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, Chaetospiridium 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, Brachpodium, 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 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.