

Characterizing Sudden Oak Death at JRBP 'O'O.

Jaden Southern, June 7 2025

Sudden Oak Death (SOD), caused by the fungal pathogen *Phytophthora ramorum*, is a disease responsible for fatal outcomes of oak trees in the western United States. Oak trees are most commonly infected with the pathogen through a vector species which can transmit the disease without suffering fatal consequences. *Umbellularia californica* or the California Bay Laurel is the primary host and source of oak infection (Kerry E. Wininger & Nathan Rank, 2019) in western US. There is currently no cure for SOD, although chemical preventative treatment has been approved by the State of California (*Sudden Oak Death*, n.d.). Better understanding of risk factors for SOD transmission can help us predict its presence and potentially deploy preventative measures.

Oak trees are a keystone species, supporting more life forms than any other North American tree genus, however, nearly one-third of all oak species are considered threatened with extinction (Liz Kimbrough, n.d.; “Species Spotlight - Oaks,” n.d.). Loss of these often centuries old trees can also increase fire risk to communities by increasing fuel loads available on forest floors. Thus, understanding the risk of SOD transmission in our woodland areas is critical to protecting and preserving the vast amounts of biodiversity held within them.

A significant portion of Jasper Ridge 'Ootchamin 'Ooyakma is made up of oak woodlands where several oak trees, *Quercus douglasii*, *Quercus agrifolia*, and *Quercus lobata* contribute significantly to the preserve ecosystem. Often, bay laurel trees carrying SOD will show leaf blight (**Figure 1**) on their leaf tips. This is due to *P. Ramorum* being a water fungus, often collecting on the tips of leaves during rainfall events. While there can be visible signs, it is not possible to know whether or not a tree is a carrier of SOD without genetic testing. Over the last

17 years, Bioblitz data has been collected at the preserve monitoring the presence and distribution of SOD in bay laurels. Each year, leaves from a number of trees are collected and submitted for genetic testing. Results of this testing data is available publicly online along with similar results for a majority of the California coastal region by UC Berkeley Pathology and Mycology Lab. While this provides a rich data set through which to better understand SOD risk, very little has been done to clean or analyze this data and better understand patterns in SOD at JRBP 'O'O.



Figure 1: “A bay laurel leaf affected by leaf blight” (Sudden Oak Death, n.d.)

Additionally, previous studies have found many factors associated with high *P. Ramorum* incidence in Bay laurels. These include high rainfall, high bay laurel density, an eastern aspect, and lower bay laurel basal area (Cobb et al., 2012; Kozanitas et al., 2022). By visiting tested bay laurels to measure their characteristics, we can further understand SOD transmission risk.

Thus, through this project, I cleaned and analyzed SOD Bioblitz data for JRBP 'O'O. I also began work on measuring bay laurel trees in the field, creating a field protocol which can be iterated on for future projects.

Materials and Methods

Data Cleaning

Raw Bioblitz data files were in the form of a KMZ Google Earth File. ArcGIS was used to clip the data to the boundaries of JRBP 'O'O, obtaining measurements of all trees tested within the preserve from 13 of the last 17 years (2009, 2010, 2011, and 2018 did not have any data). Each tree's metadata, including SOD test results, was contained in a single html string. RStudio

was used to parse the string obtaining, for each tree, latitude and longitude coordinates, collection date, and results of genetic testing for SOD.

Analysis

All coding was done using RStudio and ArcGIS Pro. All Maps were created in ArcPro. Shape files for vegetation and geology were obtained from Stanford Earthworks Jasper Ridge Biological Preserve GIS Maps & Data Collection.

Field Data

Seven trees were measured in the field for a variety of variables including location (latitude/longitude), elevation, slope, aspect, height, quality, DBH, canopy cover, and surrounding vegetation DBH within a 5 meter radius. These characteristics were determined to be accessible to measure for each tree and together give a comprehensive summary of the tree and microhabitat surrounding it.

