

Background:

I have a background in bioinformatics and plant biology and extensive experience in code development using several programming languages (prior to 2021 - C++, Bash, AWK, R - after 2021: Python, Ruby, Julia, Javascript, GO), data analysis and data science, machine and deep learning and web and application development. Following my PhD, I developed bioinformatics methods for transcriptional and post-transcriptional genomics across nuclear and organelle genomes at Fondazione Edmund Mach (Italy). I analyzed and finished multiple RNA-seq and Organelle-Seq experiments for several plant and fungal species, including *Arundo donax* (an emerging biofuel plant). Additionally, I analyzed multiple metagenomics analysis coming from the fungal and bacterial species involving ITS metagenomics, as well as the bacterial metagenomics.

Additionally, I have done a lot of work in the field of organelle genomics and have published the first Cardamine species' chloroplast genomes. I independently created an international partnership to find and create computational methods for a number of crop species. Following that, I spent two years (2014–2016) as a Research Fellow (Academic Level B) at the University of Technology, Sydney, Australia, where I developed computational methods for understanding seagrasses. Following that, I spent a short time in University of Connecticut, USA, where I analyzed the Douglas fir genome from the genome annotation to the phylogenomics and identifying genes and evolution of importance.

Since August 2017, I have worked as a Postdoctoral researcher at the Finnish Museum of Natural History and the University of Helsinki, conducting research on genome bioinformatics and sequencing the genomes of lower plants, including *Coleochaete orbicularis*, *Blasia pusilla*, *Chaetosporidium orbicularis*, *Polytrichum commune*, *Mallomonas*, and *Cryptomonas* species. My work has been focused on genome assembly, genome annotation, chloroplast genomics, and a variety of other topics. Additionally, I've worked for various other organisations, such as Edinburgh UK, to analyse the genomics data for PAFTOL species and the chloroplast genomes of the Ambrosia clade from Norway.

Since 2019, my research has shifted to examining the genomes of fungi whose species have been sequenced using NextSeq methods. This work is currently concentrated on genome assembly, annotations, marker genes, and phylogenomics of those fungi. I have assembled, annotated, and identified ITS and other phylogenomics markers, as well as performed alignments, phylogenies, and downstream analyses on the fungal genomes of over 500 different species.

The bioinformatics application of high throughput sequencing and methods to comprehend the biological and functional importance of the genes, evolution, and pathways in plants have been the main areas of my research up to this point.

From 2022-2023, I added several new skills as a career advancement and profiling to the new positions, with new developments. I learnt data science, machine and deep learning, several certification on devops and added Python and Ruby. From 2024 onwards, I worked at Universität Potsdam, Germany, where I self-learned Julia, GO, and approaches for machine and deep learning. During the time, I benchmarked PacBioHiFi genome analysis and created a complete HTML, CSS, Javascript enabled web and also coded several approaches, packages, gems in Python, Ruby, Julia, GO.

This makes me a standout candidate for the position as I work from the bioinformatics to machine and deep learning. Additionally, the inclusion of the web and the application development using the python, GO and added skills of devops makes me a versatile and an approachable candidate, who can address not only the questions pertaining to this project but across several other projects. This continuous increase in my abilities and my constant efforts to put results are a proof of itself that I am a person, who is result and goal oriented. I am open to species analysis at the genome level and also to enhance the knowledge gain.

As I worked on these plant, bacterial and fungal species, I created new computational analyses that helped identify the genes involved in abiotic and biotic interactions as well as unique genetic pathways that could help these species' genetic breeding. In addition to developing bioinformatics to clarify functional genomics, My research interests are directly related to the posted position, as well as the ongoing research projects, research activities, and my selection for the aforementioned position.

Why I should be considered:

My wide skill set and extensive experience make me a strong candidate for the offered position, and I can play a variety of role across the selected position. I have expertise motivating individuals with various mindsets to strive toward their objectives and get the desired results. During my time conducting research, I developed the skills I would need as a future scientist, including designing biological hypotheses, analyzing deep sequencing data, and interpreting its biological significance in the context of planned experiments. I offer my application for the advertised post in light of these factors. I offer my application for the advertised post in light of these factors. I consider myself to be someone with a high level of perseverance who is driven and eager to learn everything. My core teaching objective will be to help the students learn to actively think and pursue their independent thinking.

GAURAV SABLOK

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Research Interest: Highly communicative, motivated, task oriented, feature responsive, time oriented, approachable, solution seeker and initiative taker focussed professional person working on Bioinformatics, Deep Learning, DevOps, Graphs. **Bioinformatics:** genomes, transcriptomes, organelle, metagenomes and metatranscriptomes, evolutionary and phylogenome analysis. **Species:** plant, bacterial and fungal. Sequencing platform Illumina, PacBio, Oxford Nanopore. PacbioHifi. **Deep learning:** PyTorch, Tensorflow, CatBoost, XGBoost, Sklearn, Keras and other machine and deep learning. **DevOps:** Git, Docker, Kubernetes and Terraform for container orchestration. **Job Scheduler:** Skilled in both pbs and slurm. Established computing cluster and blades. **Git management:** Github commandline and GitKraken including staggging, rebasing, stashing, committing

SoftSkills: I am very pro-active in making communication and upskilling on emerging trends. Proficient in developing new approaches for better integration and minimal interactions, ease of access approaches. Profile development by reading about the latest trends in code, personal and professional development. Prefer office space work but also open to remote work 1-2 days. Efficient in time and project requirements, approaches and solving limitations.

Education/Research/Teaching Academic appointments:

1. 2024-Academic Staff Member, Universitat Potsdam, Germany
2. 2022-2023: Career Addition: Deep Learning, Data Science, Certification.
3. July 2017- Dec 2021: Postdoctoral Researcher, Finnish Museum of Natural History (Botany), Finland.
4. Aug 2016-Jan 2017: University Fellow, University of Connecticut, Storrs, USA.
5. Sept 2014-Sept 2016: Research Fellow, University of Technology Sydney, Australia.
6. Sept 2011-Sept 2014: CoCoPro, Fondazione Edmund Mach, IASMA, Italy.
7. Dec 2010-Aug 2011: Visiting Post-doc Researcher, Huazhong Agricultural University, China.
8. 2006-2009: PhD Candidate, Jai Narian Vyas University, India.

