Selcuk Journal of Agriculture and Food Sciences
http://sjafs.selcuk.edu.tr/sjafs/index
Research Article

SJAFS
(2022) 36 (Special Issue),43-47
e-ISSN: 2458-8377
DOI:10.15316/SJAFS.2022.076

Plant Viruses and Plant Growth Promoting Rhizobacteria (PGPR) Relationships: A Shiny Application

Faruk ÖNCÜ[1], Kubilay Kurtuluş BAŞTAŞ[2,*]
[1]General Directorate of Forestry, Department of Combating Forest Pests, Ankara, Türkiye
[2]Selçuk University, Faculty of Agriculture, Department of Plant Protection, Konya, Türkiye

ARTICLE INFO

Article history:
Received date: 06.12.2022
Accepted date: 14.12.2022

Keywords:
Biological Control
Database
PGPR
Plant Viruses
Shiny
Web Interface

ABSTRACT

In the face of climate change, the point of view of existing agricultural production systems is changing, and biological issues are gaining importance in terms of sustainable agriculture. Environmentally friendly biological solutions come to the forefront in the management of diseases and pests that put pressure on sustainable agriculture. It has been proven by many studies that plant growth promoting rhizobacteria (PGPR) have positive effects on plant growth, as well as reduce or prevent viral diseases. However, determining the targeted virus species, the PGPR strains used, or the plant strains tested requires a serious literature review and reading. In this study, which can be considered as a preliminary study, a database of PGPR and plant virus relations literature was created in a dynamic infrastructure that can be constantly updated, and a web interface was developed as an R/shiny application. Thanks to this preliminary study, which has examples in different fields, it is thought that it is possible for researchers to quickly access the literature on the subject, plan cost-effective projects, and identify the missing or potential points of the subject. According to the information in the database, it was determined that CMV was the most targeted virus, different strains of *Bacillus* and *Pseudomonas* genera were used the most as PGPR agent, tomato (*Solanum lycopersicum*) and cucumber (*Cucumis sativus*) were the most tested plant species, and single applications were tested more. It is thought that this and similar studies will enable researchers to gain a quick perspective on the subject, facilitate the management of the information they have acquired, and contribute to effective planning in their new studies.

1. Introduction

The threat and consequences of climate change on sustainable agriculture are becoming more visible with each passing day. In this respect, in the face of decreasing resources for ensuring food security and sustainable agriculture, more effort is needed than ever in order to protect existing assets and use them efficiently. In the activities of human beings, whose desires and needs are endless, it is essential to protect micro and macro biodiversity, as there are many points that have not been scientifically clarified, as well as the deterioration of the natural ecosystem (Chávez-Dulanto et al. 2021; Dubey et al. 2019; Nhemachena et al. 2020).

Plant growth promoting rhizobacteria (PGPR), which are a part of the natural ecosystem, directly and indirectly contribute to plant health with many interactions. PGPRs, which are of great importance for sustainable agriculture, can lead to triggering resistance against viruses or other pathogens in the host plant, thanks to their ability to affect the expression of signaling pathways or genes involved in plant defense. The discovery of this defense mechanism has revealed the possibility of using PGPRs under biological control as an alternative way to combat plant diseases. However, despite the developing technology and ever-increasing knowledge, the effects and mechanisms of PGPRs on viruses and other pathogens are not fully understood (Khoshru et al. 2020; Priya et al. 2021; Yadav 2020).

When acting with the awareness that each study contributing to the literature has a separate importance, it can be difficult to follow the studies or to control this information when the knowledge grows. In order to overcome these problems, it is necessary to follow the technological developments and ensure their use.

---

* Corresponding author email: *kbastas@selcuk.edu.tr*

However, when the data produced around the world is compared with the data processed, the difference is seen as very large. At this point, thanks to software languages such as R and Python, it becomes easier to make analyzes and inferences on the data. R software language, which is simple and fast to learn, is widely used in the academic community as it provides many uses such as statistics, analysis, modeling, bioiformatic analysis, data editing, data visualization, map creation, reproducible document creation, web environment development (Giorgi et al. 2022; Grüning et al. 2018; R Core Team 2021).