Results

Variation in the number of *Umbellularia californica* individuals tested each year and location on the preserve varied over time. Quantitative testing results can be seen in **Figure 2**. In general, testing intensity seems to be increasing over time. In the most recent year, 2024, 41 trees

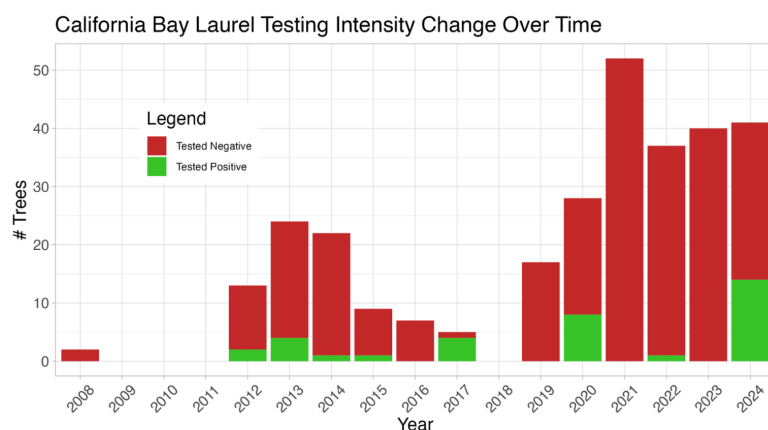


Figure 2: Stacked bar plot of testing results for *Umbellularia californica* from 2008 to 2024. Trees which tested negative are represented in red. Those which tested positive are represented in green

were tested and 14 of them tested positive for *P. Ramorum*. **Figure 3** shows the spatial distribution of testing for 6 testing years. Almost all testing was conducted on or near clearly marked trails.

Number of trees which tested

positive varied between years. Locations of positive trees also vary between years. **Figure 4** shows patterns of testing in relation to multiple variables. There seem to be no strong relationships between positive test results and slope, elevation, or aspect. Almost all testing occurred in oak woodland forests. This is also where the majority of positive trees were located. Geologically, most tested trees, and most positives, were found on either Franciscan greenstone or Whiskey hill sandstone formations.

