

Genomic Resources of Important Brassica Pathogens

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ARTICLE ID: 32

Introduction:

Brassica crops, such as rapeseed-mustard, cabbage, broccoli, and cauliflower are widely cultivated all over the world. However, these crops are highly susceptible to a range of fungal, bacterial, oomycetes and viral pathogens, which can cause significant yield losses and decrease crop quality. Therefore, the development of disease-resistant *Brassica* varieties is of great importance to ensure sustainable and efficient crop production.

In recent years, advances in genomic sequencing technologies, such as Next Generation Sequencing (NGS) techniques have enabled the identification and characterization of the genomes of important pathogens of *Brassic*as. This has led to the development of genomic resources that can be used to study the molecular mechanisms underlying pathogenicity and virulence in these organisms. By understanding the genetic basis of pathogenicity, it may be possible to develop more effective strategies for disease control, such as breeding *Brassica* crops with enhanced disease resistance. In this context, the availability of genomic resources for these pathogens is an important resource for researchers and plant breeders. This information can be useful to identify novel targets for crop breeding and to develop more efficient and sustainable strategies for disease control in *Brassica* crops. Genome sequences also help in better understanding of life-style, genome evolution of plant pathogens and they also acts as resources from which genetic information can be easily mined. In this article, we have provided an overview of the genomic resources available for various *Brassica* pathogens, and discussed how this information can be used in disease-resistant breeding programs.

Major pathogens of *Brassica* crops are as follows:

Fungal Pathogens:

- ***Alternaria brassicae***: *Alternaria brassicae* is a fungal plant pathogen that infects *Brassica* crops, including Rapeseed-mustard, cabbage, broccoli, cauliflower, and other cruciferous vegetables. It can cause a variety of diseases such as black spot, leaf

spot, and *Alternaria* head rot. The fungus produces dark-colored lesions on leaves, stems, and flowers, which can reduce plant growth, yield, and quality. The pathogen spreads through spores that can survive on infected plant debris, soil, and other surfaces for several years. It can also spread through wind, rain, and irrigation water. Warm and humid weather conditions favor the growth and spread of the fungus.

- ***Sclerotinia sclerotiorum***: *Sclerotinia sclerotiorum* is a fungal pathogen that can cause significant damage to mustard crop. The fungus produces hard, black structures called sclerotia, which can survive in the soil for several years and serve as a source of infection for new crops. Symptoms of *Sclerotinia* infection on mustard include white, fluffy growth on the stem and/or leaves, wilting, and a soft, watery rot of the affected tissue. In severe cases, the fungus can cause yield loss and even plant death.
- ***Leptosphaeria maculans***: *Leptosphaeria maculans* is a fungal pathogen that causes blackleg disease in cruciferous crops, including mustard. The disease can lead to significant yield losses, reduced crop quality, and can also reduce seed viability. Symptoms of blackleg disease on mustard include dark spots on leaves, stems, and pods, which can enlarge and turn black as the disease progresses. Infected plants may also show stunted growth and premature yellowing of leaves. The fungus survives in crop debris and can spread through wind, water, and movement of infected plant material. High humidity, wet conditions, and temperatures between 10-25°C favor the growth and spread of the fungus.

Oomycete Pathogens:

- ***Albugo candida***: *Albugo candida* is a biotrophic oomycete pathogen that causes white rust disease in mustard and other cruciferous crops. The disease can lead to significant yield losses and reduced crop quality. Symptoms of white rust disease on mustard include white pustules on leaves, stems, and pods, which can eventually turn yellow and dry up. Infected inflorescence due to hypertrophy and hyperplasia of tissue gets converted into a distorted structure popularly called as staghead. The pathogen survives in crop debris and can spread through wind, water, and movement of infected plant material. High humidity and temperatures between 10-25°C favor the growth and spread of the pathogen.

- ***Hyaloperonospora brassicae***: *Hyaloperonospora brassicae* is an *oomycete* pathogen that causes downy mildew disease in mustard and other cruciferous crops. The disease can cause significant yield losses and reduced crop quality. Symptoms of downy mildew caused by *H. brassicae* on mustard include yellowing and wilting of leaves, as well as the development of a grayish-white fuzzy growth on the underside of leaves. Infected leaves may also show small, pale spots on the upper surface. The *pathogen* survives in crop debris and can spread through wind, water, and movement of infected plant material. High humidity and temperatures between 10-20°C favor the growth and spread of the *f pathogen*.

