

## Disease Resistance Screening Metadata

### Operational screening of White pine blister rust for *Pinus strobiformis*

#### Abstract

White pine blister rust, caused by the non-native, invasive fungal pathogen *Cronartium ribicola*, has the potential to be a significant cause of mortality in southwestern white pine (*Pinus strobiformis*). Very little evaluation of this disease in southwestern white pine has been previously undertaken. Data from this project is documenting genetic resistance to the disease, including major gene resistance (MGR) conferred by a dominant *R* gene and also quantitative disease resistance (QR). We assess progeny arrays from 440 *P. strobiformis* families (19,630 seedlings), inoculated with *C. ribicola*. Subsequently, the seedlings were assessed for signs, symptoms and resulting impact in 6 common garden trials with evaluation occurring between 1 and 5 years, to determine the types and frequency of resistance across the species' range.

#### Creators

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## Keywords

White pine blister rust, *Pinus strobiformis*, Major Gene Resistance, Quantitative Resistance

## Funding of this work:

List only the **main PI of a grant** that supported this project, starting with the main grant first. Add rows to the table if several grants were involved.

PI First Name	PI Middle Initial	PI Last Name	PI ORCID ID (optional)	Title of Grant	Funding Agency	Funding Identification Number
Kristen	M.	Waring	0000-0001-9935-9432	Collaborative research: Blending ecology and evolution using emerging technologies to determine species distributions with a non-native pathogen in a changing climate	National Science Foundation	EF-1442597

## Timeframe

- 2015:
- 2021:
- Data collection ongoing:

## Geographic location

- **DESCRIPTION**
  - All maternal trees collected came from the southwestern U.S. (Texas, New Mexico, Arizona, and Colorado), specifically the Sky Islands, or Madrean Archipelago and in Mexico along the Sierra Madre Occidental.
- **BOUNDING COORDINATES**
  - North: 40.0°
  - South: 20.0°
  - East: -102.5°
  - West: -112.5°

## Taxonomic species or groups

- *Pinus strobiformis* Engelm.

## Methods

Cones from 440 open-pollinated, *P. strobiformis* trees were collected from across the species range and were sown between January 2016 and 2017 at the U.S. Department of Agriculture, Forest Service's Dorena Genetic Resource Center (Cottage Grove, Oregon, USA). Seedlings were grown for either one (for MGR trials) or two years (for QR trials), one year in 164 cm<sup>3</sup> supercell Cone-tainers™ (Ray Leach, Canby, Oregon) in family blocks in an unheated greenhouse and then transplanted to 0.9 m x 1.2 m x 0.3 m boxes outside for the second growing season. Up to 60 seedlings were available for each family, and seedlings were transplanted into family row plots in randomized complete block design with four to six blocks and up to 10 seedlings per family per block. Seedlings were inoculated in the months of September or October between the years of 2016 and 2018 with basidiospores of *C. ribicola*. Details of the standard Dorena GRC inoculation procedures are outlined elsewhere (Kegley and Snieszko, 2004; Snieszko et al., 2008; Snieszko et al., 2011). Mean inoculum density was 4,527 spores/cm<sup>2</sup>; basidiospore germination was 98.7%. Both primary and secondary needles were present on seedlings at the time of inoculation.

### *Disease trait assessment*

Following inoculation with *C. ribicola*, infected seedlings were periodically assessed for the presence of rust symptoms, with data collection ongoing. The first assessment occurred approximately 0.75 years post-inoculation and up to five assessments per trial have so far been

conducted over the course of the different trials. All seedlings were assessed for a core set of traits. Specifically, number of needle spots at first assessment, the presence/absence of needle spots at second assessment, number of cankers, number of bole infections, number of bark reactions, number of partial bark reactions, overall severity of infection, and survival. Full counts of the number and type of stem symptoms were completed at second assessment and the presence of additional stem symptoms were noted at subsequent inspections, since the growth and merging of cankers made later counts more problematic. The counts represent one point in time, and some seedlings showed stem symptoms at later assessments. Additionally, both pre-inoculation height and height present one growing season post-inoculation, recorded during the 2<sup>nd</sup> assessment.

