*. 2017;7. doi:10.3389/fpls.2016.01994
4. Pagliarani C, Vitali M, Ferrero M, Vitulo N, Incarbone M, Lovisolò C, et al. The accumulation of miRNAs differentially modulated by drought stress is affected by grafting in grapevine. *Plant Physiology*. 2017;173: 2180–2195. doi:10.1104/pp.16.01119

5. Boscari E, Vitulo N, Ludwig A, Caruso C, Mugue NS, Suci R, et al. Fast genetic identification of the Beluga sturgeon and its sought-after caviar to stem illegal trade. *Food Control*. 2017;75: 145–152. doi:10.1016/j.foodcont.2016.11.039
6. Bertoldi L, Forcato C, Vitulo N, Birolo G, De Pascale F, Feltrin E, et al. QueryOR: A comprehensive web platform for genetic variant analysis and prioritization. *BMC Bioinformatics*. 2017;18. doi:10.1186/s12859-017-1654-4
7. Rosselli R, Romoli O, Vitulo N, Vezzi A, Campanaro S, De Pascale F, et al. Direct 16S rRNA-seq from bacterial communities: A PCR-independent approach to simultaneously assess microbial diversity and functional activity potential of each taxon. *Scientific Reports*. 2016;6. doi:10.1038/srep32165
8. Corso M, Vannozzi A, Ziliotto F, Zouine M, Maza E, Nicolato T, et al. Grapevine rootstocks differentially affect the rate of ripening and modulate auxin-related genes in cabernet sauvignon berries. *Frontiers in Plant Science*. 2016;7. doi:10.3389/fpls.2016.00069
9. Corso M, Vannozzi A, Maza E, Vitulo N, Meggio F, Bouzayen M, et al. Transcriptome pathways in leaf and root of grapevine genotypes with contrasting drought tolerance. *Acta Horticulturae*. 2016;1136: 161–168. doi:10.17660/ActaHortic.2016.1136.22
10. Campagna D, Gasparini F, Franchi N, Vitulo N, Ballin F, Manni L, et al. Transcriptome dynamics in the asexual cycle of the chordate *Botryllus schlosseri*. *BMC Genomics*. 2016;17. doi:10.1186/s12864-016-2598-1
11. Alboresi A, Perin G, Vitulo N, Diretto G, Block M, Jouhet J, et al. Light remodels lipid biosynthesis in *Nannochloropsis gaditana* by modulating carbon partitioning between organelles. *Plant Physiology*. 2016;171: 2468–2482. doi:10.1104/pp.16.00599
12. Jasnic-Savovic J, Nestorovic A, Savic S, Karasek S, Vitulo N, Valle G, et al. Profiling of skeletal muscle Ankrd2 protein in human cardiac tissue and neonatal rat cardiomyocytes. *Histochemistry and Cell Biology*. 2015;143: 583–597. doi:10.1007/s00418-015-1307-5
13. Corso M, Vannozzi A, Maza E, Vitulo N, Meggio F, Pitacco A, et al. Comprehensive transcript profiling of two grapevine rootstock genotypes contrasting in drought susceptibility links the phenylpropanoid pathway to enhanced tolerance. *Journal of Experimental Botany*. 2015;66: 5739–5752. doi:10.1093/jxb/erv274
14. Campagna D, Gasparini F, Franchi N, Manni L, Telatin A, Vitulo N, et al. SATRAP: SOLiD assembler translation program. *PLoS ONE*. 2015;10. doi:10.1371/journal.pone.0137436
15. Barabaschi D, Magni F, Volante A, Gadaleta A, Simkova H, Scalabrin S, et al. Physical mapping of bread wheat chromosome 5a: An integrated approach. *Plant Genome*. 2015;8. doi:10.3835/plantgenome2015.03.0011
16. Vitulo N, Forcato C, Carpinelli EC, Telatin A, Campagna D, D'Angelo M, et al. A deep survey of alternative splicing in grape reveals changes in the splicing machinery related to tissue, stress condition and genotype. *BMC Plant Biology*. 2014;14. doi:10.1186/1471-2229-14-99
17. Martinelli VC, Kyle WB, Kojic S, Vitulo N, Li Z, Belgrano A, et al. ZASP interacts with the mechanosensing protein Ankrd2 and p53 in the signalling network of striated muscle. *PLoS ONE*. 2014;9. doi:10.1371/journal.pone.0092259
18. Lauro FM, Eloë-Fadrosch EA, Richter TKS, Vitulo N, Ferriera S, Johnson JH, et al. Ecotype diversity and conversion in *Photobacterium profundum* strains. *PLoS ONE*. 2014;9. doi:10.1371/journal.pone.0096953
19. Corteggiani Carpinelli E, Telatin A, Vitulo N, Forcato C, D'Angelo M, Schiavon R, et al. Chromosome scale genome assembly and transcriptome profiling of *nannochloropsis gaditana* in nitrogen depletion. *Molecular Plant*. 2014;7: 323–335. doi:10.1093/mp/sst120
20. Pellizzari C, Krasnov A, Afanasyev S, Vitulo N, Franch R, Pegolo S, et al. High mortality of juvenile gilthead sea bream (*Sparus aurata*) from photobacteriosis is associated with alternative macrophage activation and anti-inflammatory response: Results of gene expression profiling of early responses in the head kidney. *Fish and Shellfish Immunology*. 2013;34: 1269–1278. doi:10.1016/j.fsi.2013.02.007