Web interfaces, which facilitate the delivery of information to large masses, both in the field of biology and in many other fields, can be developed thanks to the R/shiny package (Chang et al. 2017; Jia et al. 2022). Thanks to the R/shiny package, it is possible to design a web interface capable of analysis, as well as an interactive web interface where the information in the literature or a database is compiled and shared manually or automatically. The following are examples of web interface development studies with the R/shiny package, which were created with manually compiled information; manual compilation of xenograft studies in the model organism zebrafish, ZenoFishDb (Targen et al. 2020), manual compilation of ligand-receptor pairs in plants (Xu et al. 2022), manual compilation of metadata from terrestrial metagenome studies (Corrêa et al. 2020), manual compilation of literature on Parkinson's disease (Wang et al. 2020), manual compilation of the content of transcriptomic and proteomic datasets related to fibrosis disease (Fanidis et al. 2021).

This study was carried out as a preliminary study of the idea of developing a manually compiled database and web interface in order to provide a quick overview of the basic level information about the targeted, applied and used organisms in PGPR and plant virus association research.

2. Materials and Methods

Different databases such as Web of Science (www.webofknowledge.com) and Scopus (www.scopus.com) were searched with the keywords PGPR and plant viruses. In the results of the search, the information of the studies on the relevant subject is processed in the tables in the Excel program. In order to ensure data integrity, the names and taxonomic information of plant, virus and bacterial species were taken from the National Center for Biotechnology Information (NCBI, (Schoch et al. 2020)) and International Committee on Taxonomy of Viruses (ICTV, (Walker et al. 2022)) databases and recorded in the tables.

The data were processed in R Studio v2022.07.0 (RStudio Team 2020) environment to be suitable for analysis with different packages such as tidyverse (Wickham et al. 2019) and DT (Dowle and Srinivasan 2022) developed in the R v4.2.1 (R Core Team 2021) software language. In order to create a dynamic and interactive infrastructure, a web interface was developed with the shiny (Chang et al. 2017; RStudio Team 2013) package. The plotly (Sievert 2020) package was used to visualize the data.

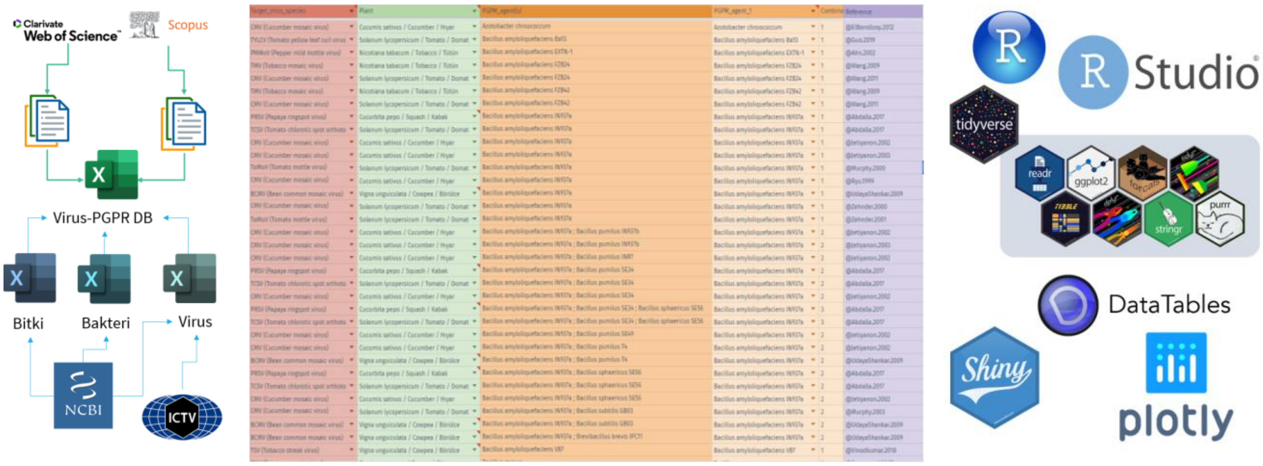
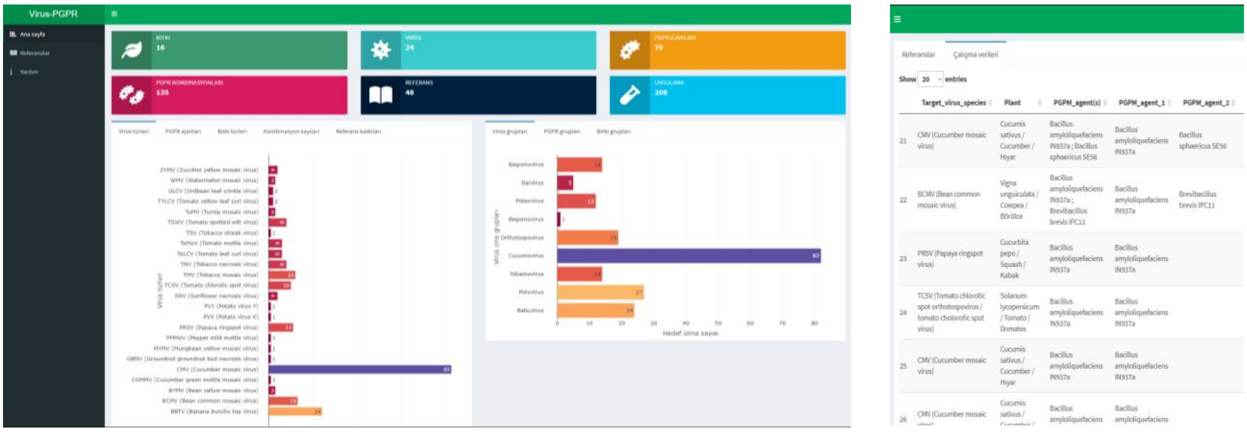


