

Survey of Lettuce Downy Mildew (*Bremia lactucae*) in Arizona to Identify Race and Fungicide Resistance

Collaborators:

PI: Stephanie Slinski, University of Arizona, Yuma Center of Excellence for Desert Agriculture

Dr. Slinski will manage the project.

Cooperator: Dr. Richard Michelmore

Dr. Michelmore will provide technical support and will evaluate *B. lactucae* isolates. This evaluation is part of a separately funded project.

Background:

Lettuce downy mildew caused by *Bremia lactucae* is an important disease that can significantly reduce the quality and marketability of lettuce. This disease is controlled using fungicides, by modifying the environment to reduce humidity, and by planting varieties containing downy mildew resistance (*Dm*) genes. *B. lactucae* evolves rapidly resulting in new races leading to the breakdown of resistance in downy mildew resistant (DMR) lettuce varieties, and fungicide resistance, threatening the available control methods. In order to ensure that breeders are developing varieties with resistance against virulent phenotypes currently in Arizona, they must know what phenotypes occur in Arizona. Dr. Richard Michelmore has provided a service to identify *B. lactucae* phenotypes or known races and has created a public database of results (<http://bremia.ucdavis.edu/>). This phenotyping includes evaluating fungicide insensitivity including oxathiapiprolin, dimethomorph, and mandipropamid. The challenge for Dr. Michelmore's group is to collect enough samples to represent the population in area. This group collects isolates in two ways: (1) by growers, breeders and Extension personnel sending infected lettuce- and (2) by planting a trap nursery.

The nurseries are composed of small plots of resistant lines from a differential series interspersed with plots of mixtures of susceptible wild and cultivated lines to serve as spreader rows. These trap crop nurseries include the *B. lactucae* differential series developed by the International Bremia Evaluation Board (IBEB, <https://worldseed.org/our-work/disease-resistance/other-initiatives/ibeb/>) and "spreader" rows of a mix of susceptible lettuce types. The *B. lactucae* differential series is a set of lettuce varieties used to identify *B. lactucae* races. They have a known susceptible and resistant reaction to races. Evaluating the differential series results in an overview of the *B. lactucae* population in an area. Planting a trap nursery with the differential series in addition to sending samples for laboratory is important because not all samples sent to the laboratory are successfully typed.

Since 2001, 43% of virulent isolates (n=202) from Arizona typed have been novel races. However, the number of isolates submitted from Arizona was low, which prevents growers from knowing if DMR varieties will perform well in Arizona and limits lettuce breeders from knowing what resistance genes need to be incorporated into varieties bred for this region.

The objectives of this project were:

1. *Identify the current races of Bremia lactucae (downy mildew of lettuce) in Yuma.*

A single trap nursery was planted in early December. The late planting was due to difficulties coordinating planting with the Fusarium wilt of lettuce trial evaluations and field day. To compensate for the single trial, plants were left in the field for longer (until March) and evaluated more frequently. Evaluations and sampling took place every week starting one month after planting.

Disease incidence was low in the 2022-2023 season. This resulted in uneven distribution of disease in the field. We were not able to confirm races present based on differential lettuce varieties planted. We were able to score plots for presence or absence of disease in one or more plot (figure 1), but the data was not consistent enough to publish. Samples were sent to UC Davis for further testing. These samples were analyzed in the lab and entered into the Bremia Database. Breeders have access to the Bremia database and can identify resistance genes that should be durable in the short term. The majority of the samples (66%) were novel races, 12% were US8 and 8% were VP-300. A single sample of US9, the US9 progenitor and VP-301 were also identified by Dr. Richard Michelmore. US8 is prevalent and widespread in AZ and CA and VP-300 remains common.

Variety	Dm Genes/R-Factors	Pathogen detection in one or more plots
PIVT1309	Dm16	N
NumDm17	Dm17	N
Colorado	Dm18	N
Salvius	Dm25	N
RYZ2164	Dm25	N
Bataille	R59	N
R4T57D	Dm 4	Y
UC DM14	Dm14	Y
NumDm15	Dm15	Y
CG Dm16	Dm16	Y
Dandie	Dm3	Y
FrRsal-1	Dm36	Y
Ninja	Dm37	Y
La Brillante	Dm50	Y
Sabine	Dm6	Y
Salinas	Dm8,13	Y
ViAE	R20	Y
ViCQ	R21	Y
Bedford	R53	Y
Balesta	R54	Y
Design	R56	Y
UC12103	R63	Y
Fenston	R65	Y

2. *Evaluate variety performance against the current population of *B. lactucae*, to determine what resistance genes are currently effective.*

Plots were evaluated two times prior to maturity and at maturity. Due to the uneven distribution of disease in the field we were not able to collect enough data to confirm variety resistance/susceptibility. Steps were taken to encourage disease spread in the field including using sprinkler irrigation and leaving the plants in the field past maturity. Despite these measures, disease spread was not uniform.

3. *Provide leaf tissue from field-grown lettuce for analysis by Dr. Richard Michelmore's laboratory at the University of California, Davis.*

Forty samples were shipped to UCDavis for typing starting in November 2022. We will continue to facilitate the shipment of samples from Arizona to UC Davis for race typing.