

Curriculum Vitae

Nicola Vitulo

1.	Personal Information.....	2
2.	Education	2
3.	Positions.....	2
4.	Teaching experience	3
5.	Foreign Experience Activity.....	3
6.	Advance teaching and workshop	3
7.	Supervision.....	4
8.	Editorial and Reviewing Activity	4
9.	Membership	4
10.	Funded Research Projects.....	5
11.	Contract research agreement and convention with research institutes.....	5
12.	Patents	5
13.	Main Research Activity	5
14.	Scientific Activity Parameters.....	6
15.	Selected Publications.....	6
16.	Full List Publications.....	7
17.	Book chapters.....	14

1. Personal Information

Name and Surname: Nicola Vitulo
Date of birth: 23 September 1976
Citizenship: Italian
Office address: Department of Biotechnology,
Università di Verona,
Strada Le Grazie 15,
37134 Verona (VR)
Phone: 045-8027892
E-mail: nicola.vitulo@univr.it

2. Education

- **21 March 2001 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 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 gets the PhD in Biotechnology.

3. Positions

Current position

- **21/12/2018-today:** Associate Professor at University of Verona, Department of Biotechnology.

Past positions

- **21/12/2015-20/01/2018:** Researcher (fixed-term researcher, type b) at University of Verona, Department of Biotechnology.
- **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”
- **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”.
- **01/04/2010-31/03/2012:** 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”
- **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”

- **01/05/2007-29/02/2008:** 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”
- **01/03/2006-30/04/2007:** 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”
- **01/01/2005-28/02/2006** he was a research grant holder at University of Padova, in the research laboratory of Prof. G. Valle.
- **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.

4. Teaching experience

- **2005-2008** “*Bioinformatics III*” MS in Molecular Biology, University of Padova.
- **2005** “*Bioinformatics*”, MS in Agro-Industrial Biotechnologies, University of Verona.
- **2009** “*Bioinformatics*” for FSE Regione Veneto n. 2120/1/4/1017/2008 Projects, “*Tecnologie per la società dell'informazione*”, University Ca' Foscari Venezia.
- **2010-2016** “*Computational Biostatistics and Bioinformatics*”, MS in Statistics, University of Padova.
- **2016-2024** “*Computational Genomics*” MS in Molecular and medical biotechnology, University of Verona.
- **2017-2024** “*Bioinformatics and biological databases*”, BS in Biotechnology, University of Verona
- **2020-2024** “*Bioinformatics*”, MS in Biotechnology for bioresources and sustainable development, University of Verona

5. 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.

6. Advance teaching and workshop

- 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: “*Introduction to molecular biology*”

DAIS - Università Ca' Foscari di Venezia, February 2, 2011, seminar title: “*Introduction to molecular biology*”

DAIS - Università Ca' Foscari di Venezia, March 30, 2011, seminar title: “*DNA sequencing using next generation technologies.*”

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

2018 Member of the organizing committee for the winter school in “*Applied Bioinformatics*”, Scuola di Dottorato in Scienze Naturali ed Ingegneristiche – PhD in Biotechnology, University of Verona, held in Canazei (TN) January 21-25, 2018.

2019 Member of the of organizing committee for the winter school in “*Understanding human genome variations and their influences on human traits. Bioinformatics insight*”, PhD School in Life and Health Sciences, held in Canazei (TN) January 13-18, 2019.

2019 “A micro Workshop on NGS Data Analysis”, title: Metabarcoding analysis: from raw reads to data interpretation, Quadram Institute, Norwich.

2022-today “*Master in Omics Data Analysis*”, topic: bioinformatics and metabarcoding analysis, University of Padova.

2024 PhD seminar at Department of Agricultural, Food, and Environmental Sciences, University of Perugia. Title: “Bioinformatics in Metagenomics: from raw reads to data interpretation”

MiCropBiomes COST Action on “Dissecting the Role of Phytobiota in Plant Health” took Verona, Italy. Title: “Bioinformatics in Metagenomics: from raw reads to data interpretation”

7. Supervision

- PhD supervisor of three students.
- PhD co-supervisor of three students.
- Thesis Supervisor of more than 10 students.