Figure 1
Work flow diagram in data collection, created main table and R packages used

3. Results and Discussion

On the main screen of the developed web interface, the total number of plant, virus and PGPR species, the sum of different single and multiple combinations, the total number of references in the database and the number of different applications are displayed. The species of plant, virus and PGPR bacteria, as well as their taxonomic groups, and the number of information provided by the references and the distribution of multiple combinations are shown in graphs (Figure 2). In addition, in the developed system, it is possible to search on the tables where the data is collected and the results can be exported. All graphics and other informative parts are updated automatically when data is added to the tables. The system can be viewed on mobile environments as well as desktops without any deterioration in graphics, and full control over all graphics and tables can be achieved.

When the graphics that are automatically generated according to the information in the database are examined, CMV (82) ranks first among 24 different virus types in terms of the targeted virus species. The targeting of CMV in many studies may be due to its ease of transport by insects and more problems due to the wide host range. The fact that virus species that cause serious damage to some warm climate plant species are also targeted, shows that the PGPR-virus issue is addressed in disease management. Bacterial species and strains used among 79 PGPR agents were classified as follows; *Bacillus amyloliquefaciens* IN937a (26), *Bacillus pumilus* SE34 (23), *Pseudomonas fluorescens* Pf 1 (18), *Pseudomonas fluorescens* CHA0 (16), *Bacillus sphaericus* SE56 (15), *Bacillus pumilus* T4 (15), *Bacillus pumilus* INR7 (11), *Bacillus pumilus* IN937b (11) and other starains (less than 10) (Figure 3).



	Target_virus_species	Plant	PGPM_agent(s)	PGPM_agent_1	PGPM_agent_2
21	CMV (Cucumber mosaic virus)	Cucumis sativus / Cucumber / Hıyar	Bacillus amyloliquefaciens IN937a ; Bacillus sphaericus SE56	Bacillus amyloliquefaciens IN937a	Bacillus sphaericus SE56
22	BCMV (Bean common mosaic virus)	Vigna unguiculata / Cowpea / Börülce	Bacillus amyloliquefaciens IN937a ; Brevibacillus brevis IPC11	Bacillus amyloliquefaciens IN937a	Brevibacillus brevis IPC11
23	PRSV (Papaya ringspot virus)	Cucurbita pepo / Squash / Kabak	Bacillus amyloliquefaciens IN937a	Bacillus amyloliquefaciens IN937a	
24	TCSV (Tomato chlorotic spot orthotospovirus / tomato cholorotic spot virus)	Solanum lycopersicum / Tomato / Domates	Bacillus amyloliquefaciens IN937a	Bacillus amyloliquefaciens IN937a	
25	CMV (Cucumber mosaic virus)	Cucumis sativus / Cucumber / Hıyar	Bacillus amyloliquefaciens IN937a	Bacillus amyloliquefaciens IN937a	
26	CMV (Cucumber mosaic	Cucumis sativus /	Bacillus amyloliquefaciens	Bacillus amyloliquefaciens	