Programming Stack:

Past: C++ (dropped 2021), Now: Bash, R, Awk, Python, Julia, GO, RUST.

Machine | Deep Learning: PyTorch, Tensorflow, XGBoost, Scikit-learn, Keras, Fastai.

Package/API Development | Documentation: Python, Julia, GO, Markdown, MkDocs, Quatro.

System Analyst: Git, Terraform, Kubernetes, Grafana, LDAP, Systemd, Apptainer, Docker, Podman.

HPC/Database: SQLite3, PostgreSQL, MongoDB, PBS, SLURM, RedHat(Fedora).

Web Development: Shiny/ShinyExpress(Python), Streamlit, Django, HUGO, Flask, HTMx.

Publications (*Corresponding Author; *Contributed Equally):

1. Yuling Yue, Gaurav Sablok, Anna Neubauer, Jaakko Hyvonen, Peter Szoevenyi (2024) Systemic response to nitrogen starvation in the cyanobacteria hosting hornwort and liverwort provides little evidence for extensive priming to the cyanobiont. bioRxiv 2024.05.22.595400; doi: <https://doi.org/10.1101/2024.05.22.595400>.
2. Zanardo, M., Giannattasio, M., Sablok, G. et al. (2023). Metabarcoding analysis of the bacterial and fungal communities during the maturation of preparation 500, used in biodynamic agriculture, suggests a rational link between horn and manure. Environ Dev Sustain <https://doi.org/10.1007/s10668-023-03144-w>
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4. Lehtonen S, Poczei P, Sablok G, Hyvönen J, Karger DN, Flores J (2020) Exploring the phylogeny of the marattialean ferns. Cladistics. 36:569-593.
5. Jike W, Li M, Zadra N, Barbaro E, Sablok G, Bertorelle G, Rota-Stabelli O, Varotto C (2020). Phylogenomic proof of Recurrent Demipolyploidization and Evolutionary Stalling of the "Triploid Bridge" in Arundo (Poaceae) Int J Mol Sci. 21:5247.
6. Sablok G, Amiryousefi A, He X, Hyvönen J and Poczei P (2019) Sequencing the Plastid Genome of Giant Ragweed (Ambrosia trifida, Asteraceae) From a Herbarium Specimen. Front. Plant Sci. 10:218
7. Jike W, Sablok G, Bertorelle G, Li M, Varotto C (2018). In silico identification and characterization of a diverse subset of conserved microRNAs in bioenergy crop Arundo donax L. Sci Rep. 8:16667.