8. Editorial and Reviewing Activity

- He is member of the Editorial board of ISRN Bioinformatics since 2022 (<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.

9. Membership

- Bioinformatics Italian Society (BITS).

10. 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.
- 2024** “Mining the biodiversity of non conventional yeasts as bioresources for innovative fermented beverages through a genomics and bioinformatics approach - NCYdiversity” PRIN: PROGETTI DI RICERCA DI RILEVANTE INTERESSE NAZIONALE – Bando 2022 PNRR, funded by European Union and Italian Ministry of University and Research.

11. Contract research agreement and convention with research institutes.

- 2018** Contract signed with the company Illycaffè S.p.A, title project “Genome sequencing and functional genomics of Coffea arabica genome”.
- 2018** Contract signed with the company Luigi Lavazza S.p.A, title project “Genome sequencing and functional genomics of Coffea arabica genome”.
- 2018** Contract signed with Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia’s National Science Agency, title project “RNA-seq transcriptomic analysis of grape”
- 2020** Contract signed with Probiotical S.p.A., Italy, title project “Statistical analyses applied to clinical trials for evaluating the efficacy of probiotic treatment.”
- 2021** Contract signed with Probiotical S.p.A., Italy, title project “Statistical analyses applied to clinical trials for evaluating the efficacy of probiotic treatment.”
- 2021** Collaboration agreement with Associazione Istituto di Genomica Applicata (IGA), Italy, title project “Assembly and annotation of the genome of Coffea arabica, Bourbon variety.”
- 2021** Collaboration agreement with the Department of Surgical, Oncological, and Gastroenterological Sciences at the University of Padua, title project “Analysis of gut microbiota changes induced by the intake of micro-encapsulated sodium butyrate in patients with chronic inflammatory bowel diseases.”
- 2023** Contract signed with Probiotical S.p.A., Italy, title project “Statistical analyses applied to clinical trials for evaluating the efficacy of probiotic treatment.”

12. Patents

- 2022** Co-inventor of the patent 'COMPOSITION IN MICRO-ENCAPSULATED FORM, BASED ON N-BUTYRIC ACID OR DERIVATIVES THEREOF, FOR TREATING CROHN'S DISEASE OR ULCERATIVE RECTAL COLITIS,' United States Patent, No. US 2022/0160665 A1.

This invention relates to a new therapeutic use of a composition based on n-butyric acid or its derivatives in microencapsulated form. The microencapsulated composition based on sodium butyrate used in the study is commercially available under the trade name Butyrose, produced by the same applicant of the present patent (SILAS.R.L.)

13. Main Research Activity

Dr. Nicola Vitulo is a associated professor 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. Prof. 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. His research interest includes the development of bioinformatics tools and the analysis of metagenomics and virome data from different ecological niches and the study of the correlation between the human gut microbiome and human health.

14. Scientific Activity Parameters

Parameters	
Number of publications	87
Total number of citations	9260
H-index contemporary	33

* Parameters from *Scopus* (last update 11/02/2025).

15. Selected Publications

1. Di Cesare F, Calgaro M, Ghini V, Squarzanti DF, De Prisco A, Visciglia A, et al. Exploring the Effects of Probiotic Treatment on Urinary and Serum Metabolic Profiles in Healthy Individuals. *JOURNAL OF PROTEOME RESEARCH*. 2023;22(12):3866–78.
2. Calgaro M, Romualdi C, Risso D, Vitulo N. benchdamic: benchmarking of differential abundance methods for microbiome data. *BIOINFORMATICS*. 2023;(1):1–3.
3. Pandolfo M, Telatin A, Lazzari G, Adriaenssens EM, Vitulo N. MetaPhage: an Automated Pipeline for Analyzing, Annotating, and Classifying Bacteriophages in Metagenomics Sequencing Data. *MSYSTEMS*. 2022;(5):1–13.
4. Guidetti C, Salvini E, Viri M, Deidda F, Amoruso A, Visciglia A, et al. Randomized Double-Blind Crossover Study for Evaluating a Probiotic Mixture on Gastrointestinal and Behavioral Symptoms of Autistic Children. *JOURNAL OF CLINICAL MEDICINE*. 2022;11(18):1–17.
5. Facchin S, Calgaro M, Pandolfo M, Caldart F, Ghisa M, Greco E, et al. Salivary microbiota composition may discriminate between patients with eosinophilic oesophagitis (EoE) and non-EoE subjects. *ALIMENTARY PHARMACOLOGY & THERAPEUTICS*. 2022;(3):1–13.
6. A Haas E, A Saad MJ, Santos A, Vitulo N, F Lemos Junior WJ, A Martins AM, et al. A red wine intervention does not modify plasma trimethylamine N-oxide but is associated with broad shifts in the plasma metabolome and gut microbiota composition. *THE AMERICAN JOURNAL OF CLINICAL NUTRITION*. 2022;(9):1–15.
7. Solito A, Bozzi Cionci N, Calgaro M, Caputo M, Vannini L, Hasballa I, et al. Supplementation with *Bifidobacterium breve* BR03 and B632 strains improved insulin sensitivity in children and adolescents with obesity in a cross-over, randomized double-blind placebo-controlled trial. *CLINICAL NUTRITION*. 2021;40(7):4585–94.