Figure 2
General view of the developed web interface and data tables page

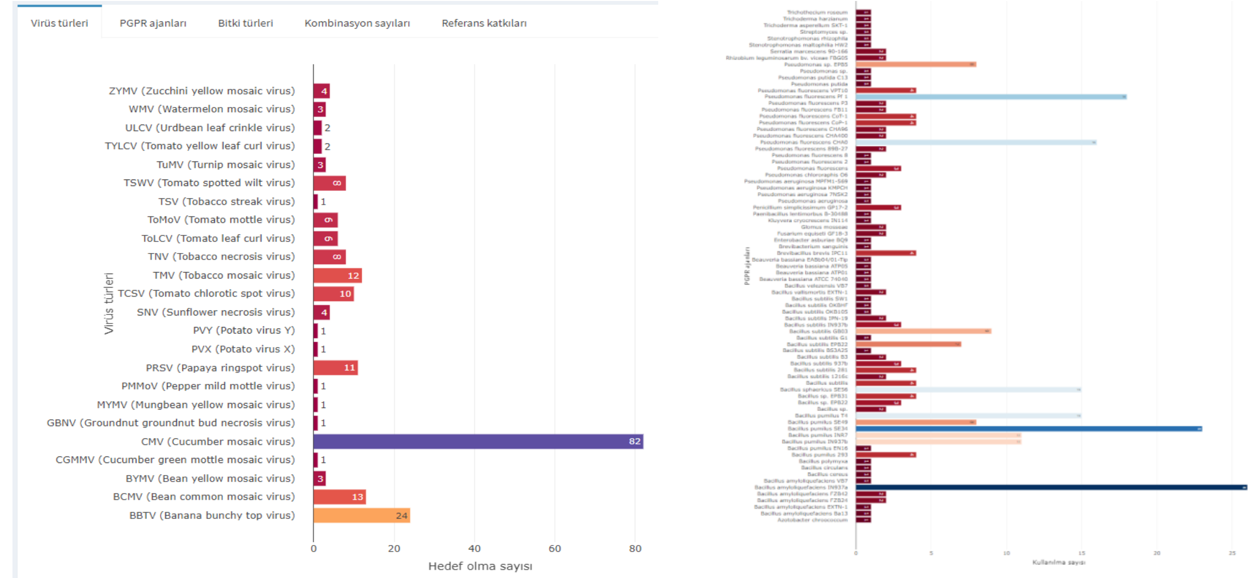


Figure 3
Graphs showing virus species and PGPR agents

On the other hand, among the 16 plant species, Solanum lycopersicum (tomato) and Cucumis sativus (cucumber) are the most studied (54-50). When it was examined how many different combinations of plants, viruses and bacteria were investigated in the studies, it was determined that the majority of them provided information in less than 10 combinations (Figure 4).

Although single (136) applications are intense in studies, multiple (72) applications are being investigated. The most common in multiple combinations are applications with two stains (63).

Cucumovirus ranks first among 9 different virus groups in terms of being a target. It is a remarkable finding that Cucumovirus (82), Potyvirus (27), and Orthotospvirus (19) genera, which include many virus species spread by vectors, are in the first place. Studies among 7 plant groups were carried out intensively on plants of the Cucurbitaceae (71) and Solanaceae (79) families. Among 15 different bacterial families, Bacilliceae (177) and Pseudomonadaceae (78) genera are used extensively in studies (Figure 5).