8. Yang K, Wen X, Mudunuri S, Varma GPS, Sablok G (2019). Diff isomiRs: Large-scale detection of differential isomiRs for understanding non-coding regulated stress omics in plants. *Sci Rep.* 9:1406
9. Zannardo M, Rosselli R, Meneghesso A, Sablok G, Stevanato P, Engel M, Altissimo A, Peserico L, Dezuani V, Concheri G, Schlöter M, Squartini A (2018) Response of Bacterial Communities upon Application of Different Innovative Organic Fertilizers in a Greenhouse Experiment Using Low-Nutrient Soil Cultivated with *Cynodon dactylon*. *Soil Syst.* 2: 52
10. Sablok G, Hayward RJ, Davey PA, Santos RP, Schliep M, Larkum A, Pernice M, Dolferus R, Ralph PJ(2018). SeagrassDB: An open-source transcriptomics landscape for phylogenetically profiled seagrasses and aquatic plants. *Sci Rep.*8(1):2749.
11. Mirzaei S, Mansouri M, Mohammadi-Nejad G, Sablok G (2018) Comparative assessment of chloroplast transcriptional responses highlights conserved and unique patterns across Triticeae members under salt stress. *Photosynth Res.* 136:357-369.
12. Kumar J, Debjyoti Sen Gupta, Gupta S, Dubey S, Gupta P, Singh NP, Sablok G. (2017). Identification, development and application of cross-species intron spanning markers in lentil. *The Crop Journal*, 6:299-305
13. Gaurav Sablok[§], Kun Yang, Chen Rui, Xiaopeng Wen (2017) tRNA derived smallRNAs: smallRNA repertoire has yet to be decoded in plants. *Front. Plant Sci.* doi: 10.3389/fpls.2017.01167
14. Florian Mattenberger, Beatriz Sabater-Muñoz, Christina Toft, Gaurav Sablok, Mario A Fares (2017) Expression properties exhibit correlated patterns with the fate of duplicated genes, their divergence, and transcriptional plasticity in *Saccharomycotina*. *DNA Research.* doi: 10.1093/dnares/dsx025
15. Salvatore Camiolo, Gaurav Sablok, Andrea Porceddu (2017) The Evolutionary Basis of Translational Accuracy in Plants. *G3: GENES, GENOMES, GENETICS.* doi: 10.1534/g3.117.040626.
16. Gaurav Sablok^{§*}, Ting-Wen Chen*, Chi-Ching Lee, Chi Yang, Ruei-Chi Gan, Jill L. Wegrzyn, Nicola L. Porta, Kinshuk C. Nayak, Po-Jung Huang, Claudio Varotto, Petrus Tang (2017) ChloroMitoCU: Codon patterns across organelle genomes for functional genomics and evolutionary applications. *DNA Research.* doi: 10.1093/dnares/dsw044
17. Kun Yang*, Gaurav Sablok*, Guang Qiao, Qiong Nie, Xiaopeng Wen (2017) isomiR2Function: An integrated workflow for identifying microRNA variants in plants. *Front. Plant Sci.* 8:322.
18. Ashish Kumar Srivastava, Gaurav Sablok, Michael Hackenberg, Uday Deshpande, Penna Suprasanna (2017) Thiourea priming enhances salt tolerance through co-ordinated regulation of microRNAs and hormones in *Brassica juncea* *Sci. Rep.* 7:4549.
19. Manoj Kumar, Matthew P. Padula, Peter Davey, Mathieu Pernice, Zhijian Jiang, Gaurav Sablok, Loretto Contreras-Porcia, Peter J. Ralph (2017) Proteome Analysis Reveals Extensive Light Stress-Response Reprogramming in the Seagrass *Zostera muelleri* (Alismatales, Zosteraceae) *Metabolism.* *Front. Plant Sci.* 7:2023.
20. Zdravka Ivanova, Gaurav Sablok, Evelina Daskalova, Gergana Zahmanova, Elena Apostolova, Galina Yahubyan, Vesselin Baev (2017) Chloroplast genome analysis of resurrection tertiary relict *Haberlea rhodopensis* highlights genes important for desiccation stress response. *Front. Plant Sci* 8:204.
21. Gaurav Sablok[§], Suresh B Mudunuri, David Edwards, Peter J Ralph (2016) Chloroplast Genomics: Expanding resources for an evolutionary conserved miniature molecule with enigmatic applications. *Current Plant Biology* 7-8:34–38.
22. Alireza Ahadi, Gaurav Sablok[§], and Gyorgy Hutvagner (2017) miRTar2GO: a novel rule-based model learning method for cell line specific microRNA target prediction that integrates Ago2 CLIP-Seq and validated microRNA–target interaction data. *Nucleic Acids Research* 45: e42
23. Xiaoyong Sun, Lin Wang, Jiechao Ding, Yanru Wang, Jiansheng Wang, Xiaoyang Zhang, Yulei Che, Ziwei Liu, Xinran Zhang, Jiazhen Ye, Jie Wang, Gaurav Sablok, Zhiping Deng, Hongwei Zhao (2016) Integrative analysis of *Arabidopsis thaliana* transcriptomics reveals intuitive splicing mechanism for circular RNA. *FEBS Letters* 590: 3510-3516.
24. Mathieu Pernice, Sutinee Sinutok, Gaurav Sablok, Audrey S. Commault, Martin Schliep, Peter I. Macreadie, Mike A. Rasheed, Peter J. Ralph (2016) Molecular physiology reveals ammonium uptake and related gene expression in the seagrass *Zostera muelleri*. *Marine Environmental Research* 122:126-134
25. Marina Zannardo, Riccardo Rosselli, Andrea Meneghesso, Gaurav Sablok, Piergiorgio Stevanato, Adriano Altissimo, Lisanna Peserico, Valentina Dezuani, Giuseppe Concheri, Michael Schlöter, Andrea Squartini (2016) Dynamics of soil prokaryotes catalyzing nitrification and denitrification in response to different fertilizers in a greenhouse experiment with *Cynodon dactylon*. *European Journal of Soil Biology* 76:83-91.
26. Debjyoti Sen Gupta, Peng Cheng, Gaurav Sablok, Dil Thavarajah, Pushparajah Thavarajah, Clarice Coyne, Shiv Kumar, Michael Baum, Rebecca McGee (2016) Development of a panel of unigene derived polymorphic EST-SSR markers in lentil using public database information. *The Crop Journal* 4: 425-433
27. Peter A. Davey, Mathieu Pernice, Gaurav Sablok, Anthony Larkum, Huey Tyng Lee, Agnieszka Golicz, David Edwards, Rudy Dolferus, Peter Ralph (2016) The emergence of molecular profiling and omics techniques in seagrass biology; furthering our understanding of seagrasses. *Functional Integrative Genomics.*16:465-80.
28. HueyTyng Lee, Agnieszka A. Golicz, Philipp E. Bayer, Yuannian Jiao, Haibao Tang, Andrew H. Paterson, Gaurav