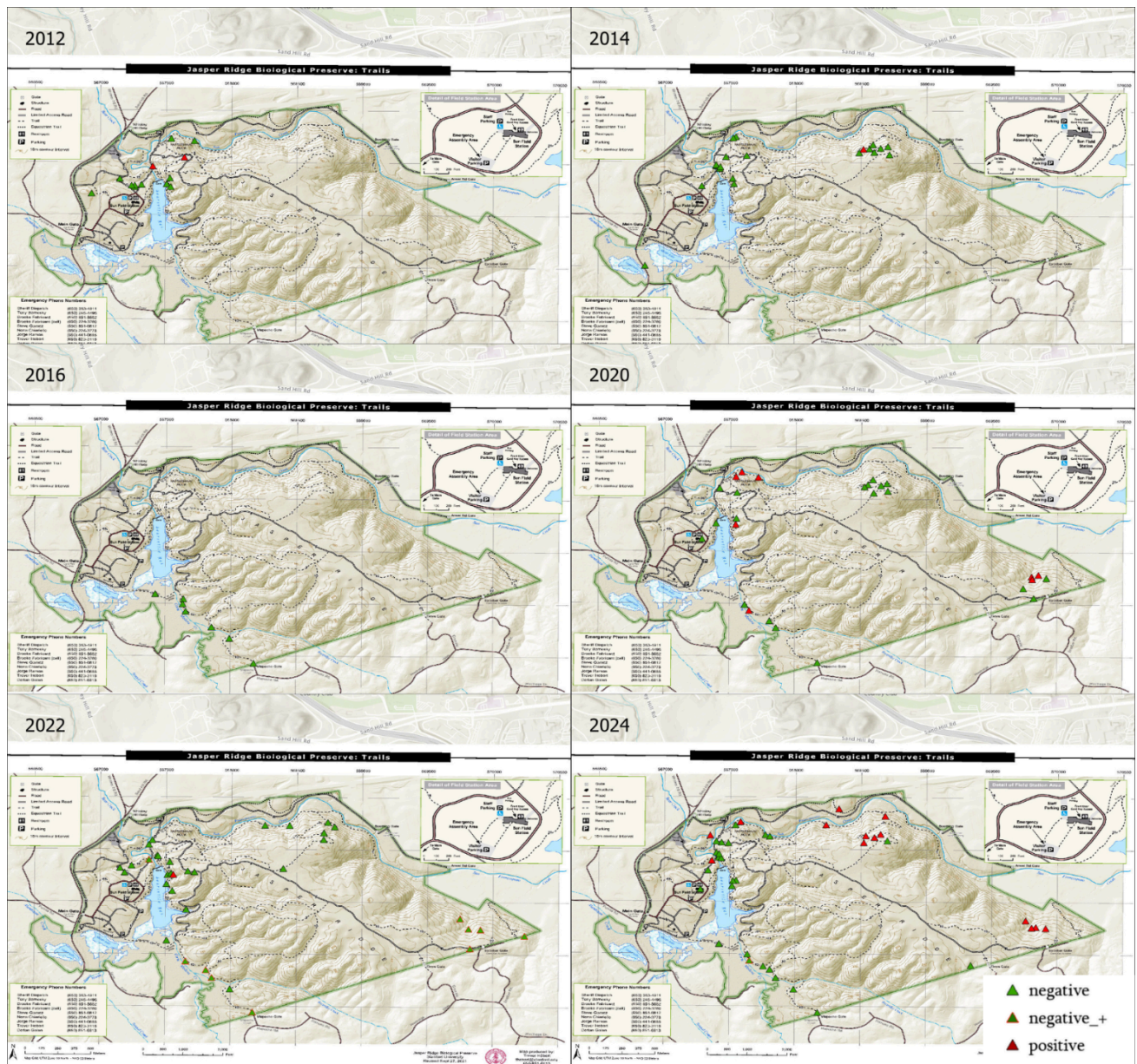


Figure 3: Locations of SOD tested bay laurel trees every even year between 2012 and 2024. Green triangles indicate trees which tested positive. Red triangles indicate trees which tested negative.