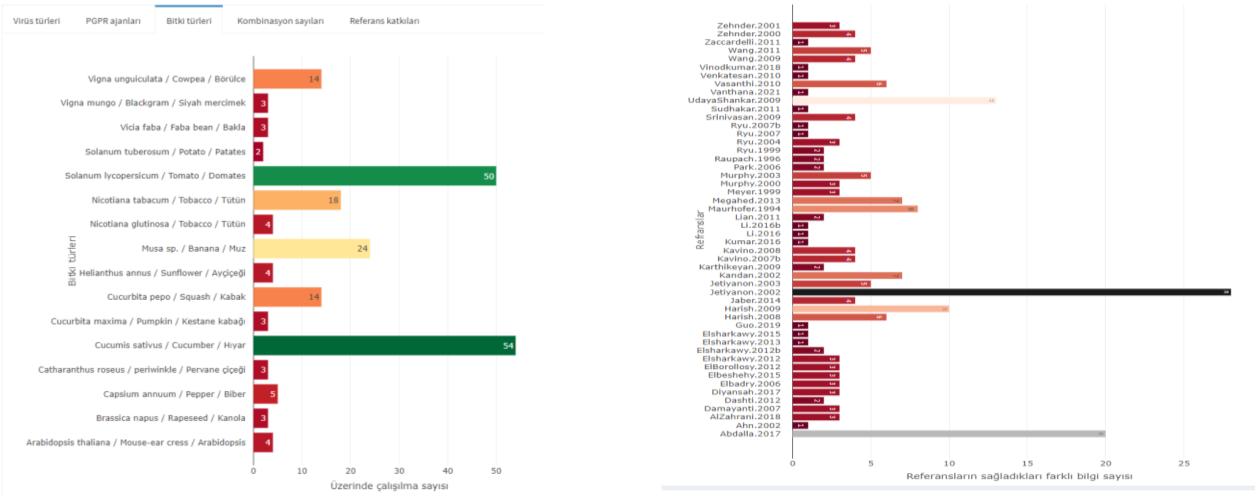


Figure 4

Graphs showing the number of studies by plant species and the number of different information provided by references

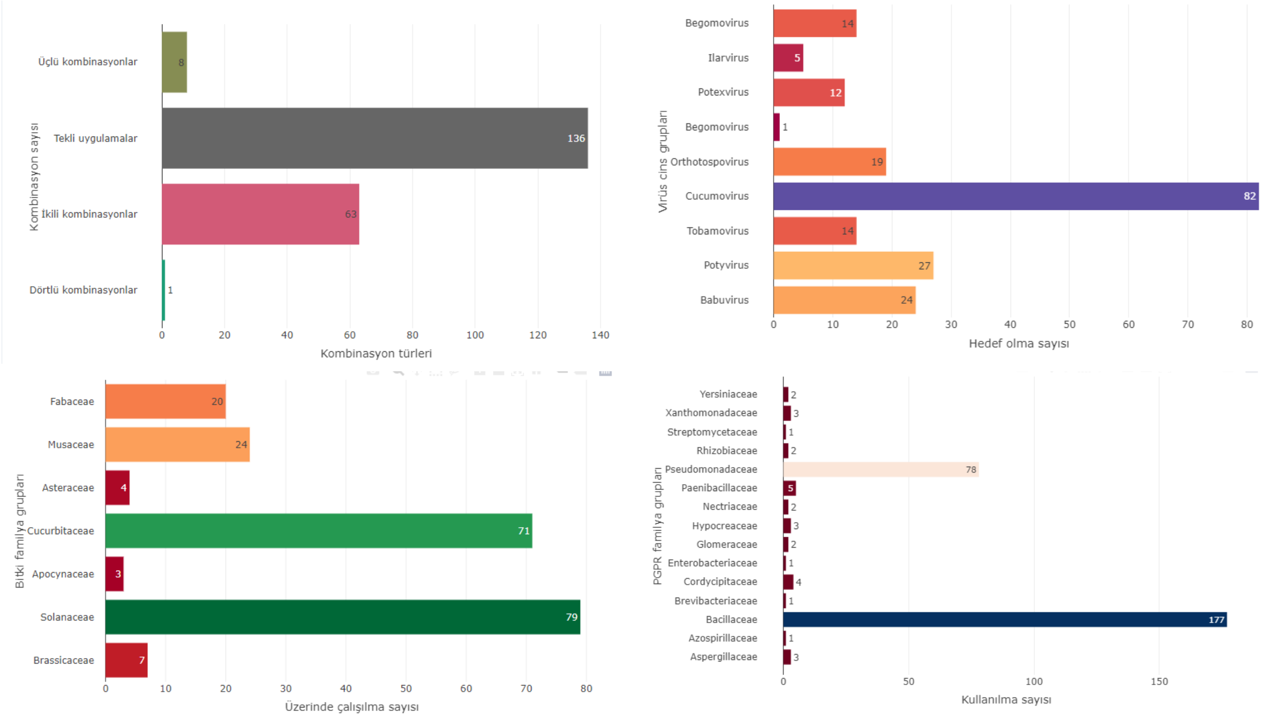


Figure 5

Graphs showing the number of single and multiple combinations, virus groups for targeting, number of studies per plant family group, and number of PGPR agents at family level

The processing and interpretation of biological data, the amount and complexity of which is rapidly increasing, becomes increasingly difficult. Thanks to the development of web interfaces and databases, it is possible to obtain information by processing biological data and make it easily accessible (Jia et al. 2022).