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 30. Gaurav Sablok, Antonio Perez, Thac Do, Tan Yew Seong, Carlos Sanchez, Nicola La Porta, Peter J. Ralph, Andrea Squartini, Antonio Munoz, Jennifer A. Harikrishna (2016) PlantFuncSSR: Integrating First and Next Generation Transcriptomics for Mining of SSR-Functional Domains Markers. *Front. Plant Sci.* 7:878.
 31. Gaurav Sablok^S, Hongwei Zhao, Xiaoyong Sun (2016) Plant Circular RNAs (circRNAs): Transcriptional regulation beyond miRNAs in plants. *Molecular Plant* 9:192-194.
 32. Salvatore Camilio, Gaurav Sablok, Andrea Porceddu (2016) Altools: a user-friendly NGS data analyser. *Biology Direct* 11:8.
 33. Yuan Fu, Michele Poli, Gaurav Sablok, Bo Wang, Yanchun Liang, Nicola La Porta, Violeta Velikova, Francesco Loreto, Mingai Li, Claudio Varotto (2016) Dissection of early transcriptional responses to water stress in *Arundo donax* L. by unigene-based RNA-Seq. *Biotechnology for Biofuels.* 9:54
 34. Biswaranjan Paital, Gaurav Sablok, Sunil Kumar, Sanjeev Kumar Singh, GBN Chainy (2016) Investigating the Conformational Structure and Potential Site Interactions of SOD Inhibitors on Ec-SOD in Marine Mud Crab *Scylla serrata*: A Molecular Modeling Approach *Interdiscip Sci Comput Life Sci* 8:312-318.
 35. Mirosław Kwasniewski, Agata Daszkowska-Golec, Agnieszka Janiak, Chwiałkowska Karolina, Nowakowska Urszula, Gaurav Sablok, Szarejko Iwona (2016) Transcriptome analysis reveals the role of the root hairs as environmental sensors to maintain plant functions under water-deficiency conditions. *Journal of Experimental Botany.* 67: 1079-1094
 36. Mir Asif Iquebal, Sarika Jaiswal, U.B. Angadi, Gaurav Sablok, Vasu Arora, Sunil Kumar, Anil Rai, Dinesh Kumar (2015) SBMDb: first whole genome putative microsatellite DNA marker database of sugarbeet for bioenergy and industrial applications. *Database: article ID bav111*.
 37. Sudhakar Srivastava, Ashish Srivastava, Gaurav Sablok, Tejaswini Deshpande, Suprasanna Penna (2015) Transcriptomics profiling of Indian mustard (*Brassica juncea*) under arsenate stress identifies key candidate genes and regulatory pathways. *Front. Plant Sci.* 6:646.
 38. Gaurav Sablok^S, Ashish K Srivastava, Suprasanna Penna, Vesselin Baev, Peter J Ralph (2015) isomiRs: Increasing evidences of isomiRs complexity in plant stress functional biology. *Front. Plant Sci.* 6:949.
 39. Xiang Jia Min, Brian Powell, Jonathan Braessler, John Meinken, Feng Yu, Gaurav Sablok (2015) Genome-wide cataloging and analysis of alternatively spliced genes in cereal crops. *BMC Genomics:* 16:721.
 40. Gaurav Sablok^S, G.V. Padma Raju, Suresh B. Mudunuri, Ratna Prabha, Dhananjaya P. Singh, Vesselin Baev, Galina Yahubyan, Peter J Ralph, Nicola La Porta (2015) ChloroMitoSSRDB 2.00: More genomes, more repeats, unifying SSRs search patterns and on-the-fly repeat detection. *Database: article ID bav084*.
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 42. Xiaoyong Sun, Fenghua Zuo, Yuanbin Ru, Jiqiang Guo, Xiaoyan Yan, Gaurav Sablok (2015) SplicingTypesAnno: Annotating and quantifying alternative splicing events for RNA-Seq data. *Computer Methods and Programs in Biomedicine* 119:53-62.
 43. Shiliang Hu*, Gaurav Sablok*, Bo Wang, Dong Qu, Enrico Barbaro, Roberto Viola, Mingai Li and Claudio Varotto (2015) Plastome organization and evolution of chloroplast genes in Cardamine species adapted to contrasting habitats. *BMC Genomics* 16:306.
 44. Mladen Naydenov, Vesselin Baev, Elena Apostolova, Nadezhda Gospodinova, Gaurav Sablok, Mariyana Gozmanova, Galina Yahubyan (2015) High-temperature effect on genes engaged in DNA methylation and affected by DNA methylation in *Arabidopsis*. *Plant Physiology and Biochemistry* 87: 102-108.
 45. Daniel A. Nielsen, Mathieu Pernice, Martin Schliep, Gaurav Sablok, Thomas C. Jeffries, Michael Köhl, Daniel Wangpraseurt, Peter J. Ralph, Anthony W.D. Larkum (2015) Microenvironment and Phylogenetic Diversity of Prochloron Inhabiting the Surface of Crustose Didemnid Ascidians. *Microenvironment and Phylogenetic Diversity of Prochloron Inhabiting the Surface of Crustose Didemnid Ascidians. Environmental Microbiology* 10:4121-32.
 46. Agnieszka A Golicz, Martin Schliep, Huey Tyng Lee, Anthony WD Larkum, Rudy Dolferus, Jacqueline Batley, Chon-Kit Kenneth Chan, Gaurav Sablok, Peter J Ralph, David Edwards (2015) Genome-wide survey of the seagrass *Zostera muelleri* suggests modification of the ethylene signalling network. *Journal of Experimental Botany* 66:1489-1498.
 47. Nicola La Porta, Gaurav Sablok, Giovanni Emilliani, Ari M Hietala, Alessio Giovannelli, Paolo Fontana, Emilio Potenza, Paolo Baldi (2015) Identification of Low Temperature Stress Regulated Transcript Sequences and Gene Families in Italian Cypress. *Molecular Biotechnology:* 57:407-418.
 48. Arturo Sánchez-Paz, Adriana Muhlia-Almazan, Reinhard Saborowski, Fernando García-Carreño, Gaurav Sablok*, Fernando Mendoza-Cano (2014) Marine viruses: the beneficial side of a threat. *Applied biochemistry and*

Biotechnology 174: 2368-2379.

49. Vesselin Baev, Ivan Milev, Mladen Naydenov, Tihomir Vachev, Elena Apostolova, Nikolay Mehterov, Mariyana Gozmanva, Georgi Minkov, Gaurav Sablok, Galina Yahubyan (2014) Insight into small RNA abundance and expression in high-and low-temperature stress response using deep sequencing in Arabidopsis. *Plant Physiology and Biochemistry* 84C: 105-114.
50. Gaurav Sablok, Yuan Fu, Valentina Bobbio, Marina Laura, Giuseppe L Rotino, Paolo Bagnaresi, Andrea Allavena, Violeta Velikova, Roberto Viola, Francesco Loreto, Mingai Li, Claudio Varotto (2014) Fuelling genetic and metabolic exploration of C3 bioenergy crops through the first reference transcriptome of *Arundo donax* L. *Plant Biotechnology Journal* 12: 554-567.
51. Vesselin Baev, Gaurav Sablok, Ivan Minkov (2014) Next generation sequencing crowd sourcing at BIOCOMP: What promises it holds for us in future? *Journal of Computational Science* 5: 325-326
52. Yachana Jha, Gaurav Sablok, MHU Turabe Fazil, R B Subramanian, Sunil Kumar (2014) Insights into differential expression of RAB18 using insilico structural analysis and interaction with GTP binding in salinity stress condition. *Journal of Molecular Recognition* 27: 521-527.
53. Piergiorgio Stevanato, Chiara Broccanello, Filippo Biscarini, Marcello Del Corvo, Gaurav Sablok, Lee Panella, Alessandra Stella, Giuseppe Concheri (2014) High-throughput RAD-SNP genotyping for characterization of sugar beet genotypes. *Plant Molecular Biology Reporter* 32:691-696.
54. Gaurav Sablok[§], Jennifer Ann Harikrishna and Xiang Jia Min (2013) Next Generation Sequencing for Better Understanding Alternative Splicing: Way Ahead for Model and Non-Model Plants *Transcriptomics* 2013: e103.
55. Gaurav Sablok[§], Ivan Milev, Georgi Minkov, Ivan Minkov, Claudio Varotto, Galina Yahubyan, Vesselin Baev (2013) isomiRex: Web-based identification of microRNAs, isomiR variations and differential expression using next-generation sequencing datasets. *FEBS Letters* 587:2629–2634.
56. Satendra Singh, Gaurav Sablok, Rohit Farmer, Atul Kumar Singh, Budhayash Gautam, Sunil Kumar (2013) Molecular dynamic simulation and inhibitor prediction of Cysteine synthase structured model as a potential drug target for Trichomoniasis. *BioMed Research International Article ID* 390920.
57. Gaurav Sablok[§], XianMing Wu, Jimmy Kuo, Kinshuk Chandra Nayak, Vesselin Baev, Claudio Varotto, Fenfeng Zhou (2012) Combinational effect of dominant mutational bias and light translational selection for translation efficiency in *Solanum lycopersicum* cv. Micro-Tom. *Genomics* 101:290-295.
58. Mehwish Yaseen, Touqeer Ahmad, Gaurav Sablok, Alvaro Standardi, Ishfaq Ahmad Hafiz (2013) Role of Carbon Sources for In Vitro Plant Growth & Development. *Molecular Biology Reports* 40: 2837-2849.
59. Mallikarjuna Rao Kovi, Gaurav Sablok, XuFeng Bai, Michael Wendell, Odd-Arne Rognli, HuiHui Yu, YongZhong Xing (2013) Expression patterns of photoperiod and temperature regulated heading date genes in *Oryza sativa*. *Computational Biology and Chemistry* 45:36-41.
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63. Touqeer Ahmad, Gaurav Sablok, Tatiana Tatarinova, Qiang Xu, Xiu Xen Deng, Wen Wu Guo (2013) Evaluation of codon biology in *Citrus* and *Poncirus trifoliata* based on Genomic Features and Frame Corrected Expressed Sequence Tags *DNA Research*. 20:135–150.
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Peer reviewed Abstracts and Posters (§Corresponding Author):

