Udai B. Singh
Ravindra Kumar
Harikesh Bahadur Singh *Editors*

Detection, Diagnosis and Management of Soil-borne Phytopathogens

Springer

Detection, Diagnosis and Management of Soil-borne Phytopathogens

Udai B. Singh • Ravindra Kumar •
Harikesh Bahadur Singh
Editors

Detection, Diagnosis and Management of Soil-borne Phytopathogens

Springer

Editors
Udai B. Singh
ICAR-National Bureau of Agriculturally Important Microorganisms
Maunath Bhanjan, Uttar Pradesh, India

Ravindra Kumar
Division of Crop Protection
ICAR-Indian Institute of Wheat and Barley Research
Karnal, Haryana, India

Harikesh Bahadur Singh
Department of Biotechnology
GLA University
Mathura, Uttar Pradesh, India

ISBN 978-981-19-8306-1 ISBN 978-981-19-8307-8 (eBook)
https://doi.org/10.1007/978-981-19-8307-8

This Springer imprint is published by the registered company Springer Nature Singapore Pte Ltd.
The registered company address is: 152 Beach Road, #21-01/04 Gateway East, Singapore 189721, Singapore

Preface

About 80,000 diseases have been reported so far on different plants throughout the world, of them majority are caused by soil-borne phytopathogens. These are categorized as soil-borne diseases leading to significant crop losses around the globe. Plant diseases in general and soil-borne diseases in particular affect a wide range of crops and pose a serious challenge to food security at the global level. Soil-borne plant pathogens are characterized as omnipresent, notorious, and difficult to manage as many produce hard resting structure as sclerotia. Early, speedy and reliable detection of plant pathogens is a prerequisite to formulate suitable and accurate management strategies for the management of these catastrophic pathogens/diseases. This book volume is very particular to soil-borne diseases, a complete package having the deep knowledge covering all spheres of soil-borne plant pathogens, viz. soil-borne diseases and their impact on agricultural trade and society, detection of soil-borne plant pathogens, diagnosis of soil-borne diseases, host–pathogen interaction during development of major soil-borne diseases, exploring the microbial resources for management of phytopathogens, and most importantly the integrated management of these soil-borne phytopathogens leading to huge impact on Indian agriculture. Descriptions of cutting-edge techniques and novel approaches for the detection and early diagnosis of soil-borne pathogens are given in detail. In the last few decades, omics approaches (transcriptomics, proteomics, metabolomics, and physionomics) have been widely used to diagnose the early infection and probe the mode of action of phytopathogens and phytotoxin (s) produced by them. Traditionally, the most prevalent techniques used to identify plant pathogens relied upon culture-based morphological approaches; these methods were laborious and time-consuming. Using more than one omics approach enhances the probability of success. In this book, we provide an overview of such omics technologies and focus on methods for their integration across multiple omics layers. As compared to studies of a single omics type, multi-omics offers the opportunity to understand the flow of information that underlies the better disease diagnosis and management strategies. The main focus of the book is on the prevalence of soil-borne disease management on various important crops with use of different strategies, including seed biopriming and microbial inoculation. Further, special attention is given to the emergence of new diseases or the re-emergence of old ones on several crops. This edited book entitled *Detection, Diagnosis and*

Management of Soil-borne Phytopathogens provides a comprehensive overview on recent developments in the area of detection, diagnosis, and management of soil-borne phytopathogens at the global level. It is going to serve as a platform for showcasing the expertise of motivated scientists and researchers working in the area of detection, diagnosis, and management of soil-borne phytopathogens and allied sectors.

In this context, the present book is a topical and timely contribution on plant–microbe interactions and offers a great scope for harnessing the beneficial interactions for agricultural sustainability. This book encompasses and addresses various issues of soil-borne plant pathogens and soil-microbe interrelationship and management of these notorious pathogens that are to be modulated either by resident microbes or by their external application. The role of OMIC in detection and diagnosis of plant pathogens is discussed in detail. Main topics include the detection and diagnosis of fungal, bacterial, and viral pathogens associated with important crop plants, role of microbes in the rhizosphere, below-ground communication among the plant, pathogens, and beneficial microbes including nematophagous fungi, rhizosphere ecosystem functioning with special reference to development of plant disease, positive interaction of the plants with the beneficial soil microorganisms for inducing plant growth, conferring biotic stress tolerance and modulating several pathways of the plants for the proper establishment and protection against major soil-borne pathogens, and host–pathogen interactions leading to the disease development in plants. Further chapters focus on the role of microbial signaling and cross-talk, biofilm formation, and antimicrobial peptides with special reference to the management of plant pathogens in the rhizosphere. The book also discusses the application of microbes in biological control of plant pathogens. Descriptions of cutting-edge techniques and novel approaches make this book unique in the area of plant protection. The book provides the latest understanding of rhizosphere microorganisms for enhanced soil and plant functions, thereby improving agricultural sustainability and food and nutritional security. The aim of the book is to compile high-quality reviews and research articles offering new insight into the application of new and safer molecules, new knowledge about the biology, ecology, and management of soil-borne pathogens, and more attention towards crop and soil health. By bringing all these areas together within the ambit of this special book volume, we hope to build cohesion between conventional and most modern approaches of science to design the future path for managing the soil-borne notorious and difficult to manage pathogens. The book covers (1) impact of soil-borne phytopathogens or soil-borne diseases on agriculture and society, (2) diagnosis and molecular detection of soil-borne pathogens, (3) host–pathogen interaction during the development of soil-borne diseases, (4) understanding the below-ground communication in the rhizosphere for better plant growth, (5) omics approaches to unravel the hidden infection, (6) microbe-mediated induced systemic resistance/tolerance to soil-borne plant pathogens, and (7) microbial inventorization for sustainable crop protection and production. We expect that the book would be useful for students, agricultural scientists, biotechnologists, plant pathologists, mycologists, and microbiologists, the farming community, scientists of R&D organizations, as

well as the teaching community and policymakers to understand the impact of plant pathogens and their role in agricultural production and national economy as a whole and provide directions for the future course of action.

Maunath Bhanjan, Uttar Pradesh, India — Udai B. Singh
Karnal, Haryana, India — Ravindra Kumar
Mathura, Uttar Pradesh, India — Harikesh Bahadur Singh

Contents

Editors and Contributors

About the Editors

Udai B. Singh presently works as a Scientist (Senior Scale) in the Plant-Microbe Interaction and Rhizosphere Biology Lab, ICAR-National Bureau of Agriculturally Important Microorganisms, Kushmaur, Maunath Bhanjan, Uttar Pradesh, India. His specialized areas are plant-microbe interactions in the rhizosphere with special reference to biotic and abiotic stress management/molecular biology/biotechnology/plant pathology. As an active researcher, Dr. Singh has published many research and review articles in the journals of national and international repute and book chapters in edited books. He has developed some microbial-based bioformulations/technologies for sustainable crop production. His team has developed databases and web-based portals for public use. His developed portal (www.mgrportal.org.in) has been awarded copyright. Dr. Singh has been awarded "DST Young Scientist" under Fast-Track Scheme, "Young Scientist award" of RASSA, New Delhi, Bharat Shiksha Ratan Award, K.P.V. Menon and Prof. K.S. Bilgrami Best Poster Award for the Year 2018 by Indian Phytopathological Society, New Delhi, and Indian Society of Mycology & Plant Pathology, Udaipur.