8. Calgaro M, Pandolfo M, Salvetti E, Marotta A, Larini I, Pane M, et al. Metabarcoding analysis of gut microbiota of healthy individuals reveals impact of probiotic and maltodextrin consumption. *BENEFICIAL MICROBES*. 2021;12(2):121–36.
9. Bordugo A, Salvetti E, Rodella G, Piazza M, Dianin A, Amoroso A, et al. Assessing Gut Microbiota in an Infant with Congenital Propionic Acidemia before and after Probiotic Supplementation. *MICROORGANISMS*. 2021;9(12):1–18.
10. Facchin S, Vitulo N, Calgaro M, Buda A, Romualdi C, Pohl D, et al. Microbiota changes induced by microencapsulated sodium butyrate in patients with inflammatory bowel disease. *NEUROGASTROENTEROLOGY AND MOTILITY*. 2020;(10):1–10.
11. Calgaro M, Romualdi C, Waldron L, Risso D, Vitulo N. Assessment of statistical methods from single cell, bulk RNA-seq, and metagenomics applied to microbiome data. *GENOME BIOLOGY*. 2020;21(1):191–221.
12. Magro DO, Santos A, Guadagnini D, de Godoy FM, Silva SHM, Lemos WJF, et al. Remission in Crohn's disease is accompanied by alterations in the gut microbiota and mucins production. *SCIENTIFIC REPORTS*. 2019;9(1):1–10.

16. Full List Publications

1. Scalabrin S, Magris G, Liva M, Vitulo N, Vidotto M, Scaglione D, et al. A chromosome-scale assembly reveals chromosomal aberrations and exchanges generating genetic diversity in *Coffea arabica* germplasm. *NATURE COMMUNICATIONS*. 2024;15(1):1–15.
2. Boscarì E, Pallo SD, Vitulo N, Scapolatiello A, Schiavon L, Cariani A, et al. MIPs: multi-locus intron polymorphisms in species identification and population genomics. *SCIENTIFIC REPORTS*. 2024;14(1):1–14.
3. Bombardi L, Salini A, Aulitto M, Zuliani L, Andreolli M, Bordoli P, et al. Lignocellulolytic Potential of Microbial Consortia Isolated from a Local Biogas Plant: The Case of Thermostable Xylanases Secreted by Mesophilic Bacteria. *INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES*. 2024;25(2):1–28.
4. Velt A, Frommer B, Blanc S, Holtgräwe D, Duchêne É, Dumas V, et al. An improved reference of the grapevine genome reasserts the origin of the PN40024 highly homozygous genotype. *G3*. 2023;13(5):1–14.
5. Quotti Tubi L, Canovas Nunes S, Mandato E, Pizzi M, Vitulo N, D'Agnolo M, et al. CK2 β Regulates Hematopoietic Stem Cell Biology and Erythropoiesis. *HEMASPHERE*. 2023;7(12):1–19.
6. Molesini B, Pennisi F, Vitulo N, Pandolfini T. MicroRNAs associated with AGL6 and IAA9 function in tomato fruit set. *BMC RESEARCH NOTES*. 2023;16(242):1–6.
7. Di Cesare F, Calgaro M, Ghini V, Squarzanti DF, De Prisco A, Visciglia A, et al. Exploring the Effects of Probiotic Treatment on Urinary and Serum Metabolic Profiles in Healthy Individuals. *JOURNAL OF PROTEOME RESEARCH*. 2023;22(12):3866–78.