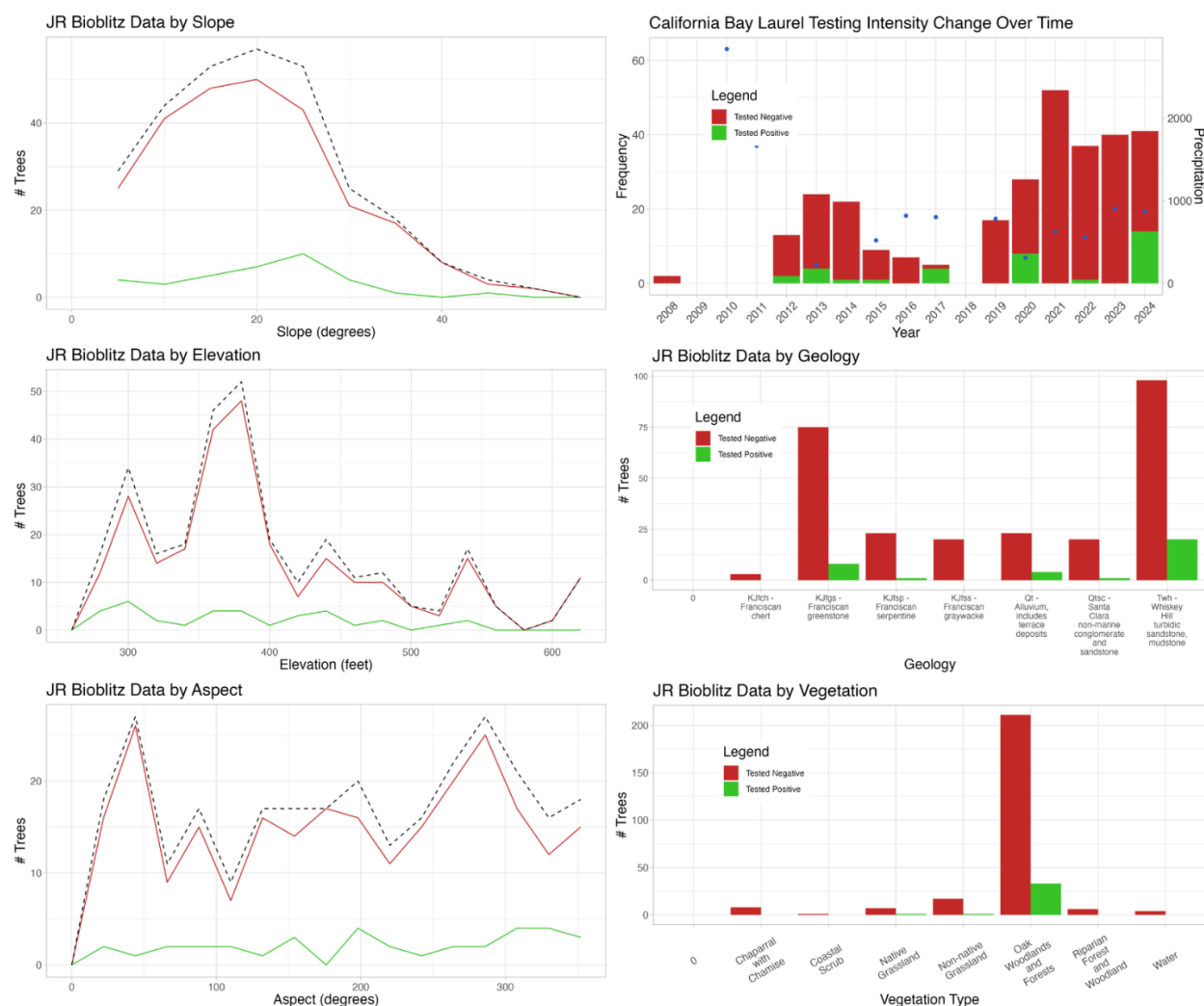


Figure 4: Trends in California Bay Laurel testing results by various variables. Red colors indicate trees which tested negative. Green indicates trees which tested positive. Black dotted line is the sum of all trees. Blue dots mark total precipitation for the year.

Discussion

The data showed important trends in testing effort and distribution over time. The number of trees tested and the number of trees testing positive have both increased over time at a similar rate. As there are significant changes in the number of trees tested each year and their location on the preserve, it is difficult to make any strong conclusions about SOD patterns over time currently. Though not shown here, according to the Bioblitz data, there is very little continuity between individual trees tested each year. This is in contradiction to the JRBP 'O'O website

which states that many of the same trees are tested each year. This indicates that a more accurate system of documenting tree location is necessary for this data in order to better understand the changes occurring in individual trees.

No strong trends were found between the number of trees which tested positive and slope, elevation, or aspect indicating none of these variables are likely correlated with SOD infection at the preserve. This study is limited by a small sample size, and a relatively small number of positive tests from which to draw strong conclusions.

While 7 trees were measured in the field, only 1 positive tree was measured making it impossible to draw any strong conclusions around the variables measured. These visits did clarify what variables are possible to measure in the field and constitute an angle for further research.

Conclusions

By cleaning this data, we are able to start to determine what patterns exist in SOD prevalence and distribution at JRBP 'O'O and thus the risk posed to the keystone oak species here. Increased testing effort and testing consistency over time will be critical to making strong predictions about SOD risk to oaks. Further directions include continuation of field measurements and further exploration and analysis of Bioblitz data.

References

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