Protists pathogens:

- ***Plasmodiophora brassicae***: *Plasmodiophora brassicae* is a soil-borne pathogen that causes clubroot disease in mustard and other cruciferous crops. The disease can cause significant yield losses and can persist in the soil for many years, making it difficult to manage. Symptoms of clubroot caused by *P. brassicae* on mustard include swelling and distortion of the roots, which can lead to stunted growth and reduced yield. Infected plants may also show yellowing and wilting of leaves, as well as the development of small, white, or yellowish-green resting spores on the surface of infected roots. The fungus survives in the soil and can spread through movement of soil, water, and infected plant material. The pathogen can persist in the soil for many years, making crop rotation and sanitation important components of management.

Bacterial Pathogens:

- ***Xanthomonas campestris pv. campestris***: *Xanthomonas campestris pv. campestris* is a bacterial pathogen that causes black rot disease in mustard and other cruciferous crops. The disease can cause significant yield losses and reduced crop quality. Symptoms of black rot include yellowing and wilting of leaves, as well as the development of V-shaped lesions on the leaves. The lesions may be surrounded by a yellow halo and can rapidly expand to cover much of the leaf surface. Infected plants may also show premature senescence and the development of small, blackened lesions on the stems and pods. The bacteria can spread through water, wind, and infected plant material. The pathogen can survive in infected crop debris and on seed surfaces,

making sanitation and the use of disease-free seed important components of management.

Genomic resources of Important *Brassica* pathogens and their further utilization

The ability to identify host resistance genes is driven by the understanding of the pathogen's genome, due to their co-evolution. Advances in genome sequencing of pathogens have led to the identification of critical pathogenicity factors which might facilitate the identification of similar resistance genes in the host. The genomic resources of *Brassica* pathogens can be extremely useful in disease-resistant breeding. Researchers can use the genomic resources to identify genes that are essential for pathogen city, and then target these genes using RNA interference or gene editing techniques to reduce pathogen virulence. In addition, identification of effector genes can help in developing new resistance genes in *Brassica* crops, which can be used for disease resistance breeding. Furthermore, genomic resources can be used to understand the genetic diversity of the pathogen populations, which can help in predicting and monitoring the emergence of new pathogenic strains. This information can be used to develop effective strategies for controlling disease outbreaks in *Brassica* crops.

Table 1: The genomic resources for important *Brassica* pathogens:

Pathogen (Disease caused)	Genome Size	Year of Sequencing	Sequencing Method	Findings related to disease resistance	Researchers
<i>Albugo candida</i> (White rust)	~39.7 Mb	2022	PacBio, Illumina	Reported significant expansion of predicted repertoire of CCG class of effectors involved in host immunity suppression.	Furzer et al. (2022)
<i>Alternaria brassicae</i> (Leaf spot)	~34.1 Mb	2019	Oxford Nanopore Technology	Reported the pathogenicity related genes in <i>Alternaria</i> species.	Rajarammo han et al. (2019)
<i>Sclerotinia</i>	~38.8	2017	PacBio,	Identified novel	Derbyshire

<i>sclerotiorum</i> (Stem rot)	Mb		Illumina	effector genes in <i>S. sclerotiorum</i> .	et al. (2017)
<i>Leptosphaeria maculans</i> (Black leg)	~45.9 Mb	2018	Oxford Nanopore Technology, Illumina, optical and genetic maps	Identified novel effector genes in AT rich regions and generated a chromosome-level assembly for <i>Leptosphaeria maculans</i> .	Dutreux et al. (2018)
<i>Plasmodiophora brassicae</i> (Club root)	~24.2 Mb	2016	PacBio	Reported a compact genome with dependency of <i>P.brassicae</i> on its host for some essential nutrients and a potential role in the regulation of host plant cytokinin and auxin.	Rolfe et al. (2016)
<i>Hyaloperonospora brassicae</i> (Downy mildew)	~72.2 Mb	2021	Illumina	Reported the <i>H. brassicae</i> genome, its metabolic pathways and genes encoding proteins of relevance for virulence.	You at al. (2021)
<i>Xanthomonas campestris pv. campestris</i> (Black rot)	~4.97 Mb	2022	Oxford Nanopore Technology	Reported variable genomic regions and virulence factors.	Chen at al. (2022)

Conclusion:

Genome sequencing of these important *Brassica* pathogens has helped in rapid characterization of plant pathogens and allowed better understanding of the plant pathogen biology. Genome sequences has provided humanity with tools that can be used during the emergence of new plant pathogens and future disease outbreaks which is very essential for livelihoods and food security. Overall, the genomic resources of *Brassica* pathogens provide a valuable tool for disease-resistant breeding, which can help in developing sustainable and efficient strategies for disease control in *Brassica* crops.

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