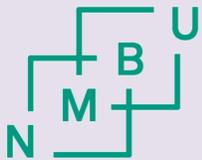


# Sensing of UV and visible light by powdery mildew pathogens



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## Introduction

- Powdery mildews caused by obligate biotroph fungal pathogens of the order Erysiphales, are a significant threat to most crops worldwide.



Fig. 1. Powdery mildew symptoms on tomato (A), strawberry (B), and cucumber (C) plants.

- Optical radiation may be an environmentally friendly alternative in management of powdery mildews.
- Short wavelength ultraviolet (250 nm – 290 nm) and red light (610 nm – 660 nm) suppress powdery mildews in a wide range of crops.

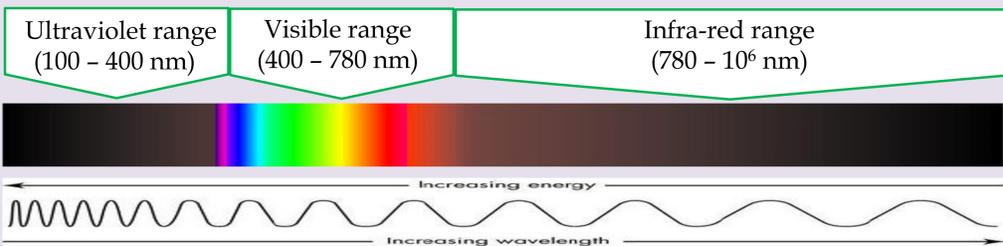


Fig. 2. Different ranges with respective wavelength of optical radiation.

- By using next generation transcriptome sequencing of *Erysiphe necator*, the presence and expression of putatively photo-responsive genes similar to phytochromes, cryptochromes, white collar, and photolyase were recently discovered.

## Objective

The powdery mildew fungi *Oidium neolycopersici*, *Podosphaera aphanis* and *Podosphaera xanthii* were selected for:

- Genome and transcriptome wide identification of photoreceptors.
- Characterization of photolyase and chryptochrome-like genes.

## Whole genome sequencing and assembly

- Genomic DNA was extracted from clean isolates.
- Quantity and quality of DNA were checked using NanoDrop and Gel electrophoresis.
- Libraries were prepared using TrueSeq Nano DNA kit (Illumina), and 150 bp paired-end sequencing was performed using Illumina NextSeq 500.
- Adapters, low quality reads and Illumina spike-in PhiX were cleaned from raw sequence data.
- Plant DNA contamination was removed by aligning sequence reads against the respective host plant genome.
- Reads that did not align with host plant genome were used for genome assembly.
- Genomes were assembled separately, and presence of core eukaryotic genes was estimated.

## Results

Table 1. Summary statistics of whole-genome assemblies, prediction and annotation

DNA	<i>Oidium neolycopersici</i>	<i>Podosphaera aphanis</i>	<i>Podosphaera xanthii</i>
# of raw reads (150 PE)	167,590,324	76,415,989	89,915,519
# of cleaned reads	150,804,907	70,598,348	82,395,014
# of reads after removing plant DNA	132,346,281	65,731,919	77,401,212
Estimated genome size	249,147,646	281,345,667	159,864,358
Assembled genome size	66,294,405	202,257,412	155,168,007
# of scaffolds	20,061	86,938	63,866
Scaffold N50	9,966	11,293	7,903
Longest scaffold (bp)	97,677	997,747	109,278
# of contigs	20,727	88,175	64,370
Contig N50	9,088	10,945	7,692
Longest contig (bp)	73,971	566,457	109,278
GC content (%)	38.97	51.72	43.27
CEGMA complete (246 KOGs) (%)	98.37	97.15	96.34
CEGMA partial (246 KOGs) (%)	100	99.59	99.19
# of protein coding transcripts	18,602	8,589	27,475
Average gene length (bp)	793	1,091	730
# of protein coding transcripts (AED < 1.0)	2,888	6,562	13,025
Average gene length (bp)	1,505	1,316	984

CEGMA - Core Eukaryotic Genes Mapping Approach. KOG - Eukaryotic orthologous groups. AED - Annotation Edit Distance.