Ravindra Kumar is currently working as a Scientist Sr. Scale (Plant Pathology) at the Division of Crop Protection, ICAR-Indian Institute of Wheat and Barley Research, Karnal-132,001 (Haryana). He received his B.Sc. (Ag.) from C.C.S. University, Meerut; and his M.Sc. (Ag.) and Ph.D. (Ag.) from the Department of Mycology and Plant Pathology, Banaras Hindu University, Varanasi, India. His areas of research interest are plant disease management, biological control, seed pathology, and plant–microbe interaction. He has published more than 35 research papers and reviews in reputed national and international journals. He has 2 textbooks, 2 edited books (one with Springer), 14 book chapters, 8 technical bulletins, and more than 50 technical/popular articles to his credit. Dr. Kumar is also a life member of the Indian Phytopathological Society, New Delhi; Indian Society of Mycology and Plant Pathology, Udaipur; Indian Society of Seed Technology, New Delhi; and Society for Advancement of Wheat and Barley Research (SAWBAR), Karnal.

Harikesh Bahadur Singh presently a Distinguished Professor, Department of Biotechnology, GLA University, Mathura. Prior to this assignment he served as Professor and Head of the Department of Mycology and Plant Pathology at the Institute of Agricultural Sciences, Banaras Hindu University. He also served the State Agriculture University, Central University, and CSIR institutes in teaching, research, and extension roles. His major research focus is on bioinoculants, biological control of plant pathogens, and nanobiotechnology. Professor Singh has been honored with several national awards for his key role in popularizing organic farming and translating agriculturally important microorganisms from lab to land. In recognition of his scientific contributions and leadership in the field of plant pathology, he has been honored with several prestigious awards, notably the CSIR Technology Prize for Biological Sciences, M. S. Swaminathan Award, Vigyan Bharti Award, Prof. V. P. Bhide Memorial Award, Scientist of Excellence Award, BRSI Industrial Medal Award, Sangam Jyoti Award, Akshyavat Samman Award, Distinguished Scientist Award, Prof. Panchanan Maheshwari Medal, Rashtriya Gaurav Award, Plant Pathology Leader Award by IPS, CSIR Award for S&T Innovation for Rural Development (CAIRD), Environment Conservation Award, Vigyan Ratna by CSTUP, and C N R Rao Award by BHU. Dr. Singh has been a fellow of the National Academy of Agricultural Sciences. Currently, he is serving as an associate/academic/board editor for journals of international repute. Dr. Singh has more than 350 publications to his credit, 34 edited books from CABI, Springer, CRC, and Elsevier, and 20 patents (USA, Canada, and PCT). He has successfully transferred several microbe-based technologies for commercial production of biopesticides to several industrial houses in India.

Contributors

Sanghmitra Aditya ICAR-Indian Agricultural Research Institute, New Delhi, India

Rashmi Aggarwal Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India

B. R. Ajesh Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra, India

M. Amrutha Lakshmi ICAR-Indian Institute of Oil Palm Research, Pedavegi, Andhra Pradesh, India

Gautam Anand Department of Plant Pathology and Weed Research, Agricultural Research Organization, The Volcani Center, Rishon LeZion, Israel

Giabardo Anita University of Georgia, Athens, GA, USA

Addanki Venkata Avinash Università degli Studi di Padova, Legnaro, PD, Italy

B. M. Bashyal Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India

Joshua Benjamin Georg-August-Universität Göttingen, Göttingen, Germany

Priya Bhargava Department of Plant Pathology, Chaudhary Sarwan Kumar Himachal Pradesh Agricultural University (CSK HPAU), Palampur, Himachal Pradesh, India

Tanmaya Kumar Bhoi Forest Protection Division, ICFRE-Arid Forest Research Institute (AFRI), Jodhpur, Rajasthan, India

Tsewang Chosdon School of Agriculture, Lovely Professional University, Phagwara, Punjab, India

Sharani Choudhury ICAR-National Institute for Plant Biotechnology, Indian Agricultural Research Institute, New Delhi, India

Sudipta Das ICAR-National Bureau of Agriculturally Important Microorganisms, Mau, Uttar Pradesh, India

Manashi Debbarma School of Crop Protection, College of Post-Graduate Studies in Agricultural Sciences, Central Agricultural University (Imphal), Umiam, Meghalaya, India

Konjengbam Sarda Devi ICAR Research Complex for NEH Region, Manipur Centre, Imphal, India

Nongthombam Olivia Devi School of Crop Protection, College of Post-Graduate Studies in Agricultural Sciences, Central Agricultural University (Imphal), Umiam, Meghalaya, India

Dalvir Kaur Dhadly Department of Plant Pathology, Punjab Agricultural University, Ludhiana, India
Department of Plant Pathology, College of Agriculture, CSKHPKV, Palampur, Himachal Pradesh, India

Abdul Gafur Sinarmas Forestry Corporate Research and Development, Perawang, Indonesia

Abhijeet Ghatak Department of Plant Pathology, Bihar Agricultural University (BAU), Bhagalpur, Bihar, India

Amrita Gupta ICAR-Indian Institute of Seed Sciences, Mau, Uttar Pradesh, India

Rupali Gupta Department of Plant Pathology and Weed Research, Agricultural Research Organization, The Volcani Center, Rishon LeZion, Israel

Monika Hajong School of Crop Protection, College of Post-Graduate Studies in Agricultural Sciences, Central Agricultural University (Imphal), Umiam, Meghalaya, India

Mohammad Jonaid Hossain Universitat Politècnica de València, Valencia, Spain

Talat Ilyas Plant-Microbe Interaction and Rhizosphere Biology Lab, ICAR-National Bureau of Agriculturally Important Microorganisms, Kushmaur, Maunath Bhanjan, Uttar Pradesh, India

K. Jayalakshmi ICAR-Directorate of Onion Garlic Research, Pune, Maharashtra, India

Parul Johri Amity Institute of Biotechnology, Amity University Uttar Pradesh, Lucknow, Uttar Pradesh, India
Department of Biotechnology, Dr. Ambedkar Institute of Technology for Handicapped, Kanpur, Uttar Pradesh, India

Monika Karn Department of Plant Pathology, Dr Yashwant Singh Parmar University of Horticulture and Forestry (YSPUH&F), Nauni, Solan, Himachal Pradesh, India

