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 anlaysis 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 spent 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*, *Chaetospiridium 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, 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.

From 2022-2023, i added several new skills as a carrier 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. 2024 onwards, I worked at Universitat Potsdam, Germany, where I am currently based and working on my code and approach development, submitting applications for position and self-learnt Julia, GO and Javascript, adding Java (if needed) and approaches for machine and deep learning. During the time, I benchmarked PacBioHifi genome analysis 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 and javascript with added skills of deployment using the 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 also learning ArcPy to link the geospatial analysis and deep learning approaches to merge the analysis. 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, I have also created a number of marker-based strategies. 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 2024.

GAURAV SABLOK
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ORCID: https://orcid.org/0000-0002-4157-9405
WOS: https://www.webofscience.com/wos/author/record/C-5940-2014

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 inlcuding stagging, rebasing, stashing, commiting
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.

Areas of Interest:

Bioinformatics,Deep Learning,RAG,Language Models and Graphs.
Priority Language: Python, R, Ruby, Julia, Javascript, Shell, Awk, Nextflow
Machine/Deep Learning:PyTorch, Tensorflow, XGBoost, Scikit-learn, Keras, LightGBM, Fastai.
Package Development: Python, Julia, Ruby.
API Development using FASTAPI
Documentation: Markdown, ReadTheDocs, MkDocs, Jekyll, Github Pages, Quatro

DevOPs
Priority Language: Shell, NuShell, Awk, Python, Nodejs
Code Management: Git, GitKraken.
Application deployment: Docker
Orchestration:Terraform, Kubernetes.
Database Management: SQlite3, MySQL, MongoDB.
HPC management: PBS and SLURM as job scheduler

Web Develpoment:
Priority Language: Ruby on Rails, Streamlit, Python Shiny/ShinyExpress, Django, Julia, Flask, HTML, Javascript

Application Development:
Priority Language: Learning Electron, PyQT, PyGTK, Typescript

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 (JNVU), India.

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.
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6. 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**.
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8. Zanardo M, Rosselli R, Meneghesso A, **Sablok G**, Stevanato P, Engel M, Altissimo A, Peserico L, Dezuani V, Concheri G, Schloter 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**
9. 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.
10. 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**.
11. 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**
12. **Gaurav Sablok$**, Kun Yang, Chen Rui, Xiaopeng Wen (2017) tRNA derived smallRNAs: smallRNA reportoire has yet to be decoded in plants. **Front. Plant Sci. doi: 10.3389/fpls.2017.01167**
13. Florian Mattenberger, Beatriz Sabater-Muñoz, Christina Toft, **Gaurav Sablok**, Mario A Fares (2017) Expression properties exhibit correlated patterns with the fate of duplicated genes, their divergence, and transcriptional plasticity in Saccharomycotina. **DNA Research. doi: 10.1093/dnares/dsx025**
14. Salvatore Camiolo, **Gaurav Sablok**, Andrea Porceddu (2017) The Evolutionary Basis of Translational Accuracy in Plants. G3: GENES, GENOMES, GENETICS. **doi: 10.1534/g3.117.040626.**
15. **Gaurav Sablok$***, 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**
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method for cell line specific microRNA target prediction that integrates Ago2 CLIP-Seq and validated microRNA–target interaction data. **Nucleic Acids Research 45: e42**

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24. Marina Zanardo, Riccardo Rosselli, Andrea Meneghesso, **Gaurav Sablok**, Piergiorgio Stevanato, Adriano Altissimo, Lisanna Perserico, Valentina Dezuani, Giuseppe Concheri, Michael Schloter, 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**.
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29. **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**.
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34. Miroslaw Kwasniewski, Agata Daszkowska-Golec, Agnieszka Janiak, Chwialkowska 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**
35. 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**.
36. 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**.
37. **Gaurav Sablok**[$], 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**.
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Biomedicine 119:53-62.

42. 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**.
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45. 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**.
46. 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**.
47. 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**.
48. 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. P**lant Physiology and Biochemistry 84C: 105-114**.
49. **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**.
50. 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**
51. 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**.
52. 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.**
53. **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.**
54. **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**.
55. 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**.
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splicing events in Brachypodium distachyon. **DNA Research. 20: 163-171**.

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71. G Sablok[§], P Gahlot, AK Gupta, Pareek K and NS Shekhawat (2009) Extraction of PCR-usable DNA using modified CTAB method from the Resource Trees adapted to arid environment sustainability. **Plant Omics Journal 2:103-109**.