- Presence of genes similar to all major classes of photoreceptor genes, including photolyase, cryptochrome, white color, phototropins, phytochrome and UVR8 were identified.
- All three *de novo* assembled genomes have three putative genes similar to photolyase-chryptochrome domains.

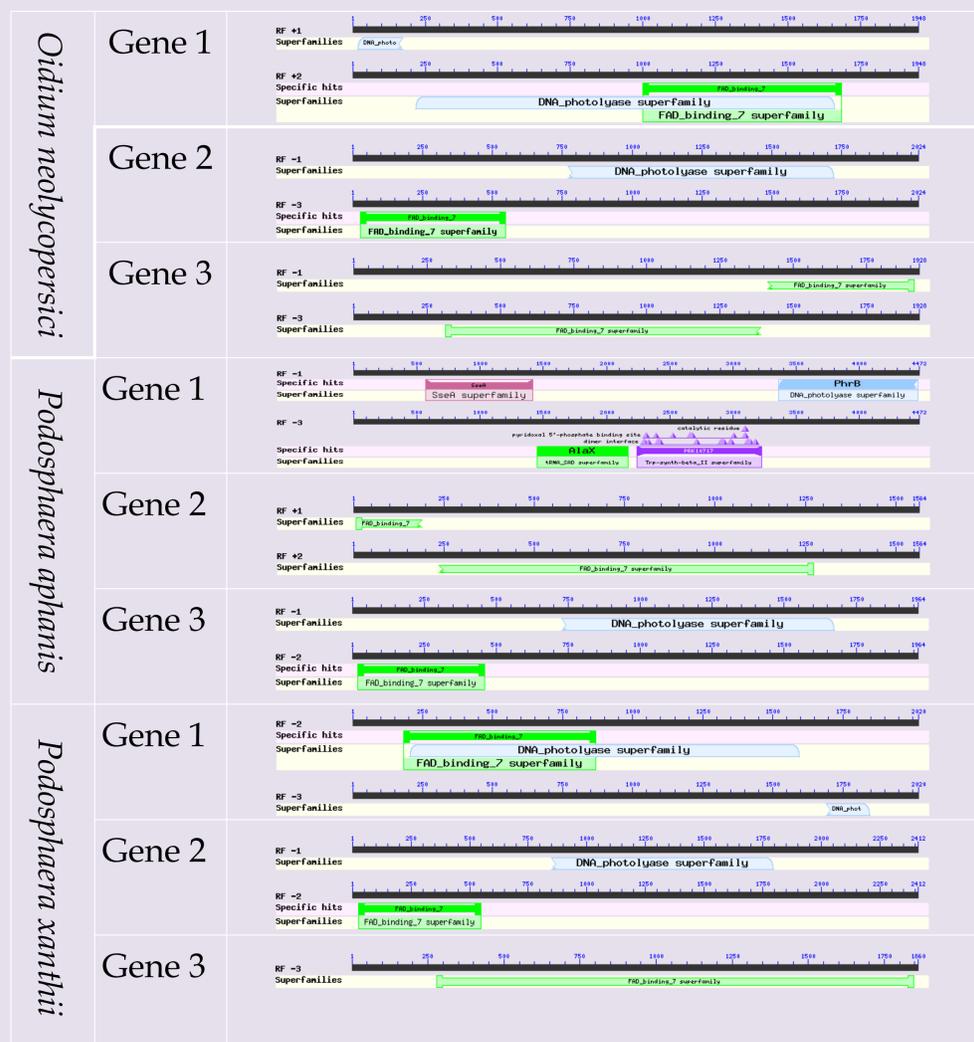


Fig.3. NCBI conserved domain search for photolyase-chryptochrome like putative genes identified in *Oidium neolycopersici*, *Podosphaera aphanis*, and *Podosphaera xanthii*.

- Current research focus on characterization and biological functions of these photoreceptors in powdery mildew fungi.
- Findings of this work could help to better design optical architecture for effective management of powdery mildews in a wide range of crops.