Abhijeet S. Kashyap ICAR-National Bureau of Agriculturally Important Microorganisms, Mau, Uttar Pradesh, India

Prem Lal Kashyap ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India

J. Keerthana Indira Gandhi Krishi Viswavidyalaya, Raipur, Chattisgarh, India

Ifrah Khan Forest Protection Division, ICFRE-Arid Forest Research Institute (AFRI), Jodhpur, Rajasthan, India

Noopur Khare Faculty of Biotechnology, Institute of Bio-Sciences and Technology, Shri Ramswaroop Memorial University, Lucknow, Uttar Pradesh, India

Ankush Kumar ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India

Ravindra Kumar Division of Crop Protection, ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India

Sudheer Kumar ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India

Usha Kumari Department of Agricultural Chemicals, ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India

V. Mageshwaran ICAR-National Bureau of Agriculturally Important Microorganisms, Kushmaur, Mau Nath Bhanjan, Uttar Pradesh, India

Prasanta Kumar Majhi Odisha University of Agriculture and Technology, Regional Research and Technology Transfer Station (RRTTS), Keonjhar, Odisha, India

Dipali Majumder School of Crop Protection, College of Post-Graduate Studies in Agricultural Sciences, Central Agricultural University (Imphal), Umiam, Meghalaya, India

Deepti Malviya Plant-Microbe Interaction and Rhizosphere Biology Lab, ICAR-National Bureau of Agriculturally Important Microorganisms, Kushmaur, Maunath Bhanjan, Uttar Pradesh, India

Gaddam Manoj Citrus Center, Texas A&M University Kingsville, Weslaco, TX, USA

Pradeep Manyam S V Agricultural College, Tirupati, Andhra Pradesh, India

Nazia Manzar ICAR-National Bureau of Agriculturally Important Microorganisms, Mau, Uttar Pradesh, India

Manish Mathur Amity University Uttar Pradesh, Lucknow, India

Yalavarthi Nagaraju ICAR-National Bureau of Agriculturally Important Microorganisms, Mau, Uttar Pradesh, India

B. K. Namriboi Department of Plant Pathology, GBPUA&T, Pantnagar, Uttarakhand, India

Rakesh Pandey Department of Microbial Technology and Nematology, CSIR-Central Institute of Medicinal and Aromatic Plants, Lucknow, India

Rahat Parveen Faculty of Biotechnology, Institute of Bio-Sciences and Technology, Shri Ramswaroop Memorial University, Lucknow, Uttar Pradesh, India

Neeta Pathaw ICAR Research Complex for NEH Region, Manipur Centre, Imphal, India

S. T. Prashantha Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India

Upasna Priya Department of Plant Pathology, Bihar Agricultural University (BAU), Bhagalpur, Bihar, India

Jai P. Rai Department of Mycology and Plant Pathology, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India

Atiraj Rathi Forest Protection Division, ICFRE-Arid Forest Research Institute (AFRI), Jodhpur, Rajasthan, India

Manda Raghavendra Reddy Wageningen University and Research, Wageningen, The Netherlands

Aradhana Sagwal ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India

Pramod K. Sahu Plant-Microbe Interaction and Rhizosphere Biology Lab, ICAR-National Bureau of Agriculturally Important Microorganisms, Kushmaur, Maunath Bhanjan, Uttar Pradesh, India

R. Saranya ICAR-Central Arid Zone Research Station, Jaisalmer, Rajasthan, India

M. S. V. Satyanarayana School of Crop Protection, College of Post-Graduate Studies in Agricultural Sciences, Central Agricultural University (Imphal), Umiam, Meghalaya, India

Khanna Sayesha Universitat Politècnica de València, Valencia, Spain

Zaryab Shafi Plant-Microbe Interaction and Rhizosphere Biology Lab, ICAR-National Bureau of Agriculturally Important Microorganisms, Kushmaur, Maunath Bhanjan, Uttar Pradesh, India

Mohammad Shahid Plant-Microbe Interaction and Rhizosphere Biology Lab, ICAR-National Bureau of Agriculturally Important Microorganisms, Kushmaur, Maunath Bhanjan, Uttar Pradesh, India

N. Sharath ICAR-Directorate of Onion Garlic Research, Pune, Maharashtra, India

Shikha Sharma Department of Plant Pathology, Punjab Agricultural University, Ludhiana, India
Department of Plant Pathology, College of Agriculture, CSKHPKV, Palampur, Himachal Pradesh, India

Susheel Kumar Sharma ICAR Research Complex for NEH Region, Manipur Centre, Imphal, India
Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India

Ravi Kumar Shekhar ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India

Alok K. Singh ICAR-National Bureau of Agriculturally Important Microorganisms, Mau, Uttar Pradesh, India

Dikchha Singh ICAR-National Bureau of Agriculturally Important Microorganisms, Mau, Uttar Pradesh, India

G. P. Singh ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India

Harikesh Bahadur Singh Department of Biotechnology, GLA University, Mathura, Uttar Pradesh, India

Harsh V. Singh Plant-Microbe Interaction and Rhizosphere Biology Lab, ICAR-National Bureau of Agriculturally Important Microorganisms, Kushmaur, Maunath Bhanjan, Uttar Pradesh, India

Indar Singh Forest Protection Division, ICFRE-Arid Forest Research Institute (AFRI), Jodhpur, Rajasthan, India

Raghuveer Singh ICAR Research Complex for NEH Region, Arunachal Pradesh Centre, Basar, Telangana, India

S. K. Singh ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India

Sachidanand Singh Department of Biotechnology, Vignan's Foundation for Science, Technology and Research (Deemed to be University), Guntur, Andhra Pradesh, India
Department of Biotechnology, Smt. S. S. Patel Nootan Science and Commerce College, Sankalchand Patel University, Visnagar, Gujarat, India

Sangeeta Singh Forest Protection Division, ICFRE-Arid Forest Research Institute (AFRI), Jodhpur, Rajasthan, India

Satyendra Pratap Singh Pharmacognosy Division, CSIR-National Botanical Research Institute, Lucknow, India

Udai B. Singh ICAR-National Bureau of Agriculturally Important Microorganisms, Maunath Bhanjan, Uttar Pradesh, India

Diksha Sinha Department of Plant Pathology, Chaudhary Sarwan Kumar Himachal Pradesh Agricultural University (CSK HPAU), Palampur, Himachal Pradesh, India

Seweta Srivastava School of Agriculture, Lovely Professional University, Phagwara, Punjab, India

Sushanti Thokchom School of Crop Protection, College of Post-Graduate Studies in Agricultural Sciences, Central Agricultural University (Imphal), Umiam, Meghalaya, India