8. Calgaro M, Romualdi C, Risso D, Vitulo N. benchdamic: benchmarking of differential abundance methods for microbiome data. *BIOINFORMATICS*. 2023;(1):1–3.
9. Quotti Tubi L, Mandato E, Canovas Nunes S, Arjomand A, Zaffino F, Manni S, et al. CK2 β -regulated signaling controls B cell differentiation and function. *FRONTIERS IN IMMUNOLOGY*. 2022;13:1–25.
10. Pandolfo M, Telatin A, Lazzari G, Adriaenssens EM, Vitulo N. MetaPhage: an Automated Pipeline for Analyzing, Annotating, and Classifying Bacteriophages in Metagenomics Sequencing Data. *MSYSTEMS*. 2022;(5):1–13.
11. Molesini B, Pennisi F, Cressoni C, Vitulo N, Dusi V, Speghini A, et al. Nanovector-mediated exogenous delivery of dsRNA induces silencing of target genes in very young tomato flower buds. *NANOSCALE ADVANCES*. 2022;4(21):4542–53.
12. Guidetti C, Salvini E, Viri M, Deidda F, Amoruso A, Visciglia A, et al. Randomized Double-Blind Crossover Study for Evaluating a Probiotic Mixture on Gastrointestinal and Behavioral Symptoms of Autistic Children. *JOURNAL OF CLINICAL MEDICINE*. 2022;11(18):1–17.
13. Facchin S, Calgaro M, Pandolfo M, Caldart F, Ghisa M, Greco E, et al. Salivary microbiota composition may discriminate between patients with eosinophilic oesophagitis (EoE) and non-EoE subjects. *ALIMENTARY PHARMACOLOGY & THERAPEUTICS*. 2022;(3):1–13.
14. Facchin S, Calgaro M, Pandolfo M, Caldart F, Ghisa M, Vitulo N, et al. Editorial: non-invasive testing for EoE —does microbiome testing hold the key? Authors’ reply. *ALIMENTARY PHARMACOLOGY & THERAPEUTICS*. 2022;56(4):729–30.
15. A Haas E, A Saad MJ, Santos A, Vitulo N, F Lemos Junior WJ, A Martins AM, et al. A red wine intervention does not modify plasma trimethylamine N-oxide but is associated with broad shifts in the plasma metabolome and gut microbiota composition. *THE AMERICAN JOURNAL OF CLINICAL NUTRITION*. 2022;(9):1–15.
16. Vandelle E, Ariani P, Regaiolo A, Danzi D, Lovato A, Zadra C, et al. The Grapevine E3 Ubiquitin Ligase VriATL156 Confers Resistance against the Downy Mildew Pathogen *Plasmopara viticola*. *INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES*. 2021;22(2):940–58.
17. Solito A, Bozzi Cionci N, Calgaro M, Caputo M, Vannini L, Hasballa I, et al. Supplementation with *Bifidobacterium breve* BR03 and B632 strains improved insulin sensitivity in children and adolescents with obesity in a cross-over, randomized double-blind placebo-controlled trial. *CLINICAL NUTRITION*. 2021;40(7):4585–94.
18. Guardini Z, Dall’Osto L, Barera S, Jaberri M, Cazzaniga S, Vitulo N, et al. High Carotenoid Mutants of *Chlorella vulgaris* Show Enhanced Biomass Yield under High Irradiance. *PLANTS*. 2021;10(5):1–25.
19. Giovannoni M, Larini I, Scafati V, Scortica A, Compri M, Pontiggia D, et al. A novel *Penicillium sumatraense* isolate reveals an arsenal of degrading enzymes exploitable in algal bio-refinery processes. *BIOTECHNOLOGY FOR BIOFUELS*. 2021;14(1):1–20.