Having a good command of the literature plays an important role in carrying out successful studies in order to avoid repetitions unintentionally, to identify deficiencies or potential points, to plan correctly and to manage resources well (Antezana et al. 2009; Satyahadewi and Perdana 2021). Biological solutions such as PGPR are gaining more and more importance in the control of viral diseases for which there is no effective control method (Khoshru et al. 2020; Maksimov et al. 2019; Priya et al. 2021).

When the data are evaluated, although generally positive results are obtained from PGPRs in the control of plant virus diseases, it takes time for the expected effect to occur and emerge due to various limitations and deficiencies. Although it has many shortcomings, there is a need to plan different studies for the development of this emerging system. In addition, with the ideas that our study gives to the researchers, it is hoped that they will carry out similar studies on different subjects in order to evaluate the literature more effectively.

4. References

Antezana E, Kuiper M, Mironov V (2009). Biological knowledge management: the emerging role of the

Semantic Web technologies. Brief Bioinformatics 10:392–407. https://doi.org/10.1093/bib/bbp024

Chang W, Cheng J, Allaire J, Xie Y, McPherson J (2017). Shiny: web application framework for R. R package version 1:2017

Chávez-Dulanto PN, Thiry AAA, Glorio-Paulet P, Vögler O, Carvalho FP (2021). Increasing the impact of science and technology to provide more people with healthier and safer food. Food Energy Secur 10. https://doi.org/10.1002/fes3.259

Corrêa FB, Saraiva JP, Stadler PF, da Rocha UN (2020). TerrestrialMetagenomeDB: a public repository of curated and standardized metadata for terrestrial metagenomes. Nucleic Acids Res 48:D626-D632. https://doi.org/10.1093/nar/gkz994

Dowle M, Srinivasan A (2022). data.table: Extension of ‘data.frame‘ https://r-datatable.com, https://Rdatatable.gitlab.io/data.table, https://github.com/Rdatatable/data.table

Dubey A, Malla MA, Khan F, Chowdhary K, Yadav S, Kumar A, Sharma S, Khare PK, Khan ML (2019). Soil microbiome: a key player for conservation of soil health under changing climate. Biodivers Conserv 28:2405–2429. https://doi.org/10.1007/s10531-019-01760-5

Fanidis D, Moulos P, Aidinis V (2021). Fibromine is a multi-omics database and mining tool for target discovery in pulmonary fibrosis. Sci Rep 11:21712. https://doi.org/10.1038/s41598-021-01069-w

Giorgi FM, Ceraolo C, Mercatelli D (2022). The R Language: An Engine for Bioinformatics and Data Science. Life (Basel) 12. https://doi.org/10.3390/life12050648

Grüning B, Dale R, Sjödin A, Chapman BA, Rowe J, Tomkins-Tinch CH, Valieris R, Köster J (2018). Bioconda: sustainable and comprehensive software distribution for the life sciences. Nat Methods 15:475–476. https://doi.org/10.1038/s41592-018-0046-7

Jia L, Yao W, Jiang Y, Li Y, Wang Z, Li H, Huang F, Li J, Chen T, Zhang H (2022). Development of interactive biological web applications with R/Shiny. Brief Bioinformatics 23. https://doi.org/10.1093/bib/bbab415

Khoshru B, Mitra D, Khoshmanzar E, Myo EM, Uniyal N, Mahakur B, Mohapatra PKD, Panneerselvam P, Boutaj H, Alizadeh M, Cely MVT, Senapati A, Rani A (2020). Current scenario and future prospects of plant growth-promoting rhizobacteria: an economic valuable resource for the agriculture revival under stressful conditions. Journal of Plant Nutrition 43:3062–3092. https://doi.org/10.1080/01904167.2020.1799004