Jyotsana Tilgam ICAR-National Bureau of Agriculturally Important Microorganisms, Mau, India
ICAR-National Institute for Plant Biotechnology, Indian Agricultural Research Institute, New Delhi, India

Rajesh K. Tiwari Amity University Uttar Pradesh, Lucknow, India

Ratan Tiwari ICAR-Indian Institute of Wheat and Barley Research, Karnal, Haryana, India

Mala Trivedi Amity University Uttar Pradesh, Lucknow, India

Shaloo Verma ICAR-National Bureau of Agriculturally Important Microorganisms, Mau, Uttar Pradesh, India

Shailesh K. Vishwakarma Plant-Microbe Interaction and Rhizosphere Biology Lab, ICAR-National Bureau of Agriculturally Important Microorganisms, Kushmaur, Maunath Bhanjan, Uttar Pradesh, India

Vipula Vyas Forest Protection Division, ICFRE-Arid Forest Research Institute (AFRI), Jodhpur, Rajasthan, India

Bavita Yadav Plant-Microbe Interaction and Rhizosphere Biology Lab, ICAR-National Bureau of Agriculturally Important Microorganisms, Kushmaur, Maunath Bhanjan, Uttar Pradesh, India

Dinesh Yadav Department of Biotechnology, Deen Dayal Upadhyaya Gorakhpur University, Gorakhpur, Uttar Pradesh, India

Manoj Kumar Yadav ICAR-Indian Agricultural Research Institute, Regional Station, Karnal, Haryana, India

Soil-Borne Viruses: Outlook on Community and Recent Advances in Detection

1

Shikha Sharma, Dalvir Kaur Dhadly, Neeta Pathaw, Konjengbam Sarda Devi, Raghuveer Singh, and Susheel Kumar Sharma

Abstract

Plant viruses are transmitted via various means, and a number of them belonging to different genera are transmitted through soil. The soil-borne viruses are found throughout the world and infect a variety of economically important crops including wheat, potato, fruit crops, barley, etc. Control strategies to minimize the losses caused due to viruses in general are very few, and the very persistence nature of these viruses makes them more difficult to be understood and managed. Research on the diversity of soil-borne viruses is still lacking. Early and reliable detection of plant pathogens is prerequisite to design an effective and sustainable disease management strategy. Traditionally, symptomatology, indexing, or visual methods were used for detection of viruses. But these techniques are time-consuming and laborious. Recent advances in molecular detection strategies

S. Sharma (✉)
Department of Plant Pathology, College of Agriculture, CSKHPKV, Palampur, Himachal Pradesh, India

Department of Plant Pathology, Punjab Agricultural University, Ludhiana, Ludhiana, India
e-mail: shikhasharmapp@hillagric.ac.in

D. K. Dhadly
Department of Plant Pathology, Punjab Agricultural University, Ludhiana, Ludhiana, India

N. Pathaw · K. S. Devi
ICAR Research Complex for NEH Region, Manipur Centre, Imphal, India

R. Singh
ICAR Research Complex for NEH Region, Arunachal Pradesh Centre, Basar, Telangana, India

S. K. Sharma (✉)
ICAR Research Complex for NEH Region, Manipur Centre, Imphal, India

Division of Plant Pathology, ICAR-Indian Agricultural Research Institute, New Delhi, India

U. B. Singh et al. (eds.), *Detection, Diagnosis and Management of Soil-borne Phytopathogens*, https://doi.org/10.1007/978-981-19-8307-8_1

offer to improve accuracy and reliability and overcome the abovementioned limitations. The nucleic acid and protein-based detection techniques as well as development of onsite detection assays, viz., next-generation sequencing, DNA fingerprinting, isothermal amplification, serology, and biochemical assays, have revolutionized the outlook on detection of plant viruses due to their high degree of specificity and reliability.

Keywords

Soil-borne Viruses · ssRNA · Virus indexing · Next generation sequencing · DNA fingerprinting · Isothermal amplification · Serology

1.1 Introduction

The transmission of the majority of the plant viruses is via biological vectors mainly arthropods onto the aerial parts of the plant (Hull 2013). However, some viruses that are also transmitted via soil are referred to as soil-borne viruses (SBVs), which cause diseases in many important crops, viz., potato, wheat, fruit crops, barley, groundnut, sugar beet, etc. SBVs are ubiquitous in nature and if once established in the field, their eradication can be very difficult, hence causing yield losses in many crops (Roberts 2014). Similar to other proteins, viruses, due to their nucleo-proteinaceous properties, can be adsorbed by colloidal particles in the soil, e.g., clays, and this phenomenon keeps them infective for longer periods of time. Currently, there are few effective arsenals against SBVs at our disposal like cultivation of resistant varieties and chemical control, while resistant cultivars are limited in number. Moreover, chemical control is expensive and leads to environmental and health hazards (Roberts 2014). The transmission of SBVs can be either via abiotic means or via biotic means including soil-inhabiting organism, viz., fungi, plasmodiophorids, and nematodes. A total of 15 genera of viruses including two unassigned genera are soil-borne belonging to families *Secoviridae*, *Potyviridae*, *Ophioviridae*, *Tombusviridae*, and *Virgaviridae* or unassigned family.

Hewitt et al. (1958) were the pioneers in discovering that soil-borne fanleaf virus of grapevine, vectored by *Xiphinema index* in 1958. This discovery started the search on nematodes vectoring SBVs. However, earlier in 1886, Mayer (1886) proposed the idea of soil transmission of viruses. The soil-borne viruses are distinct from other viruses because they are subjected to different anatomy, patterns of gene expression, external environmental conditions, and anti-viral defense in the roots than the shoot region of the plant (Andika et al. 2016). Surprisingly, all the known SBVs transmitted by vectors have RNA as their genomic nucleic acid (positive sense (+) single-stranded RNA (ssRNA) genome) except for the two genera of viruses, viz., *Ophiovirus* and *Varicosavirus*, whose member viruses are composed of negative sense (−) ssRNA genomes (Verchot-Lubicz 2003; Kormelink et al. 2011). The difficulty in studying these viruses leaves us with scanty knowledge *w.r.t.* their biology, and it is highly likely that there can be more unknown genera of viruses