Peer reviewed Abstracts and Posters ([§]Corresponding Author):

1. Gaurav Sablok, Xiaolan He, Mari Miranto, Elina Peltomaa, Robin Sleith, Kenneth Karol, Charles Delwiche, Neil Bell, Lars Paulin, Peter Poczai, Jaakko Hyvönen (2019) First draft genome assembly of Coleochaete orbicularis (2019) 5th Conference on Plant Genome Evolution Conference, Spain.
2. Gaurav Sablok**,** Xiaolan He, Mari Miranto, Jorge R. Flores, Elina Peltomaa, Robin Sleith, Kenneth Karol, Charles Delwiche, Neil Bell, Lars Paulin, Peter Poczai, Jaakko Hyvönen (2019) Mitogenomics of *Blasia pusilla* as a tool for agricultural productivity. 3rd Agriculture and Climate Change Conference. Budapest, Hungary P102
3. Gaurav Sablok**,** Xiaolan He, Mari Miranto, Elina Peltomaa, Jorge R. Flores, Robin Sleith, Kenneth Karol, Charles Delwiche, Neil Bell, Lars Paulin, Peter Poczai, Jaakko Hyvönen (2019) Gametophytic transcriptomics of an early embryophyte (*Blasia pusilla*) and comparative landscape of gametophyte evolution. The 3rd International Symposium on Frontiers in Molecular Science - RNA Regulatory Networks 26–28 June 2019, Lisbon, Portugal.
4. Gaurav Sablok, Andres Orejuela, Xiaolan He, Jaakko Hyvönen, Tiina Särkinen, Péter Poczai **(2019)** Complete plastid genome sequence of African nightshade (*Solanum scabrum)* and its comparative plastomics across Solanales. ESEB Congress 2019, Turku, Finland.
5. Gaurav Sablok**,** Xiaolan He, Mari Miranto, Elina Peltomaa, Robin Sleith, Kenneth Karol, Charles Delwiche, Neil Bell, Lars Paulin, Peter Poczai, Jaakko Hyvönen (2018) Plastomics of charophycean *Coleochaete orbicularis* and embryophyte *Blasia pusilla*. European Conference on Computational Biology, poster 541.
6. Gaurav Sablok**,** Xiaolan He, Mari Miranto, Elina Peltomaa, Neil Bell, Lars Paulin, Peter Poczai, Jaakko Hyvönen **(2018)** The first draft genome of Blasia pusilla using SMRT sequencing. EMBO Plant Evo Abstract number: 74.
7. Ganesh Nikalje, Ashish Kumar Srivastava, **Gaurav Sablok**, Tukaram Nikam and Suprasanna Penna (2015) Integrating RNA transcriptome wide and microRNA analyses for the identification of molecular regulators associated with high salt tolerance in Sesuvium portulacastrum (L.) poster presented in 3rd International Plant Physiology Congress, JNU, New Delhi, India pp. 202.
8. Yuan Fu, Michele Poli, Gaurav Sablok, Violeta Velikova, Yanchun Liang, Francesco Loreto, Mingai Li, Claudio Varotto (2016) Dissection of early transcriptional responses to water stress in Arundo donax L. by unigene-based RNA-Seq. Proceedings of the Joint Congress SIBV-SIGA. Milano, Italy – 8/11 September, 2015. ISBN 978-88-904570-5-0