Maksimov IV, Sorokan AV, Burkhanova GF, Veselova SV, Alekseev VY, Shein M, Avalbaev AM, Dhaware PD, Mehetre GT, Singh BP, Khairullin RM (2019). Mechanisms of Plant Tolerance to RNA Viruses Induced by Plant-Growth-Promoting Microorganisms. Plants (Basel) 8. https://doi.org/10.3390/plants8120575

Nhemachena C, Nhamo L, Matchaya G, Nhemachena CR, Muchara B, Karuaihe ST, Mpandeli S (2020). Climate Change Impacts on Water and Agriculture Sectors in Southern Africa: Threats and Opportunities for Sustainable Development. Water 12:2673. https://doi.org/10.3390/w12102673

Priya P, Aneesh B, Harikrishnan K (2021). Genomics as a potential tool to unravel the rhizosphere microbiome interactions on plant health. J Microbiol Methods 185:106215. https://doi.org/10.1016/j.mimet.2021.106215

R Core Team (2021). R: A Language and Environment for Statistical Computing: R Foundation for Statistical Computing

RStudio Team (2013). shiny: Easy web applications in R

RStudio Team (2020). RStudio: Integrated Development Environment for R

Satyahadewi N, Perdana H (2021). Web Application Development for Inferential Statistics using R Shiny. In: Proceedings of the 1st International Conference on Mathematics and Mathematics Education (ICMMEd 2020). Atlantis PressParis, France

Schoch CL, Ciufo S, Domrachev M, Hotton CL, Kannan S, Khovanskaya R, Leipe D, Mcveigh R, O’Neill K, Robbertse B, Sharma S, Soussov V, Sullivan JP, Sun L, Turner S, Karsch-Mizrachi I (2020). NCBI Taxonomy: a comprehensive update on curation, resources and tools. Database (Oxford) 2020. https://doi.org/10.1093/database/baaa062

Sievert C (2020). Interactive web-based data visualization with r, plotly, and shiny, 1st edn. Chapman & Hall/CRC the R series. Chapman & Hall/CRC, Boca Raton

Targen S, Kaya T, Avci ME, Gunes D, Keskus AG, Konu O (2020). ZenoFishDb v1.1: A Database for Xenotransplantation Studies in Zebrafish. Zebrafish 17:305–318. https://doi.org/10.1089/zeb.2020.1869

Walker PJ, Siddell SG, Lefkowitz EJ, Mushegian AR, Adriaenssens EM, Alfenas-Zerbini P, Dempsey DM, Dutilh BE, García ML, Curtis Hendrickson R, Junglen S, Krupovic M, Kuhn JH, Lambert AJ, Łobocka M, Oksanen HM, Orton RJ, Robertson DL, Rubino L, Sabanadzovic S, Simmonds P, Smith DB, Suzuki N, van Doorslaer K, Vandamme A-M, Varsani A, Zerbini FM (2022). Recent changes to virus taxonomy ratified by the International Committee on Taxonomy of Viruses (2022). Arch Virol 167:2429–2440. https://doi.org/10.1007/s00705-022-05516-5

Wang C, Chen L, Zhang M, Yang Y, Wong G (2020). PDmethDB: A curated Parkinson’s disease associated methylation information database. Comput Struct Biotechnol J 18:3745–3749. https://doi.org/10.1016/j.csbj.2020.11.015

Wickham H, Averick M, Bryan J, Chang W, McGowan L, François R, Grolemund G, Hayes A, Henry L, Hester J, Kuhn M, Pedersen T, Miller E, Bache S, Müller K, Ooms J, Robinson D, Seidel D, Spinu V, Takahashi K, Vaughan D, Wilke C, Woo K, Yutani H (2019). Welcome to the Tidyverse. JOSS 4:1686. https://doi.org/10.21105/joss.01686

Xu C, Ma D, Ding Q, Zhou Y, Zheng H-L (2022). PlantPhoneDB: A manually curated pan-plant database of ligand-receptor pairs infers cell-cell communication. Plant Biotechnol J. https://doi.org/10.1111/pbi.13893

Yadav AN (2020). Plant Microbiomes for Sustainable Agriculture: Current Research and Future Challenges. In: Plant Microbiomes for Sustainable Agriculture. Springer, Cham, pp 475–482.