Based on the level and severity of infection with white pine blister rust, each tree was also assigned a severity classification at each assessment. The classification assigns a seedling a numeric value that assesses the severity of damage from 0, no infection, to 9, dead from rust with classes designated by the degree to which a canker has encircled the bole of the seedling and expanded vertically. For example, a tree that is infected with blister rust (presence of needle spots and a canker) with intermediate severity, a normal canker encircling >50% but <100% of the bole but little vertical expansion, would receive a rating of 4. The severity rating and the disease trait phenotypes are standard measurements recorded as part of rust inspections at the USDA Dorena GRC. The severity rating for each seedling is dynamic and can change (increase or decrease) with each subsequent assessment, reflecting the degree of rust progression or resistance response. Seedlings can have one or many stem symptoms and the severity provides a composite look at the progression of all infections present at each point in time.

## Data Table

**Table name:** (Operational Trial Phenotypes)

**Table description:** (Raw phenotype/disease trait scores for Southwestern white pine trial)

Column name	Description	Unit or code explanation or date format	Missing value code
<u>Inspection Codes</u>	Missing tree - X Unable to assess trait of interest- Z		
HT#	Height to nearest half (0.5) cm of tree at inoculation, bottom of new growth		
Needle shed	Presence/absence of needle shed	0 = absent 1 = present	

(Nshed# or <u>NS#</u> )		? possible Nshed difficult to tell	
Spot count secondary's ( <u>Spts sec1</u> )	Count up to 50 then groups of 25	51-75 spots then enter 75, 76-100 spots then enter 100, etc.	
Spot count primary's ( <u>Spts pri1</u> )	Count up to 50 then groups of 25		
Canker count secondary's ( <u>CC sec1</u> )	Number of cankers from secondary needle infection		
Canker count primary's ( <u>CC pri1</u> )	Number of cankers from primary needle infection		
Primary needles lammas ( <u>Pri Lam1</u> )	Presence/absence of primary needles on lammas growth	0 = absent 1 = present	
SPTS2	spots at inspection 2	0 = absent 1 = present	
Damage (DM)	1st digit of the two-digit DMSV code.	0 = none 1 = Animal 2 = Mechanical 3 = Disease, Non-blister rust 4 = Disease, Blister Rust 5 = Insect 9 = Unknown	
Severity (SV#)	2nd digit of the two-digit DMSV code.	0 = No infection or damage 1 -3 = Minimal rust/damage impact 4 = intermediate rust/damage impact 5-6 = intermediate rust/damage	

		impact with girdling 7-8 = Severe impact (large lesion growth vertical, and encircling stem) 9 = Dead	
Vigor (Vig#):	Health status of tree	1 = Tree alive and vigorous 2 = Tree alive and sickly 3 = Tree recently dead (bark intact, easy to count cankers) 4 = Tree dead more than a few years 5 = Tree dead or missing; unable to determine presences of rust 6 = Top dead	
CM#	Canker merge status	0 = cankers not merged 1 = cankers merged and count is reasonable 2 = cankers merged and count is unreliable	
BiFG#	count of bole infections on fixed growth		
ncFG#	count of normal cankers on fixed growth		
pbrFG#	count of partial bark reactions on fixed growth		
brFG#	count of bark reactions on fixed growth		
bi18L	count of boled infections on 2017 lammas		
nc18L	count of normal cankers on 2017 lammas		
pbr18L	count of partial bark reactions on 2017 lammas		
br18L	count of bark reactions on 2017 lammas		
biLG#	count of boled infections on previous year lammas		
ncLG#	count of normal cankers on previous year lammas		
pbrLG#	count of partial bark reactions on previous year lammas		
brLG#	count of bark reactions on previous year lammas		

Common Abbreviations	19L 2019 lammas present aec aecia present b bent bc bole canker bn brown needles chl chlorotic cm cankers merged dlt dead limb tips dnt dead needle tips dr#### dead of rust in year #### dunk dead unknown cause fk forked FL flecks hpnc high primary needle cast id insect damage md mechanical damage mt multi-top ns needle shed obd old bud damage primary needle senescence pns (not shed) ps pseudospots pyc pycnia present questionable primary/secondary needle qps canker source rs red spots sf swollen fascicles sm small tb tuberculina tdabc top dead above bole canker tdunk top dead unknown cause v or ver validated/verified		

## Notes and Comments

Sy specific columns include dates (e.g. bi18L where 18 indicates sow year 17 trial had measurements of traits on year 2018 growth.) Some trials will have alternate measures.