9. Min XJ, Powell B, Braessler J, Meinken J, Yu F, Sablok G (2015) Genome-wide comparative analyses of alternative splicing genes in cereal plants. Great Lakes Bioinformatics (GLBIO2015), May 16-18, Purdue University, Indiana.
10. Ralph P, Schliep M, Pernice M, Sinutok S, Webster L, Elgetti Brodersen K, Trevathan-Tackett S, Manojlovic B, Apichanangkool P, Sablok G, Davey P, Chotikarn P, Thomson A, Macreadie P, Rasheed M, Chartrand K, Larkum A (2014) System biology approach to understanding seagrass loss. The 11th International Seagrass Biology Workshop, Sanya, China.
11. M. A. Iquebal, Sarika, U. B. Angadi, Vasu Arora, Gaurav Sablok, Sunil Kumar, Anil Rai and Dinesh Kumar (2014), SBMDb: First whole genome based DNA microsatellite database of sugarbeet for bioenergy and industrial application. Proceedings of 2nd National Conference on Converging Technologies Beyond 2020 (2CTB-2010), University Institute of Engineering and Technology, Kurukshetra University, Kurukshetra, Haryana. Pp. 359
12. Antonella Cristofori, Nicola La Porta, Gaurav Sablok, Elisa Pellegrini, Paolo Baldi, Christina Nali, Fabiana Cristofolini, Elena Gottardini (2014). 454 sequencing to assess the differential expression of genes due to ozone stress in Viburnum lantana L.. In: Parrotta, J.E.; Moser, C.F.; Scherzer, A.J.; Koerth, N.E.; Lederle, D.R. (eds.) Sustaining forests, sustaining people: the role of research: XXIV IUFRO World Congress, Salt Lake City, USA: Commonwealth forestry association: 376. http://hdl.handle.net/10449/24993.
13. Nicola La Porta, Gaurav Sablok, Massimo Pindo, Andrea Squartini (2014). 454 Pyrosequencing analyses of mountain forest soils reveal a high fungal diversity and a rapid response to successional stages. In: Parrotta, J.E.; Moser, C.F.; Scherzer, A.J.; Koerth, N.E.; Lederle, D.R. (eds.) Sustaining forests, sustaining people: the role of research: XXIV IUFRO World Congress, Salt Lake City, USA: Commonwealth forestry association: 166. handle: http://hdl.handle.net/10449/24992.
14. Ashish K Srivastava, Gaurav Sablok, Micheal Hackenberg, U Deshpande, P Suprasanna (2014) Redox mediated regulation of microRNA, hormone homeostasis and its significance for regulating salt tolerance in Brassica juncea. "Poster Presentation" in Next Generation Scientist Conference held at John Innes Centre, Norwich, UK.
15. Piergiorgio Stevanato, Kelley Richardson, Lee Panella, Gaurav Sablok, Chiara Broccanello, Filippo Biscarini, Marcello Del Corvo, Alessandra Stella and Massimo Saccomani (2013) Identification Of SNPs Linked To Key Root Traits In Sugar Beet. Plant & Animal Genome XXI, San Diego, CA.
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 Schloter, 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 Zottele, 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, (9^{th}-13^{th} September, 2012), Basel, Switzerland. Poster D8.
19. Emiliani G, Sablok G, La Porta N. (2013) Comparative genomic analyses of rot fungi: insights into the evolution of specialized functions. In: Proceedings XIII Conference Root and Butt Rot of Forest Trees, IUFRO Working Party 7.02.01, 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. 55-57.
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, Sujan 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 2^{nd} 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. **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).
2. **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: ttp://www.springer.com/in/book/9781493972760).
3. **Gaurav Sablok** et al. Plant Metallomics and Functional Omics: A system perspective (Springer, 2018).
4. Tatiana V. Tatarinova and **Gaurav Sablok** (2012) DNA methylation Challenges and Mechanism, Nova Publishers, USA. ISBN: 978-1-62417-128-4

Book Chapters:

1. 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.
2. 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).
3. **Sablok G**, Sun K, Sun H. NAMS (2019) Noncoding Assessment of long RNAs in Magnoliophyta Species. Methods Mol Biol. 1933:257-264.
4. **Sablok G**, Yang K, Wen X (2019) Protocols for miRNA Target Prediction in Plants. Methods Mol Biol.1970:65-73.

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 Bimolecular 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.ysu.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

Invited talks and Presentations:

1. 2014 – Invited by European Union COST action programme to deliver my finding on "Variations in stress-regulated smallRNA transcriptomics of Arabidopsis thaliana", Sofia, Bulgaria.
2. 2012 – Invited to deliver a Keynote lecture on Plant and Pathogen Genomics: NGS and Cross talks at International Conference on Bioinformatics and System Biology, BIOCOMP, Varna, Bulgaria.
3. 2013 – Invited to deliver a lecture on Genome-wide landscape of alternative splicing events in Brachypodium distachyon at 1st International Brachypodium Conference, Modena, Italy.
4. 2012 – Invited to deliver a Keynote lecture on Plant and Pathogen Genomics: NGS and Cross-talk at CRIBI, University of Padova, Italy.
5. 2011 – Invited Keynote lecture on Alternative splicing, GC Biology and Evolution of Codon Biology in plant and viral genomes and their potential applications at Shenyang Agricultural University, Shenyang, China.
6. 2011 – Presented an oral presentation on Multivariate analysis revealed translational selection and mutational bias in Heterobasidion irregulare at XIII IUFRO Conference on Root and Butt Rot of Forest trees. Trento, Italy
7. 2011 – Presented an oral presentation on Comparative genomic analysis of rot fungi: insights into the evolution of specialized functions at XIII IUFRO Conference on Root and Butt Rot of Forest trees. Trento, Italy

References:

1. Jaakko Hyvönen (Employer)
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   University of Helsinki, Finland.
   Email: jaakko.hyvonen@helsinki.fi

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