21. Engström PG, Steijger T, Sipos B, Grant GR, Kahles A, Räscht G, et al. Systematic evaluation of spliced alignment programs for RNA-seq data. *Nature Methods*. 2013;10: 1185–1191. doi:10.1038/nmeth.2722
22. Capomaccio S, Vitulo N, Verini-Supplizi A, Barcaccia G, Albiero A, D'Angelo M, et al. RNA sequencing of the exercise transcriptome in equine athletes. *PLoS ONE*. 2013;8. doi:10.1371/journal.pone.0083504
23. Campagna D, Telatin A, Forcato C, Vitulo N, Valle G. PASS-bis: A bisulfite aligner suitable for whole methylome analysis of Illumina and SOLiD reads. *Bioinformatics*. 2013;29: 268–270. doi:10.1093/bioinformatics/bts675
24. Sato S, Tabata S, Hirakawa H, Asamizu E, Shirasawa K, Isobe S, et al. The tomato genome sequence provides insights into fleshy fruit evolution. *Nature*. 2012;485: 635–641. doi:10.1038/nature11119
25. Vitulo N, Albiero A, Forcato C, Campagna D, Dal Pero F, Bagnaresi P, et al. First survey of the wheat chromosome 5A composition through a next generation sequencing approach. *PLoS ONE*. 2011;6. doi:10.1371/journal.pone.0026421
26. Negrisolo E, Kuhl H, Forcato C, Vitulo N, Reinhardt R, Patarnello T, et al. Different phylogenomic approaches to resolve the evolutionary relationships among model fish species. *Molecular Biology and Evolution*. 2010;27: 2757–2774. doi:10.1093/molbev/msq165
27. Ferrareso S, Milan M, Pellizzari C, Vitulo N, Reinhardt R, Canario AVM, et al. Development of an oligo DNA microarray for the European sea bass and its application to expression profiling of jaw deformity. *BMC Genomics*. 2010;11. doi:10.1186/1471-2164-11-354
28. Capomaccio S, Verini-Supplizi A, Galla G, Vitulo N, Barcaccia G, Felicetti M, et al. Transcription of LINE-derived sequences in exercise-induced stress in horses. *Animal Genetics*. 2010;41: 23–27. doi:10.1111/j.1365-2052.2010.02094.x
29. Campagna D, Albiero A, Bilardi A, Caniato E, Forcato C, Manavski S, et al. PASS: A program to align short sequences. *Bioinformatics*. 2009;25: 967–968. doi:10.1093/bioinformatics/btp087
30. Lauro FM, Tran K, Vezzi A, Vitulo N, Valle G, Bartlett DH. Large-scale transposon mutagenesis of *Photobacterium profundum* SS9 reveals new genetic loci important for growth at low temperature and high pressure. *Journal of Bacteriology*. 2008;190: 1699–1709. doi:10.1128/JB.01176-07
31. Ferrareso S, Vitulo N, Mininni AN, Romualdi C, Cardazzo B, Negrisolo E, et al. Development and validation of a gene expression oligo microarray for the gilthead sea bream (*Sparus aurata*). *BMC Genomics*. 2008;9. doi:10.1186/1471-2164-9-580
32. Vitulo N, Vezzi A, Romualdi C, Campanaro S, Valle G. A global gene evolution analysis on Vibrionaceae family using phylogenetic profile. *BMC Bioinformatics*. 2007;8. doi:10.1186/1471-2105-8-S1-S23
33. Vitulo N, Vezzi A, Galla G, Citterio S, Marino G, Ruperti B, et al. Characterization and evolution of the cell cycle-associated mob domain-containing proteins in eukaryotes. *Evolutionary Bioinformatics*. 2007;3: 121–158.
34. Jaillon O, Aury J-M, Noel B, Policriti A, Clepet C, Casagrande A, et al. The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. *Nature*. 2007;449: 463–467. doi:10.1038/nature06148
35. Simonato F, Campanaro S, Lauro FM, Vezzi A, D'Angelo M, Vitulo N, et al. Piezophilic adaptation: a genomic point of view. *Journal of Biotechnology*. 2006;126: 11–25. doi:10.1016/j.jbiotec.2006.03.038
36. Vezzi A, Campanaro S, D'Angelo M, Simonato F, Vitulo N, Lauro FM, et al. Life at depth: *Photobacterium profundum* genome sequence and expression analysis. *Science*. 2005;307: 1459–1461. doi:10.1126/science.1103341
37. Romualdi C, Vitulo N, Del Favero M, Lanfranchi G. MIDAW: A web tool for statistical analysis of microarray data. *Nucleic Acids Research*. 2005;33: W644–W649. doi:10.1093/nar/gki497