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16. Gaurav Sablok, Massimo Pindo, Nicola La Porta, Andrea Squartini (2013) Soil Fungal Diversity In Six Spruce Forests: A Metagenomic Approach. Collocazione: c9.12.17 - ID Contributo: #157 at Multifunctional management of mountain forests in Europe - the role of ecosystem services. In: Proceedings of the 9th SISEF National Congress "Multifunzionalità degli Ecosistemi Forestali Montani: Sfide e Opportunità per la Ricerca e lo Sviluppo" (Tonon G, Ventura M, Bucci G eds). Bolzano (Italy).
17. Marina Zanardo, Riccardo Rosselli, Andrea Meneghesso, Gaurav Sablok, Piergiorgio Stevanato, Chiara Broccanello, Andreas Hofmann, Marion Engel, Adriano Altissimo, Lisanna Perserico, Valentina Dezuani, Giuseppe Concheri, Michael Schlöter, Andrea Squartini (2013) Effect of different fertilizers on soil microbial communities analyzed by 16S T-RFLP and 454 sequencing. Code: 837 at V International Conference on Environmental, Industrial and Applied Microbiology, Madrid, Spain.
18. Gaurav Sablok, Fabio Zotte, Nicola La Porta, Ari M Hietala, Carl Grunnar Fossdal, Andrey Kajava (2012) FungPROTDB: Database of homorepeats in fungal proteomes and secretomes. ECCB'12-European Conference on Computational Biology, (9th-13th September, 2012), Basel, Switzerland. Poster D8.
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20. Sablok G, Nayak KC, Potenza E, Emiliani G, La Porta N (2013) Multivariate analysis revealed translational selection and mutational bias in *Heterobasidion annosum* genome. In: Proceedings XIII Conference. Root and Butt Rot of Forest Trees, IUFRO Working Party 7.02.01, September Firenze - S. Martino di Castrozza (Trento), Italy, edited by P. Capretti, C. Comparini, M. Garbelotto, N. La Porta, A. Santini, Firenze University Press, 2013, ISBN 978-88-6655-352-6, pp. 58-61.
21. Martina Popova, Suresh B Mudunuri, Sujana Patnana, Vesselin Baev, Gaurav Sablok[§] (2012) ChloroMitoSSRDB: open source repository of perfect and imperfect repeats in organelle genomes for evolutionary genomics presented at International Conference on Bioinformatics and System Biology, BIOCOMP, Varna, Bulgaria. F1000 Posters 2012, 3: 1466
22. Piergiorgio Stevanato, Daniele Trebbi, Chiara Broccanello, Giuseppe Concheri, Andrea Squartini, Massimo Saccomani, Gaurav Sablok (2012) High-throughput SNP genotyping in sugar beet. International Conference on Bioinformatics and System Biology, BIOCOMP, Varna, Bulgaria. F1000 Posters 2012, 3: 1513.
23. G Sablok[§], Amit K. Gupta and N S Shekhawat (2010) SPAR and SP-SSR Markers based Genetic Relatedness and Interspecies Diversity revealed in *Acacia's* of Western Rajasthan at 2nd International Symposium on Genomics of Plant Genetic Resources, Bologna, Italy. Poster No-281.
24. Sablok G[§], Priyanka Gahlot, Amit Kumar Gupta, K Pareek and N.S. Shekhawat (2009) Standardization of Protocol for PCR Usable DNA From *Acacia nilotica* For Molecular Characterization and Sustainability of Arid Region Species at The PTCA (Plant Tissue Culture Association of India) meeting at IHBT, Palampur.
25. Sablok G[§], Priyanka Gahlot, Amit Kumar Gupta and N.S. Shekhawat (2008) Bioinformatics Identification of eSNPs/Indels in the 1467 expressed sequence tags (ESTs) of the *Prosopis juliflora*: A study on the Drought Tolerant Plant at International conference on Plant Biotechnology and Molecular Biology. Department of Biotechnology Kakatiya University Warangal.