20. Fattore N, Bellan A, Pedroletti L, Vitulo N, Morosinotto T. Acclimation of photosynthesis and lipids biosynthesis to prolonged nitrogen and phosphorus limitation in *Nannochloropsis gaditana*. *ALGAL RESEARCH*. 2021;58:1–11.
21. Fasani E, DAL CORSO G, Zorzi G, Vitulo N, Furini A. Comparative analysis identifies micro-RNA associated with nutrient homeostasis, development and stress response in *Arabidopsis thaliana* upon high Zn and metal hyperaccumulator *Arabidopsis halleri*. *PHYSIOLOGIA PLANTARUM*. 2021;173(3):920–934–934.
22. De Jesus Inacio L, Merlanti R, Lucatello L, Bisutti V, Carraro L, Larini I, et al. Natural contaminants in bee pollen: DNA metabarcoding as a tool to identify floral sources of pyrrolizidine alkaloids and fungal diversity. *FOOD RESEARCH INTERNATIONAL*. 2021;146(110438):1–12.
23. de Almeida OGG, Vitulo N, De Martinis ECP, Felis GE. Pangenome analyses of LuxS-coding genes and enzymatic repertoires in cocoa-related lactic acid bacteria. *GENOMICS*. 2021;113(4):1659–70.
24. D’Inca E, Cazzaniga S, Foresti C, Vitulo N, Bertini E, Galli M, et al. VvNAC33 promotes organ de-greening and represses vegetative growth during the vegetative-to-mature phase transition in grapevine. *NEW PHYTOLOGIST*. 2021;231(2):726–46.
25. Calgaro M, Pandolfo M, Salvetti E, Marotta A, Larini I, Pane M, et al. Metabarcoding analysis of gut microbiota of healthy individuals reveals impact of probiotic and maltodextrin consumption. *BENEFICIAL MICROBES*. 2021;12(2):121–36.
26. Bordugo A, Salvetti E, Rodella G, Piazza M, Dianin A, Amoroso A, et al. Assessing Gut Microbiota in an Infant with Congenital Propionic Acidemia before and after Probiotic Supplementation. *MICROORGANISMS*. 2021;9(12):1–18.
27. Urciuolo A, Serena E, Ghua R, Zatti S, Giomo M, Mattei N, et al. Engineering a 3D in vitro model of human skeletal muscle at the single fiber scale. *PLOS ONE*. 2020;15(5):1–10.
28. Scalabrin S, Toniutti L, Di Gaspero G, Scaglione D, Magris G, Vidotto M, et al. A single polyploidization event at the origin of the tetraploid genome of *Coffea arabica* is responsible for the extremely low genetic variation in wild and cultivated germplasm. *SCIENTIFIC REPORTS*. 2020;10(1):4642–54.
29. Pinosio S, Marroni F, Zuccolo A, Vitulo N, Mariette S, Sonnante G, et al. A draft genome of sweet cherry (*Prunus avium* L.) reveals genome-wide and local effects of domestication. *PLANT JOURNAL*. 2020;(4):1–10.
30. Palumbo F, Vitulo N, Vannozzi A, Magon G, Barcaccia G. The Mitochondrial Genome Assembly of Fennel (*Foeniculum vulgare*) Reveals Two Different *atp6* Gene Sequences in Cytoplasmic Male Sterile Accessions. *INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES*. 2020;21(13):4664–74.
31. Facchin S, Vitulo N, Calgaro M, Buda A, Romualdi C, Pohl D, et al. Microbiota changes induced by microencapsulated sodium butyrate in patients with inflammatory bowel disease. *NEUROGASTROENTEROLOGY AND MOTILITY*. 2020;(10):1–10.