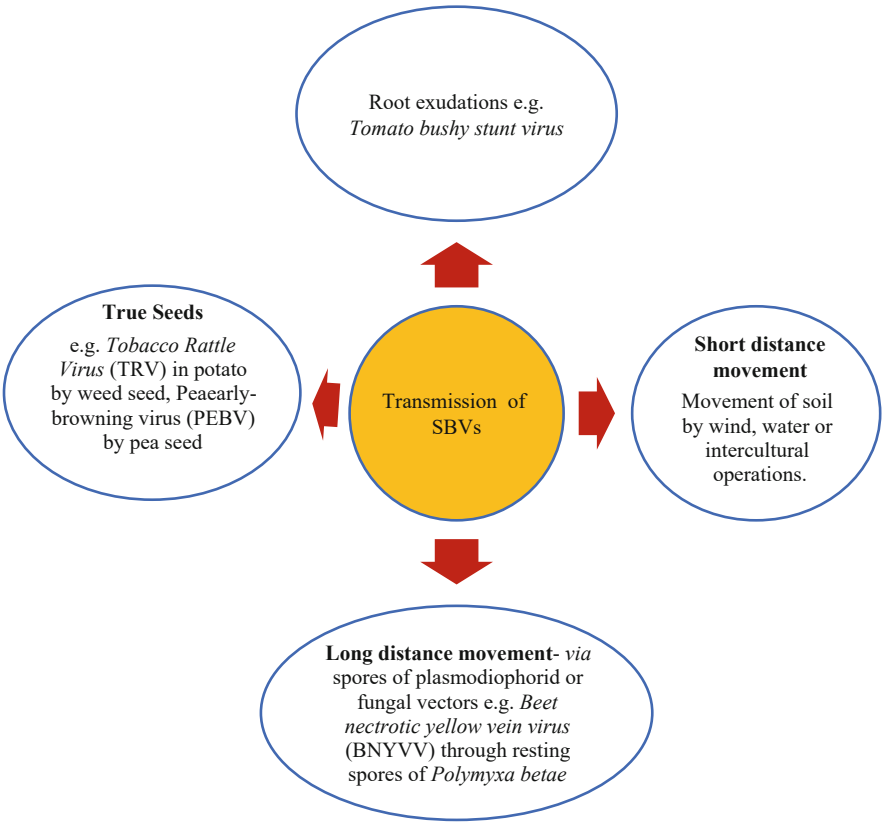

Fig. 1.1 Diagrammatic representation of transmission and movement of soil-borne viruses (SBV)

which may belong to category of soil-borne in nature (Roberts 2014; Andika et al. 2016).

The viruses enter the plant system either via injury on roots created by feeding of nematodes or during colonization of soil-inhabiting fungi. Upon entering the plants, the virus travels upwards using plant's vascular system after producing disease symptoms on the roots, e.g., *Beet necrotic yellow vein virus* (BNYVV; genus *Benyvirus*) causes Rhizomania disease in sugarbeet. Rhizomania disease causes excessive growth of side roots and rootlets while taproots remain stunted (Tamada et al. 1999). Symptoms can also be produced on aerial parts of the plant due to pathogenesis of roots, e.g., yellow mosaic symptoms accompanied with stunting of plants are produced on winter cereal crops due to infection of *Barley yellow mosaic virus* (BaYMV; genus *Bymovirus*) (Kühne 2009). Another example of aerial symptomatology due to virus infection is by *Peanut clump virus* (PCV) which belongs to genus *Pecluvirus*. The infection of PCV leads to appearance of mottling and chlorotic rings on leaves and stunting of infected plants (Thouvenel and Fauquet 1981; Dieryck et al. 2009) (Fig. 1.1 and Table 1.1).

Table 1.1 Crop yield losses caused due to soil-borne virus (SBVs) around the world

Genus	Species	Yield loss (%)	Reference
Bymovirus	*Barley yellow mosaic virus* (BaYMV)	50%	Huth and Lesemann (1978)
	Barley mild mosaic virus (BaMMV)	>50%	Ketta et al. (2011) Cox et al. (2014)
	Wheat spindle streak mosaic virus (WSSMV)	Up to 80%	Drumm-Myers et al. (1993)
	Wheat yellow mosaic virus (WYMV)	20–44%	Palmer and Brakke (1975)
Furovirus	*Oat mosaic virus* (OMV) *Oat golden stripe virus* (OGSV)	>50% or even 100%	Walker et al. (1998)
Nepovirus	*Grapevine fanleaf virus* (GFLV)	~80%	Martelli and Savino (1991)

1.2 Transmission of Soil-Borne Viruses (SBVs)

Plant viruses require living organisms or viral vectors to carry them. The transmission of plant viruses to their host plants take place via many biotic vectors; however, abiotic transmission is also reported. The main vectors for SBVs are chytrids, plasmodiophorids, and nematodes. Member viruses of genus *Tombusvirus* are transmitted without a vector except *Cucumber necrosis virus* (CNV) which in nature is transmitted by zoospores of *Olpidium bornovanus* (Kakani et al. 2003). As far as abiotic transmission of SBV is concerned, the viruses are released into the soil along with root exudates, and from thereon they enter healthy roots through root injuries inflicted either via different arthropods or agricultural implements, e.g., *Cymbidium ringspot virus* (CymRSV), *Tomato bushy stunt virus*, and *Petunia asteroid mosaic virus* (PetAMV; genus *Tombusvirus*). Among genus *Carmovirus*, *Cucumber soil-borne mosaic virus* and *Galinsoga mosaic virus* (GMV) also show non-vector transmission (Sarwar et al. 2020). Major biotic vectors of SBVs are discussed further in this chapter.

1.2.1 Chytrid Fungi

Olpidium spp. are the vectors of all fungi-transmitted viruses. They belong to division Chytridiomycota also commonly called as chytrids and are true fungi-producing flagellated zoospores. Members of this fungal group are symptomless obligate intracellular root parasites, but *Olpidium bornovanus* has been shown to independently cause root disease (Stanghellini et al. 2010). The major families of SBVs are *Ophioviridae* and *Tombusviridae* and one phylogenetically unassigned virus. Out of all fungi-transmitted plant viruses, *Tobacco necrosis virus* (TNV genus *Necrovirus*) causing diseases in tobacco and many other crop species worldwide,

viz., bean stipple streak disease and Tulip augusta disease in tulips, is transmitted by *Olpidium brassicae* and holds paramount importance (Roberts 2014).

1.2.1.1 Mechanism of Transmission.

There are two modes by which virus transmission can take place.

(a) **In vitro transmission**: Here, the zoospores acquire the virus from the aqueous medium present outside the root system of plants.
(b) **In vivo transmission**: In this mode, zoospores acquire the virus during co-infection of the plant roots by both fungus and SBVs. The viruses involved in this type of transmission are a nuisance to control as the virus is present in the resting spores of the fungus and it can retain infectivity for decades, e.g., transmission of *Lettuce big vein virus* (LBVV) by *O. brassicae* (Campbell 1996; Rochon et al. 2004; Rochon 2009) (Table 1.2).

Table 1.2 Soil-borne viruses (SBVs) transmitted by *Olpidium* spp.