Edited and Authored Books:

1. **Sablok G**, Sun K, Sun H. NAMS (2019) Noncoding Assessment of long RNAs in Magnoliophyta Species. *Methods Mol Biol.* 1933:257-264.
2. **Sablok G**, Yang K, Wen X (2019) Protocols for miRNA Target Prediction in Plants. *Methods Mol Biol.* 1970:65-73.
3. **Gaurav Sablok** et al. *Plant Metallomics and Functional Omics: A system perspective* (Springer, 2018).
4. Mariyana Gozmanova, Vesselin Baev, Elena Apostolova, **Gaurav Sablok**, Galina Yahubyana (2017) Growing diversity of plant micro RNAs and MIR-derived small RNAs. *Plant Epigenetics* 49-67 (Springer, doi: 10.1007/978-3-319-55520-1_3).
5. **Gaurav Sablok**, Hikmet Budak, Peter J Ralph (2017) *Brachypodium Genomics: Advances and Development in understanding the genetic base of the model plant.* *Methods in Molecular Biology* (Springer: <http://www.springer.com/in/book/9781493972760>).
6. **Gaurav Sablok**, Sunil Kumar, Saneyoshi Uneo, Jimmy Kuo, Claudio Varotto (2015) *Advances in the Understanding of Biological Sciences using Next Generation Sequencing (NGS) Approaches* (Springer: <http://www.springer.com/us/book/9783319171562>).

7. Tatiana V. Tatarinova and **Gaurav Sablok** (2012) DNA methylation Challenges and Mechanism, Nova Publishers, USA. ISBN: 978-1-62417-128-4
8. NS Shekhawat and **Gaurav Sablok** (2008) Plant Physiology and Biochemistry: Growth and Development. NSDL NISCAIR: 1-83. doi: <http://nsdl.niscair.res.in/123456789/379>.

Fellowships and Travel Grants (Chronological Order):

1. 2014-2016: UTS Internal Start-up Grant (\$20K) Project Role: Principal Investigator.
2. 2015-2016: KARORA: Graphic driven platform independent proteomics workflow for spectral libraries (2016) University of Technology Sydney (\$15K) Project Role: Principal Investigator.
3. 2012-2014: Awarded CoCoPro Fellowship for “Developing NGS tools and techniques for large scale methods implementation in transcriptomics and genomics.
4. 2011-2012: Awarded EU Postdoctoral Fellowship (BIOMASFOR) “Enhancing biomass potential for European forest using NGS technologies”.
5. 2012: Awarded travel grant by European Conference on Computation Biology, Swiss Institute of Bioinformatics (ECCB, 2012) for presenting FungPROTDB: Database of protein homo-repeats in fungal proteomes and secretomes.
6. 2010-2011: Chinese Fellowship “Developing transcriptomics tools for Disopyros kaki”.
7. 2011: Awarded Prestigious DS Kothari Post-Doctoral Fellowship by Department of Science and Technology, Government of India (Award Number BL/10/0057) on Identification of potential stress related microRNAs in Wheat and Pennisetum. Project Role: Principal Investigator.
8. 2006-2009: Awarded University Research Fellowship on Doctoral Dissertation, Computational Mining of Phyto-Diversity Resources of Rajasthan and Analysis of Simple Sequence Repeats (SSR’s), Biotechnology Centre, Jai Narian Vyas University, India.
9. 2009: “Molecular Characterization and Prediction of Interspecies Diversity in Acacia’s for Sustainable Rehabilitation through Agroforestry”- F7(7)/DST/SP/2009/343-355. Funding: State Department of Science and Technology, Rajasthan, India. Project Role: Principal Investigator.
10. 2008: Molecular Characterization of the Prosopis cineraria: A sustainable move towards conservation of Biodiversity of Arid Regions”- P35/DST/2008/2227. Funding: State Department of Science and Technology, Rajasthan, India. Project Role: Principal Investigator.

Grant Reviewer:

1. Ohio Agricultural Research and Development Center (OARDC) (2014), Ohio Plant Biotechnology Consortium, USA.
2. Reviewed WHITE proposal (2018) from Chargée de Projets Scientifiques, Agence Nationale de la Recherche, France.

Educational Service as Peer Reviewer in ISI Journals:

I am serving/served as Ad-hoc reviewer for following ISI journals: Silvae Genetica (Germany); Bioinformatics, (Oxford Journal); International Journal of Bioinformatics Research; African Journal of Biotechnology; 3Biotech (Springer); Molecular Biology Reports (Springer); Frontiers in Bioinformatics and Computational Biology (Frontiers); Genomics (Elsevier), Plant Omics Journal, Antonie van Leeuwenhoek Journal of Microbiology (Springer), Plant Molecular Biology Reporter (Springer), Journal of Aquatic Animal Health (Taylor and Francis), Frontiers in Genetics (Frontiers), Frontiers in Statistical Genetics (Frontiers), RNA Biology (Lande Sciences), Journal of Genetics and Genomics (Springer); Computational Molecular Biology; Journal of Structural Biology (Elsevier), Molecular Genetics and Genomics (Springer). PLOSONE, Database (Oxford Journal), Journal of Fish Diseases (Wiley), Canadian Journal of Microbiology (NRC Press), Interdisciplinary Sciences: Computational Life Sciences (Springer), Journal of Biomolecular and Structural Design (Taylor and Francis), DNA Research (Oxford Journal), Nucleic Acid Research (Oxford Journal), PeerJ, BMC Genomics, Functional and Integrative Genomics, The Plant Journal, Scientific Reports, Current Plant Biology, Journal of Forest Research.

Bioinformatics Resources:

1. ChloroMitoSSRDB and ChloroMitoSSRDB 2.00: Webserver cum Database of Chloroplast and Mitochondrial microsatellites available at www.mcr.org.in/chloromitossrdb.
2. Plant Alternative Splicing Database: Alternative splicing database containing the splice patterns of Brachypodium available at <http://proteomics.yasu.edu/altsplice/>.
3. IsomiRex: Webserver for identification of the microRNA, differential expression and isomiRs from smallRNA dataset available at <http://bioinfo1.uni-plovdiv.bg/isomiRex/>.
4. SBMDB: World first Sugarbeet microsatellite database containing polymorphic SSRs for sugarbeet genome: <http://cabindb.iasri.res.in/sbmdb>.
5. PlantFuncSSRs: Functional SSRs in Plants: www.bioinfocabd.upo.es:3000.

