

The scientific community is faced with the difficulty of understanding how plants in the field react to ecological stress and various simultaneous environmental cues. A deeper knowledge of the complex trait genomics and functional connections at the level of system biology can be created with the advent of NGS technologies and the application of high-throughput bioinformatics tools. In recent years, it has been clear that different ecological responses are present among ecological ecotypes. However, it is still unclear how and by what mechanism the ecological ecotypes respond to the complex natural surroundings differently. I have a background in bioinformatics and plant biology, as well as a lot of experience. I spent 3.5 years developing bioinformatics methods for comprehending the transcriptional and post-transcriptional genomics across nuclear and organelle genomes at Fondazione Edmund Mach in Italy after completing my PhD. I took involved in and finished multiple RNA-seq and Organelle-Seq experiments for several plant species, including *Arundo donax* (an emerging biofuel plant). Additionally, I have done a lot of work in the field of organelle genomics and have published the first Cardamine species' chloroplast genomes. Additionally, while working at FEM, I independently created an international partnership to find and create computational methods for a number of crop species. After that, I spent four years (2014–2016) as a Research Fellow (Academic Level B) at the University of Technology, Sydney, where I developed computational methods for understanding seagrasses.

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*, *Mallomonas*, and *Cryptomonas* species. My work has focused on genome assembly, chloroplast genomics, and a variety of other topics. Additionally, I've worked for various other organisations, collaborating with Edinburgh UK, to analyse the genomics data for PAFTOL species and the chloroplast genomes of the *Ambrosia* clade. 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, markers 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. My research focuses on how the complex structure of the plant system may be understood via gene and pathway evolution, as well as how the post-transcriptional machinery functions to control the complicated trait genomics. My research has also been concentrated on comprehending the biology of non-coding RNA and the function of translational genomics in plants. To understand the plant system biology, I have developed bioinformatics methodologies, apps, and novel approaches that combine computational and wet lab methods. I have developed bioinformatics techniques, programmes, and novel strategies combining computational and wet lab methodologies to comprehend plant system biology in order to solve these concerns. By advancing knowledge of the genetic and molecular underpinnings of plant variation at the transcriptional, translational, or post-translational level, I intend to increase our capacity to predict how different species will react to environmental changes and climate change. Using bioinformatics and functional validation techniques in plants, my work during my graduate career and during my postdoc postings has built a framework for understanding linkages between genetics, environmental change, and functional variation. The key to comprehending this adaptation is the development and integration of methods, such as merging transcriptional, post-transcriptional, and methods to link transcriptional and post-transcriptional interactions for a better understanding of the relationships between genotype and phenotype.

Finally, by utilising genomics and bioinformatics techniques, my work with model plants like *Arabidopsis*, *Brachypodium*, *Cereal*, *Legumes*, and non-model crop species aims to build dynamic models to understand the genetic and signalling pathways that can link natural genetic variation and establish the unique ecological ecotypes. As I worked on these plant species, I created new computational analyses that helped me 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, I have also created a number of marker-based strategies and, more recently, intron-spanning markers to advance the genetics of cereals and legumes. My research interests are directly related to the posted position, as well as the ongoing research projects, research activities, and my selection for the Bioinformatics position. My wide skill set and extensive experience make me a strong candidate for the offered position, and I can play a variety of roles inside the department and amongst the departments as a

whole. 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, analysing deep sequencing data, and interpreting its biological significance in the context of planned experiments. I also gained experience managing grants, working in a lab, and collaborating with others. I offer my application for the advertised post in light of these factors. I have always made an effort to further my knowledge in any area of applied plant genomics and bioinformatics, which provides fresh perspectives on how plants function and how they respond to environmental changes. I consider myself to be someone with a high level of perseverance who is driven and eager to learn everything there is to know about plants and to advance the field of biology.

Teaching Statement

I have dealt with a number of students during my research career so far, primarily to encourage them to pursue careers in research. As part of research collaboration, I have encountered students who are self-motivated or students who require motivation, and this natural mix of students has helped me to comprehend and address the essential question in teaching - how to spark students' interest in research and help them understand the value of the contributions they will make after completing their education.

As a teaching assistant at the university level for my first teaching position following my Master's and throughout my PhD, I was able to develop strategies that I can use to practically focus students on understanding the relevance of each subject, actively learn fundamental concepts, develop a systems' thinking, and acquire practical skills and experience. My postdoctoral experiences have given me the opportunity to mentor and assist students who are interested in research, inspiring them to succeed in plant genomics and bioinformatics. I frequently discuss student-developed genomics and bioinformatics methods as part of independent partnerships since they can be utilised to advance the genomics platform for plants, and more recently, for specific crops. In order to share what I have learned, encourage students to think for themselves, and aid in the development of young professionals so that they can foster their interest in improving plant genomics to the best of its ability, I am looking forward to the opportunity to teach in the plant genomics and bioinformatics undergraduate major as well as other graduate groups.

I am looking forward to a teaching opportunity in the plant genomics and bioinformatics undergraduate major and other graduate groups to share what I have learned, inspire students to develop independent thinking and assist in the development of young professionals to foster their interest in improving the plant genomics to the best of its form. By putting a lot of effort into research-driven classroom instruction, I strive to achieve a variety of research goals. I make an effort to ensure that students understand the challenging ideas in plant genomics and bioinformatics, as well as how to apply those ideas to actual issues. As the majority of outstanding ideas come from independent thought, I also promote logical and critical thinking. My core teaching objective will be to help the students learn to actively think and pursue their independent thinking. Throughout my research career, I have generated independent thoughts and effective independent collaborations. The majority of classroom instruction today is centred on earning grades, but I wish to start initiatives that link classroom instruction to research topics, so that a trained candidate might be encouraged further to pursue scientific objectives.

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

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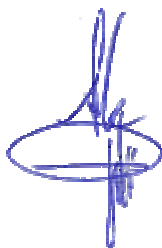
Legnaro, October 1st 2022

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", written over a horizontal line.

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

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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

Letter of Reference to Dr. Gaurav SABLOK

August 30th, 2022

PhD Dr. Nicola La Porta
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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 is positioned centrally below the typed name.



**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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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

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
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