32. Calgaro M, Romualdi C, Waldron L, Risso D, Vitulo N. Assessment of statistical methods from single cell, bulk RNA-seq, and metagenomics applied to microbiome data. *GENOME BIOLOGY*. 2020;21(1):191–221.
33. Balzan S, Carraro L, Merlanti R, Lucatello L, Capolongo F, Fontana F, et al. Microbial metabarcoding highlights different bacterial and fungal populations in honey samples from local beekeepers and market in north-eastern Italy. *INTERNATIONAL JOURNAL OF FOOD MICROBIOLOGY*. 2020;334:108806–13.
34. Vitulo N, Lemos WJF, Calgaro M, Confalone M, Felis G, Zapparoli G, et al. Bark and Grape Microbiome of *Vitis vinifera*: Influence of Geographic Patterns and Agronomic Management on Bacterial Diversity. *FRONTIERS IN MICROBIOLOGY*. 2019;9:3203–14.
35. Magro DO, Santos A, Guadagnini D, de Godoy FM, Silva SHM, Lemos WJF, et al. Remission in Crohn's disease is accompanied by alterations in the gut microbiota and mucins production. *SCIENTIFIC REPORTS*. 2019;9(1):1–10.
36. Lovato A, Pignatti A, Vitulo N, Vandelle E, Polverari A. Inhibition of Virulence-Related Traits in *Pseudomonas syringae* pv. *actinidiae* by Gunpowder Green Tea Extracts. *FRONTIERS IN MICROBIOLOGY*. 2019;10:1–17.
37. Fasoli M, Richter C, Zenoni S, Bertini E, Vitulo N, Dal Santo S, et al. Unraveling the key molecular events of grape berry ripening. In: *Acta Horticulturae*. PO BOX 500, 3001 LEUVEN 1, BELGIUM: INT SOC HORTICULTURAL SCIENCE; 2019. p. 241–8.
38. Bargelloni L, Babbucci M, Ferraresso S, Papetti C, Vitulo N, Carraro R, et al. Draft genome assembly and transcriptome data of the icefish *Chionodraco myersi* reveal the key role of mitochondria for a life without hemoglobin at subzero temperatures. *COMMUNICATIONS BIOLOGY*. 2019;2(1):1–11.
39. Pauletto M, Manousaki T, Ferraresso S, Babbucci M, Tsakogiannis A, Louro B, et al. Genomic analysis of *Sparus aurata* reveals the evolutionary dynamics of sex-biased genes in a sequential hermaphrodite fish. *COMMUNICATIONS BIOLOGY*. 2018;1(1):119–31.
40. Palumbo F, Vannozzi A, Vitulo N, Lucchin M, Barcaccia G. The leaf transcriptome of fennel (*Foeniculum vulgare* Mill.) enables characterization of the t-anethole pathway and the discovery of microsatellites and single-nucleotide variants. *SCIENTIFIC REPORTS*. 2018;8(1):10459–70.
41. Palumbo F, Galla G, Vitulo N, Barcaccia G. First draft genome sequencing of fennel (*Foeniculum vulgare* Mill.): identification of simple sequence repeats and their application in marker-assisted breeding. *MOLECULAR BREEDING*. 2018;38(10):38–49.
42. Nigris S, Baldan E, Tondello A, Zanella F, Vitulo N, Favaro G, et al. Biocontrol traits of *Bacillus licheniformis* GL174, a culturable endophyte of *Vitis vinifera* cv. Glera. *BMC MICROBIOLOGY*. 2018;18(1):133–48.
43. Fasoli M, Richter CL, Zenoni S, Bertini E, Vitulo N, Dal Santo S, et al. Timing and Order of the Molecular Events Marking the Onset of Berry Ripening in Grapevine. *PLANT PHYSIOLOGY*. 2018;178(3):1187–206.