6. miRTar2GO: microRNA prediction using CLIP-seq: <http://mirtar2go.org>.
7. ChloroMitoCU: Organelle centric platform for browsing thousands of pre-compiled codon patters across organelle genomes: <http://chloromitocu.cgu.edu.tw/>.
8. SplicingTypesAnno: annotating and quantifying alternative splicing events for RNA-Seq data available from: <http://sourceforge.net/projects/splicingtypes/>.
9. NAGNAG Splicing: Identification and quantification of the NAGNAG splicing events from: <http://genome.sdau.edu.cn/research/software/nagnag.html>.
10. ALTools: <http://sourceforge.net/projects/altools/files/?source=navbar>
11. KARORA: Java enabled Pathovariance system for Mass-spectrometry data.
12. AquaticPlantDB: First repository for Aquatic plants: <http://115.146.91.129/index.php>
13. isomiR2Function: <https://github.com/347033139/isomiR2Function>

References:

1. Jaakko Hyvönen (Employer)
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3. Nicola La Porta (Employer)
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4. Claudio Varotto, PhD (Employer)
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To whom it may concern

Based on four yrs (plus one year in a project led by a local junior colleague) that Dr. Sablok worked here in Helsinki I can say that he seems to have excellent wet lab and bioinformatic skills. He was in charge of extracting organellar and whole genome of several species (material grown in the lab and also those collected in the wild). He produced genome data for numerous eukaryotes (various "algae", fungi and plants) working in collaboration with numerous colleagues locally, and abroad. This data unfortunately remains to large extent unpublished, partly due to the covid pandemic. However, several posters with Gaurav Sablok as a lead author were prepared to be presented in international meetings that he attended. Dr. Sablok mostly worked in genome bioinformatics, in collaboration with laboratories providing these services locally, but also contacted commercial company in the Netherlands to get their services in providing estimate of the genome size. Our project did not have funds to support students/junior researchers, only research costs and salary to Sablok's post doc position, and thus I am unfortunately not able to evaluate this kind of activities.

Helsinki, 9.viii.2022



Jaakko Hyvönen
professor of botany

To whom it may concern,

I have known the applicant Dr Gaurav Sablok since 2018. He worked as a postdoctoral researcher in the project “*Two genomes to discover the keys to embryophyte success*” funded by the Academy of Finland, which enabled his research in Helsinki for three years. Dr Sablok is hard-working researcher with specialized skills in bioinformatics and genome analysis. Our co-operation has produced several publications with some of them highly cited within very short time. I see Dr Sablok as a good fit for the position in the **Research Centre in Biodiversity and Genetic Resources**, therefore I fully support his application.



Prof Péter Poczai, PhD, habil.
Curator, Associate Professor
Chair of the Systematics & Evolution
Research Programme

31.07.2022

CIBIO

Research Center in Biodiversity and Genetic Resources
Portugal

Reference letter for Dr. Gaurav Sablok

Dr. Gaurav Sablok worked in an Academy of Finland financed project "Evolution of early-diverging basidiomycetes - diversity and wood decay in Pucciniomycotina" as a postdoc researcher in 2021. I coordinated that project, and Dr. Sablok's role was data management and conducting bioinformatics analyses of genomic data of fungi. During the project, he arranged sequencing of hundreds of genomic samples, handled large amounts of Illumina sequences, troubleshooted fragmented and contaminated data, assembled genomes, and run various analyses on them. He clearly has good knowledge of relevant software, scripting and HPC computing environments.

Helsinki, 12 August 2022,



Otto Miettinen

Curator of fungi
Associate professor, PhD
Finnish Museum of Natural History
University of Helsinki, Finland
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**UNIVERSITY
OF TURKU**

27 September 2022

To whom it may concern,

Dr. Gaurav Sablok has participated as an expert in my project "Using complete plastomes to study the phylogenetics of early fern lineages" funded by the Finnish Cultural Foundation. In the project Dr. Sablok was mainly responsible for the bioinformatics and genome structure analyses. His contribution for the project during the years 2018-2020 was important and I found him very cooperative and capable. I can therefore warmly recommend him for any similar job.

The above mentioned project resulted in the following scientific publication: Lehtonen, S., Poczai, P., Sablok, G., Hyvönen, J., Karger, D.N., Flores, J. 2020. Exploring the phylogeny of the marattialean ferns. *Cladistics*, 36: 569–593.

Sincerely,

A handwritten signature in blue ink, appearing to read 'Samuli Lehtonen'.

Samuli Lehtonen

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October 13, 2022

To whom it may concern,

Dr Gaurav Sablok – statement of support

I worked with Dr Sablok between 2017 and 2021 when he was employed as a postdoctoral researcher at the Finnish Museum of Natural History, Helsinki, and also during a research visit he made to the Royal Botanic Garden Edinburgh in early 2020. Dr Sablok has extensive expertise in bioinformatics, genome assembly and the design of markers for plant phylogenetics projects. Our collaboration involved the design of next-generation baits for a proposed phylogenetic study of the moss genus *Pogonatum* as well as other studies within the family Polytrichaceae.

Dr Sablok is extremely enthusiastic, productive and technically competent and would be a valuable addition to any research team engaged with plant bioinformatics and phylogenomics.

Sincerely,

Neil Bell
Research Bryologist
Royal Botanic Garden Edinburgh

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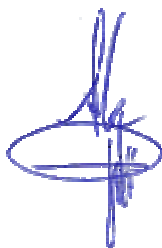
Legnaro, October 1st 2022

TO WHOM IT MAY CONCERN

Dear Sirs,

I hereby endorse the scientific qualities of Gaurav Sablok, with whom I have had very fruitful collaborative interactions during the period from the beginning of 2012 to the end of 2017. In those years I have had the opportunity to appreciate his skills in bioinformatics, covering the aspects of programming and data elaboration applied to several different topics of plant, animal and microbial genomics and metagenomics as well as in presenting research and methodology reports in public seminars. He demonstrated a high level of both operative and decisional autonomy, an active initiative and a good competence in tackling complex scientific problems. I can therefore recommend his proficiency and professional capabilities in this field.