38. De Pittà C, Tombolan L, Dell'Orto MC, Accordi B, Kronnie GT, Romualdi C, et al. A leukemia-enriched cDNA microarray platform identifies new transcripts with relevance to the biology of pediatric acute lymphoblastic leukemia. *Haematologica*. 2005;90: 890–898.
39. Campanaro S, Vezzi A, Vitulo N, Lauro FM, D'Angelo M, Simonato F, et al. Laterally transferred elements and high pressure adaptation in *Photobacterium profundum* strains. *BMC genomics*. 2005;6.
40. Campanaro S, Vezzi A, Vitulo N, Lauro FM, D'Angelo M, Simonato F, et al. Laterally transferred elements and high pressure adaptation in *Photobacterium profundum* strains. *BMC Genomics*. 2005;6. doi:10.1186/1471-2164-6-122
41. Campagna D, Romualdi C, Vitulo N, Del Favero M, Lexa M, Cannata N, et al. RAP: A new computer program for de novo identification of repeated sequences in whole genomes. *Bioinformatics*. 2005;21: 582–588. doi:10.1093/bioinformatics/bti039

13. Book chapters

1. Valle G., **Vitulo N.**, Vannozzi A., Telatin A., Lucchin M. (2014). Il genoma dei portainnesti: similarità e differenze con *Vitis vinifera*. In: Progetto AGER-SERRES : strategie innovative per la selezione di nuovi portainnesti di vite, Edition: First Edition December 2014, Publisher: Edizioni l'informatore agrario, Editors: Attilio Scienza, Osvaldo Failla, Luca Espen, pp.75-85

Verona, 21/06/2017

NICOLA VITULO