44. De Iudicibus S, Lucafò M, Vitulo N, Martelossi S, Zimbello R, De Pascale F, et al. High-Throughput Sequencing of microRNAs in Glucocorticoid Sensitive Paediatric Inflammatory Bowel Disease Patients. *INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES*. 2018;19(5):1399–409.
45. Cecchin M, Benfatto S, Griggio F, Mori A, Cazzaniga S, Vitulo N, et al. Molecular basis of autotrophic vs mixotrophic growth in *Chlorella sorokiniana*. *SCIENTIFIC REPORTS*. 2018;8(1):1–13.
46. Ambrosino L, Ruggieri V, Bostan H, Miralto M, Vitulo N, Zouine M, et al. Multilevel comparative bioinformatics to investigate evolutionary relationships and specificities in gene annotations: an example for tomato and grapevine. *BMC BIOINFORMATICS*. 2018;19(Suppl 15):435–51.
47. Vitulo N, Dalla Valle L, Skobo T, Valle G, Alibardi L. Transcriptome analysis of the regenerating tail versus the scarring limb in lizard reveals pathways leading to successful versus unsuccessful organ regeneration in amniotes. *DEVELOPMENTAL DYNAMICS*. 2017;(2):1–50.
48. Vitulo N, Dalla Valle L, Skobo T, Valle G, Alibardi L. Downregulation of lizard immunogenes in the regenerating tail and myogenes in the scarring limb suggests that tail regeneration occurs in an immuno-privileged organ. *PROTOPLASMA*. 2017;(6):1–15.
49. 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;7:1994–2010.
50. Santi C, Molesini B, Guzzo F, Pii Y, Vitulo N, Pandolfini T. Genome-Wide Transcriptional Changes and Lipid Profile Modifications Induced by *Medicago truncatula* N5 Overexpression at an Early Stage of the Symbiotic Interaction with *Sinorhizobium meliloti*. *GENES*. 2017;8(12):1–23.
51. Pagliarani C, Vitali M, Ferrero M, Vitulo N, Incarbone M, Lovisolo C, et al. The Accumulation of miRNAs Differentially Modulated by Drought Stress Is Affected by Grafting in Grapevine. *PLANT PHYSIOLOGY*. 2017;173(4):2180–95.
52. 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;75:145–52.
53. 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(1):225–35.
54. 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;6:32165–76.

55. 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(2016):69–82.
56. 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):161–8
57. 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(1):275–91.
58. 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(4):2468–82.
59. 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(6):583–97.
60. 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(19):5739–52.
61. Campagna D, Gasparini F, Franchi N, Manni L, Telatin A, Vitulo N, et al. SATRAP: SOLiD Assembler TRANslation Program. *PLOS ONE*. 2015;10(9):275–91.
62. Barabaschi D, Magni F, Volante A, Gadaleta A, Šimková H, Scalabrin S, et al. Physical Mapping of Bread Wheat Chromosome 5A: An Integrated Approach. *THE PLANT GENOME*. 2015;8(3):1–24.
63. 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(1):1–16.
64. Martinelli VC, Kyle WB, Kojic S, Vitulo N, Zhaohui L, Belgrano A, et al. ZASP interacts with the mechanosensing protein Ankrd2 and p53 in the signalling network of striated muscle. *PLOS ONE*. 2014;9(3):1–18.
65. Lauro FM, Eloie Fadrosch EA, Richter TKS, Vitulo N, Ferriera S, Johnson JH, et al. Ecotype diversity and conversion in *Photobacterium profundum* strains. *PLOS ONE*. 2014;9(5):1–10.
66. 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(2):323–35.

67. 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(5):1269–78.
68. Engström P, Steijger T, Sipos B, Grant G, Kahles A, Alioto T, et al. Systematic evaluation of spliced alignment programs for RNA-seq data. *NATURE METHODS*. 2013;10(12):1185–91.
69. 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(12):1–14.
70. 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(2):268–70.
71. 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(7400):635–41.
72. 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(10):1–13.
73. 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(12):2757–74.
74. Ferraresso 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(1):354–70.
75. 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(2):23–7.
76. Campagna D, Albiero A, Bilardi A, Caniato E, Forcato C, Manavski S, et al. PASS: a program to align short sequences. *BIOINFORMATICS*. 2009;25(7):967–8–968.
77. 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(5):1699–709.

78. Ferraresso 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;9:580–94.
79. 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 Suppl 1(Suppl 1):1–16.
80. 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 ONLINE. 2007;3:121–58.
81. Jaillon O, Aury JM, Noel B, Policriti A, Clepet C, Casagrande A, et al. The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. NATURE. 2007;449(7161):449–55.
82. 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(1):11–25.
83. 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(5714):1459–61.
84. Romualdi C, Vitulo N, Del Favero M, Lanfranchi G. MIDAW: a web tool for statistical analysis of microarray data. NUCLEIC ACIDS RESEARCH. 2005;33(Web Server issue):644–9.
85. De Pittà C, Tombolan L, Campo Dell'Orto M, Accordi B, te Kronnie G, 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(7):890–8.
86. 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(1):122–36.
87. 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(5):582–8.

17. 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, 11/02/2025

Prof. Nicola Vitulo

A handwritten signature in black ink, appearing to read 'Nicola Vitulo', written in a cursive style.