Prof. Andrea Squartini

A handwritten signature in blue ink, appearing to be "A. Squartini".

ENDORSEMENT LETTER FOR Dr. GAURAV SABLOK

To whom it may be of concern

It is a great pleasure to write this endorsement letter for Dr. Gaurav Sablok, which was a post-doctoral researcher in my group some years ago.

Gaurav is a brilliant computer scientist, possibly the most talented bioinformatician I have ever met and worked with. He is very fast and highly productive. He can tackle a multitude of different computational problems with ease and high accuracy, ranging from RNA-Seq and microRNA identification to plastome assembly and codon usage. He is very fast in assessing the new programs that are best suited to address a specific computational problem, developing pipelines that are both robust and effective. He is experienced in the management of computational clusters, making him a very versatile figure in any kind of setting requiring high throughput computation.

For all these reasons, I strongly recommend Dr. Gaurav Sablok to any bioinformatic group, as I am sure that he will be a precious asset for the development of reliable high-throughput data analyses.

Please do not hesitate to contact me directly if you are interested in having more information on him.

Best regards,



Claudio Varotto

Head of the Ecogenomics Unit
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Letter of Reference to Dr. Gaurav SABLOK

August 30th, 2022

PhD Dr. Nicola La Porta
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Email: nicola.laporta@fmach.it

To whom it may concern.

I feel glad and excited to write a recommendation letter for Dr. Gaurav Sablok to support his applications for a position in any relevant Research Institution worldwide.

Dr. Gaurav Sablok was selected in a competitive call by my Institution (FEM) and was working with my group, Environmental Biotechnology Platform, for ca. two years during 2011-2012. He was working with me on several aspects of Biostatistics and Computational Biology. He was hired under the BIOMASFOR project, a 550 K€ project funded by CARITRO Bank Foundation, which was successfully completed and scientifically appreciated.

Under my supervision, he developed the ChloroMitoSSRDB, which has already been published in *DNA Research* (2013; DOI: 10.1093/dnares/dss038) and recently upgraded to ChloroMitoSSRDB 2.0 on *Database Oxford* (2015; DOI: 10.1093/database/bav084). In both papers, he worked meticulously on writing codes, developing the pipelines, and writing the manuscript. In further two works his skills in conceiving and designing the experiments, using innovative analysis tools to analyzed the data and to write the papers provided a very fast, deep and comprehensive extraction and evaluation of useful information from the raw data, that brought to a fast acceptance of the papers published in *Molecular Biotechnology* (DOI: 10.1007/s12033-014-9833-2 and *Biotechnology for Biofuels* (DOI: 10.1111/efp.12248). Recently a fifth and sixth papers were published on *Frontiers of Plant Science*, dealing respectively with PlantFuncSSRs to identify functional-based genic variability among the species of interest, which might be of particular interest in developing functional markers in plants and analyzed data for the transcriptome analysis to identify the genes and the related expression in ozone stress conditions in plants. Additionally, there are several other works, where his contribution to the data analysis was crucial, if not fundamental, and are currently in the step of submission to several peer-reviewed international journals. Under my supervision, he worked on the metagenomics of the soil fungal dynamics using the NGS. He analyzed all the data generated through the projects that were afterwards presented in a scientific conference and submitted for publication on *Fungal Diversity* journal. In total he published with my group 8 peer reviewed papers, with 5 of them as first author. In all these publications his role was determinant, as was also stated in the Author contribution chapters.

He has effectively demonstrated a thorough knowledge of Linux operating systems and is quite experience in developing computational pipelines for the analysis. In additions, he writes effective lines for codes, installing new servers and maintaining the servers for downstream analysis of the project data in BASH, Perl and R (Statistical analysis). He has meticulously analyzed the data and also identified new ways to analyze and interpret the data for successful meaningful publication. In general he has very brilliant skills in writing manuscripts and projects, not at all so common at his age. His credentials, rigorous scientific approach, and first-rate analytical and problem-solving skills equip him to offer the necessary qualifications mix you require to be a member of any cutting-edge project team. Because his continuous and passionate reading of the most recent scientific high quality literature, he was well aware and expert of the most updated tools implemented in metagenomics, genomics and transcriptomic analysis and was an esteemed and valued member of my group.

In addition, I want to clarify you that he quitted the job at FEM as PostDoc researcher and his collaboration with me, only because the conclusion of the project. Definitely I would employ him in case of an other project related to his excellent skills.

Unfortunately at that time there was not possibility to apply any tenure track or permanent position in my Institution. I would sure re-hire him for future projects if granted by funding agency.

Also the his ability to collaborate with other researchers and staff members is open and truly honest both with internal and external colleagues, as well as with the project leader, and actively stimulating new ideas and innovative approaches. At the same time, I can testify that he is very respectful and professional with the Institution to which he belongs. About acute problems, I don't think it is the real case. Perhaps sometime he is working too much and he is demanding too much from himself. Also sometime he can be quite anxious for work problems, at least from my point of view. But I guess that with the coming age he has improved in these respects.

In general he works hardly and seriously with strong working ethics. At the same time, he also motivates team members to submit the papers to journal of higher reputation. I strongly feel glad on mentoring him and based on my observations, he is an autonomous and independent observer and thinker for doing effective science. At FEM, his interaction within a multi-disciplinary project teams from different countries, with diverse traditions and cultures has certainly fortified those skills. I strongly encouraged and recommend the application of Dr. Sablok to any relevant lab position at Universities or other Research bodies.

Please feel free to contact me, even by phone if you like, for any further clarifications.

Best regards,

Nicola La Porta

A handwritten signature in black ink, reading "Nicola La Porta". The signature is written in a cursive, flowing style with some capitalization and stylized lettering.