Family	Genus	Virus species	Vector
Ophioviridae	*Ophiovirus*	· *Freesia sneak virus* (FreSV) · *Lettuce ring necrosis ophiovirus* (LRNVOO) · *Mirafiori lettuce big-vein virus* (MLBVV) · *Tulip mild mottle mosaic virus* (TMMV)	*Olpidium*
Tombusviridae	*Carmovirus*	· *Melon necrotic spot virus* (MNSV)	*Olpidium*
	Dianthovirus	· *Carnation ringspot virus* (CRSV)	*Olpidium*
	Tombusvirus	· *Cucumber necrosis virus* (CNV) · *Cymbidium ringspot virus* (CyRSV) · *Petunia asteroid mosaic virus* (PetAMV) · *Tomato bushy stunt virus* (TBSV)	*Olpidium* and abiotic means of transfer
	Necrovirus	· *Beet black scorch virus* (BBSV) · *Chenopodium necrosis virus* (ChNV) · *Tobacco necrosis virus A* (TNV-A) · *Tobacco necrosis virus D* (TNV-D)	*Olpidium*
	Varicosavirus	· *Lettuce big-vein associated virus* (LBVaV)	*Olpidium*

1.2.2 Plasmodiophorids

The plasmodiophorids are placed in order Plasmodiophorales under family Plasmodiophoraceae and compose of microorganisms that are intracellular parasites of algae, oomycetes, and higher organisms. The nuclei of these parasites undergo the peculiar "cruciform" kind of nuclear division and further give rise to a plasmodium or multinucleate protoplast, hence named as plasmodiophorids (Sarwar et al. 2020). They are known to cause growth deformities in the root region, e.g., *Plasmodiophora brassicae* (soil-borne protist pathogen), inciting "club-root disease" of crucifers as well as transmit plant viruses. The different members of class Plasmodiophoromycetes, viz., *Polymyxa betae*, *P. graminis*, and *Spongospora subterranean* are known to transmit a number of viruses on temperate as well as tropical crops (Maraite 1991). Once categorized as fungi, now they are classified in the *Rhizaria* in phylum Cercozoa. Their affinity with the protozoans can be proved by studying the structure of zoospores, synaptonemal complex using electron microscopes, and rDNA sequence data for some species (Neuhauser et al. 2010).

1.2.2.1 Life Cycle

Plasmodiophorids exhibit complex life cycle and lacks complete understanding. It is composed of the following stages:

1. Zoosporic stage.
2. Plasmodia formation inside host cells.
3. Formation of resting spore.

1.2.2.2 Plasmodiophorid-Vectored Viruses

Approximately 20 species of 5 genera of SBVs, viz., *Benyvirus* (family unassigned) and *Bymovirus* (family *Potyviridae*), *Furovirus*, *Pecluvirus*, and *Pomovirus* (family *Virgaviridae*), are transmitted by plasmodiophorid fungi (Adams et al. 2009). The plasmodiophorid-transmitted viruses contain multi-segmented (2–5 RNA components) positive sense single-stranded RNA (ssRNA) genome. Except for bymoviruses which have flexuous filamentous geometry, other genera are rod shaped (Sarwar et al. 2020).

The genera *Polymyxa* and *Spongospora* are reported to transmit SBVs. The genus *Polymyxa* has worldwide prevalence including all those organisms which are obligate intracellular parasites of *Poaceae* (*P. graminis*) and *Chenopodiaceae* (*P. betae*) family. These 2 genera vector 15 most economically important SBVs (Roberts 2014). The different *Polymyxa* species can be further classified into different ribotypes (based on the rDNA sequence data) which differ in terms of host specificity and vector specificity. *Barley yellow mosaic virus* (BaYMV; genus *Bymovirus*) and *Barley mild mosaic virus* (BaMMV; genus *Bymovirus*) vectored by *P. graminis* are widely prevalent SBVs in Japan and whole of Europe causing yield losses of 70% or more. The shift to autumn-sown barley from spring-sown can be a reason of outbreaks of BaYMV and BaMMV in Western Europe, as the early-sown autumn barley seeds before emergence remain in the soil for longer time, which makes them

more susceptible to SBV infection. *P. graminis* is capable of transmitting *Benyvirus*, *Rice stripe necrosis virus* (RSNV), bymoviruses, furoviruses, and pecluviruses, while the remaining benyviruses, *Beet soilborne virus* (BSBV), and Beet virus Q (BVQ) are transmitted by *P. betae* (Sarwar et al. 2020). Morphologically, *P. graminis* and *P. betae* are indistinguishable but we can differentiate between them at molecular level. Twelve different viruses in the genera *Benyvirus*, *Bymovirus*, *Furovirus*, and *Pecluvirus* are reported to be transmitted by both *P. graminis* and *P. betae* (Mayo and Pringle 1998). Unlike *Polymyxa*, the genus *Spongospora* includes the species which are both vectors and plant pathogen, e.g., *S. subterranea*, which causes powdery scab disease in potato and also act as vector of *Potato mop-top virus* (PMTV; (genus *Pomovirus*; Jones and Harrison 1969) inciting "Spraing disease" in potatoes. Two member species of the genus are both plant pathogens and "fungal" virus vectors: *S. subterranea* f. sp. *subterranea* and *S. subterranean* f. sp. *nasturtii* (Merz et al. 2005). PMTV was first detected in the USA in 2003 and has spread to cooler areas of Europe (northern and central), Andean region of South America, Israel, Canada, and Japan (Jacobi et al. 1995; Lambert et al. 2003). The increasing incidence and spread of powdery scab disease is believed to be a reason for increased prevalence of PMTV worldwide. *S. subterranean* f. sp. *nasturtii* transmits *Watercress yellow spot virus* (WYSV) which holds great economic importance in France and England (Arnold et al. 1995; Walsh et al. 1988) (Table 1.3).

1.3 Nematodes

Nematodes are roundworms belonging to phylum Nematoda. Plant-parasitic nematodes belong to two major families *Longidoridae* and *Trichodoridae*, involved in transmitting viruses from genera *Nepovirus* and *Tobravirus*, respectively. Both the families include migratory ecto-parasitic nematodes of the root system. The name "*Nepovirus*" is deduced from "Nematode-transmitted polyhedral viruses," these viruses are polyhedral or isometric in shape while "tobraviruses" are straight tubular rod shaped. There are 22 longidorids (10 *Longidorus*, 1 *Paralongidorus*, and 11 *Xiphinema* species) and 14 trichodorids (5 *Trichodorus*, 9 *Paratrichodorus* spp.) known to vector plant viruses (Sarwar et al. 2020).

1.3.1 Transmission of Viruses by Nematodes

The nematodes can obtain the virus while feeding on infected plants, e.g., *Xiphinema index* can acquire the *Grapevine fanleaf virus* (GFLV) within 5–15 min of feeding on infected vines while for other nematodes an acquisition feeding period of 24 h might be needed. Following acquisition, the nematodes can immediately transmit the virus onto healthy plants (roots) without any latent period (Schellenberger et al. 2010). The nematodes can lose the virus within the first few months post acquisition; however, they can stay viruliferous for up to 1 year provided the nematodes are

Table 1.3 Plasmodiophorid-transmitted SBVs

Family	Genus	Species	Vector
Potyviridae	*Bymovirus*	· *Barley mild mosaic virus* (BaMMV) · *Barley yellow mosaic virus* (BaYMV) · *Oat mosaic virus* (OMV) · *Rice necrosis mosaic virus* (RNMV) · *Wheat spindle streak virus* (WSSV) · *Wheat yellow mosaic virus* (WYMV)	*Polymyxa*
Virgaviridae	*Furovirus*	· *Chinese wheat mosaic virus* (CWMV) · *Japanese soil-borne wheat mosaic virus* (JSBWMV) · *Oat golden stripe virus* (OGSV) · *Soil-borne cereal mosaic virus* (SBCMV) · *Soil-borne wheat mosaic virus* (SBWMV) · *Sorghum chlorotic spot virus* (SrCSV)	*Polymyxa*
	Pecluvirus	· *Peanut clump virus* (PCV) · *Indian peanut clump virus* (IPCV)	*Polymyxa*
	Pomovirus	· *Beet soil-borne virus* (BSBV) · *Beet virus Q* (BVQ)	*Polymyxa*
		· *Broad bean necrosis virus* (BBNV) · *Potato mop-top virus* (PMTV)	*Spongospora*
Unassigned	*Benyviridae*	· *Tobacco rattle virus* (TRV) · *Beet necrotic yellow vein virus* (BNYVV) · *Beet soil-borne mosaic virus* (BSBMV) · *Rice stripe necrosis virus* (RSNV)	*Polymyxa*
	Unassigned	· *Watercress yellow spot virus* (WYSV) · *Watercress chlorotic leaf spot virus* (WCLSV)	*Spongospora*
		· *Aubian wheat mosaic virus* (AWMV)	*Polymyxa*

stored (in vitro) at low temperatures without their host. Nematode-transmitted viruses are neither transstadial nor transovarian in nature (Sarwar et al. 2020).

1.3.1.1 Trichodorid-Transmitted Viruses

The genera *Trichodorus* and *Paratrichodorus* belonging to family Trichodoridae are mainly involved in transmission of SBVs. Both the nematodes are short in size ranging from 0.5 to 1.5 mm in length. Out of the total 75 species, only 14 species are reported as vectors of tobraviruses (Ploeg et al. 1992; Ploeg and Decraemer 1997). Only the didelphic trichodorid genera, i.e., having two ovaries, possess virus vector species. Trichodorids are present worldwide in the freely draining fields having usually sandy soils. *Trichodorus* genus is mainly found in the temperate region, whereas *Paratrichodorus* predominates the tropical and sub-tropical region. They contain a non-axial ventrally curved mural tooth or onchiostyle that can only pierce up to the epidermal cells of the root tip (Siddiqi 2002; Sarwar et al. 2020). They are plant root feeders which aggregate 1–3 mm behind the apical meristem around the zone of elongation. The feeding leads to necrosis and stunting of the roots manifested in the form of stubby roots followed by exhibition of other symptoms,

Table 1.4 Tobraviruses and their trichodorid vectors

Virus species	Nematode vector
Pea early browning virus (PEBV)	· *Paratrichodorus anemones* · *P. teres* · *P. pachydermus* · *Trichodorus primitivus* · *T. viruliferous*
Pepper ringspot virus (PepRSV)	· *P. minor*
Tobacco rattle virus (TRV)	· *P. allius* · *P. teres* · *P. anemones* · *P. hispanus* · *P. pachydermus* · *P. tunisiensis* · *P. minor* · *P. namus* · *T. primitivus* · *T. viruliferous* · *T. similis* · *T. cylindricus*

viz., wilting and chlorosis of the foliage. The secretions of the nematodes injected into the meristem during feeding may also lead to stubby root condition (Yeates et al. 1993; Oliveira et al. 2004). Among the viruses transmitted by this group, *Tobacco rattle virus* (TRV) has the widest host range (Roberts 2014). This virus is responsible for "corky ringspot" disease of potato tubers (Table 1.4).

1.3.1.2 Longidorid-Transmitted Viruses

Among *Longidoridae* family genera, viz., *Xiphinema*, *Paralongidorus*, and *Longidorus*, are reported to be virus vectors. Longidorids are larger in size reaching length of 2–12 mm (*Longidorus* and *Paralongidorus*) or even up to 1.6–6.0 mm (*Xiphinema*) in their adult stage (Sarwar et al. 2020). Compared to trichodorids, they are less restricted by soil type and are usually found in sandy and loamy soils. The members of this family bear a long hollow spear known as stylet which helps in penetrating and feeding on the plant roots. They feed at or behind the plant root tips exclusively and inject their secretions leading to galling or hyperplasia in the root region. The effects of their feeding are visible on the aerial parts of the plant as well (Griffin and Epstein 1964). On underground or roots of plants, necrosis and discoloration of the meristematic as well as cortical tissue is also evident. With few exceptions like *Cherry rasp leaf virus* (CRLV) and *Strawberry latent ringspot virus* (SLRSV) (formerly placed under *Nepovirus* now categorized in *Cheravirus* genus), they have been proven to transmit 13 out of 38 known nepoviruses (Roberts 2014). Among these, seven are transmitted by *Longidorus* species, one by *Paralongidorus*, and nine by *Xiphinema* (Roberts 2014; Sarwar et al. 2020). Many viruses are transmitted by longidorids, i.e., *Tomato ringspot virus* (ToRSV), *Tobacco ring spot virus* (TRSV), *Peach rosette mosaic virus* (PRMV), *Cherry*

Table 1.5 Transmission of plant viruses by longidorid vectors

Genus	Species	Nematode vector
Cheravirus	*Cherry rasp leaf virus*	*Xiphinema*
Unknown	*Strawberry latent ringspot virus*	*Xiphinema*
Nepovirus	*Arabis mosaic virus* *Artichoke Italian latent virus* *Beet ringspot virus* *Cherry leaf roll virus* *Cherry rosette virus* *Grapevine fanleaf virus* *Mulberry ringspot virus* *Peach rosette mosaic virus* *Raspberry ringspot virus* *Tobacco ringspot virus* *Tomato black ring virus* *Tomato ringspot virus*	*Xiphinema* and *Longidorus*

leafroll virus (CLRV), *Cherry rasp leaf virus* (CRLV), *Arabis mosaic virus* (ArMV), *Grapevine fanleaf virus* (GFLV), *Tomato black ringspot virus* (TBRSV), and *Raspberry ringspot virus* (RRSV) (Table 1.5).

1.4 Detection of Soil-Borne Viruses (SBVs)

For timely and effective management of soil-borne diseases, there is a need for fast and accurate detection tools (DeShields et al. 2018). Diagnosis of soil-borne diseases is limited and hugely hindered because of the vast soil environment as compared to plant mass, and factors like nutrient and moisture status of the soil can also influence the diagnosis (Panth et al. 2020). The field of plant disease diagnostics has seen a dramatic change from visual inspection and identification of plant disease which relied on signs and symptoms to robust serological techniques like enzyme-linked immunosorbent assay (ELISA) and molecular methods like polymerase chain reaction (PCR) (Balodi et al. 2017). Among molecular detection methods, PCR and particularly the RT-PCR (real-time PCR)-based methods form the basic protocol of many diagnostic laboratories across the world owing to their accuracy and sensitivity (DeShields et al. 2018). Fomitcheva and Kühne (2019) were successful in developing a sensitive serological, i.e., Western Blot analysis and duplex RT-PCR-based method to detect and differentiate between the sugarbeet SBVs, viz., BNYVV and BSBMV. Simultaneous detection of three SBVs in wheat mainly CWMV, JSBWMV, and WYMV using reverse transcription loop-mediated isothermal amplification reaction (RT-LAMP) was reported by Fukuta et al. (2013). However, costly equipment and skilled personnel are needed to employ these laboratory techniques. On the other hand, on-site testing tools give results at the farmers' field and can be performed by the grower himself. Lateral flow devices (LFDs) like the Immunostrip and pocket diagnostic are the leading methods with respect to on-site pathogen detection as they are simple and one-step assays but they are not completely reliable.

LAMP is another such cheap method which involves simple colorimetric analysis (DeShields et al. 2018). DeShields et al. (2018) outlined protocol for on-site detection of potato soil-borne pathogens which involved the following steps:

1. Magnetic bead-based nucleic acid extraction.
2. Portable real-time PCR (fluorogenic probe-based assay).
3. Quantitative data analysis using a laptop/computer.

This protocol enabled the detection of even as less as 100 copies of pathogen's DNA. A CRISPR-Cas12a-based detection system has recently been developed for detecting BNYVV in sugarbeet roots by Ramachandran et al. (2021). In this approach, viral RNA amplification is achieved by single-step isothermal RT-recombinase polymerase amplification (RPA) method followed by confirmation of the RT-RPA amplicon sequence identity with BNYVV sequence. Afterward, the RT-RPA reaction products are diluted ten-fold serially and 5 μL from each dilution is used further as template in the CRISPR-Cas12a reaction containing fluorescently labeled ssDNA reporter. The reaction is incubated at 37 °C. A strong fluorescence signal was deducted from infected roots than healthy roots which decreased linearly in reactions having increased levels of serial dilutions (Ramachandran et al. 2021).

1.5 Management of SBVs

Soil-borne bymoviruses are agronomically important in barley and wheat crops responsible for huge amount of yield losses annually (Campbell 1996; Kühne 2009; Kanyuka et al. 2003). Continuous efforts are being made to find resistance genes against these pathogens in the breeding programs of several countries (Takahashi et al. 1973; Ruan et al. 1984; Zhou and Cao 1985; Götz and Friedt 1993; Ordon and Friedt 1993). So far, a total of 18 resistance genes have been identified in barley against BaMMV and BaYMV. Resistance (R) gene *rym3* is identified from mutant cultivar 'Ishuku Shirazu' or 'Ea 52' which is derived from cultivar 'Chikurin Ibaraki 1' via mutagenesis (Saeki et al. 1999; Ordon et al. 2005, 2009; Kai et al. 2012). However, resistance conferred by these genes except $Rym14^{Hb}$, $Rym16^{Hb}$, Rym17, rym18, and $eIF4E_{HOR3298}$ is short lived and overcome by new races of the viruses, e.g., demise of *rym4* gene in European winter barley varieties by BaYMV-2 race (Kühne et al. 2003; Kanyuka et al. 2005; Habekuß et al. 2008; Kim et al. 2011; Arai et al. 2018). This has led to a search for durable resistance sources. One such way is pyramiding of resistance genes like *rym5* and *rym1/11-d* present in landrace 'Mokusekko 3', which offers complete resistant to all the reported isolates of BaMMV and BaYMV (Kanyuka et al. 2005; Habekuß et al. 2008; Kim et al. 2011; Arai et al. 2018; Shi et al. 2019). Rupp et al. (2019) reported that silencing of *TaeIF(iso)4E* and *TaeIF4G* genes provide resistance to WSMV, TriMV (*Triticum mosaic virus*), and SbWMV in wheat lines. These genes code for the Eukaryotic initiation factors (eIFs) which are required by the RNA viruses for

Table 1.6 List of some of the R genes/QTLs against cereal SBVs

S. No.	Resistance gene/QTL	Crop	Donor	SBV	Reference
1.	*YmYF*	Wheat	Yangfu 9311 (China)	WYMV	Liu et al. (2005)
2.	*Ymlb*	Wheat	Ibis (Netherland)	WYMV	Nishio et al. (2010)
3.	*Qssm-mtpsa-7BS*	Wheat	Dic2 (Emmer wheat)	WSSMV	Holtz et al. (2017)
4.	*rym1*	Barley	Mokusekko 3 (China)	BaMMV/ BaYMV	Okada et al. (2003) Yang et al. (2014)
5.	$rym^{b}_{HOR4224}$	Barley	HOR4224 (Japan)	BaMMV	Perovic et al. (2014)
6.	$Rym14^{Hb}$	Barley	*Hordeum bulbosum* (wild relative)	BaMMV/ BaYMV	Ruge et al. (2003)

Table 1.7 Cultural and physical measures of SBVs control

S. No.	Type of control	Strategy	Reference
1.	Cultural control	· Rogueing of diseased plants · Selection of less-susceptible cultivars · Culture on heavy types of soil, e.g., done in tulips · Change of planting date, e.g., late planting is done for autumn planted bulbs · Soil disinfection against TRV in gladiolus	Asjes (1974)
2.	Physical control		Luvisi et al. (2015)
	(a) Heat treatment	· *Potato virus Y* can be managed by steam treatment and soil solarization using ethylene-vinylacetate or high efficiency infrared films up to 20 cm of soil depth	
	(b) Air pressure	· Maintenance of matric potential of -40 kPa in field obstructs the movement of *P. graminis* zoospores vectoring SBVs within the soil	Cadle-Davidson et al. (2003)

movement between cells, replication of their genome, and production of viral proteins (Diaz-Pendon et al. 2004) (Tables 1.6 and 1.7).

1.6 Conclusion

Plant diseases have a significant impact on sustainable crop production, and over the years, even after improved chemical control, resistance development, and improvements in technology have been introduced to protect crop plants, plant diseases continue to cause severe reductions in crop yield and quality. There are a number of pests and diseases that affect crop plants. The soil-borne virus group is a particularly important pathogen that causes severe crop yield losses. Typically, these