

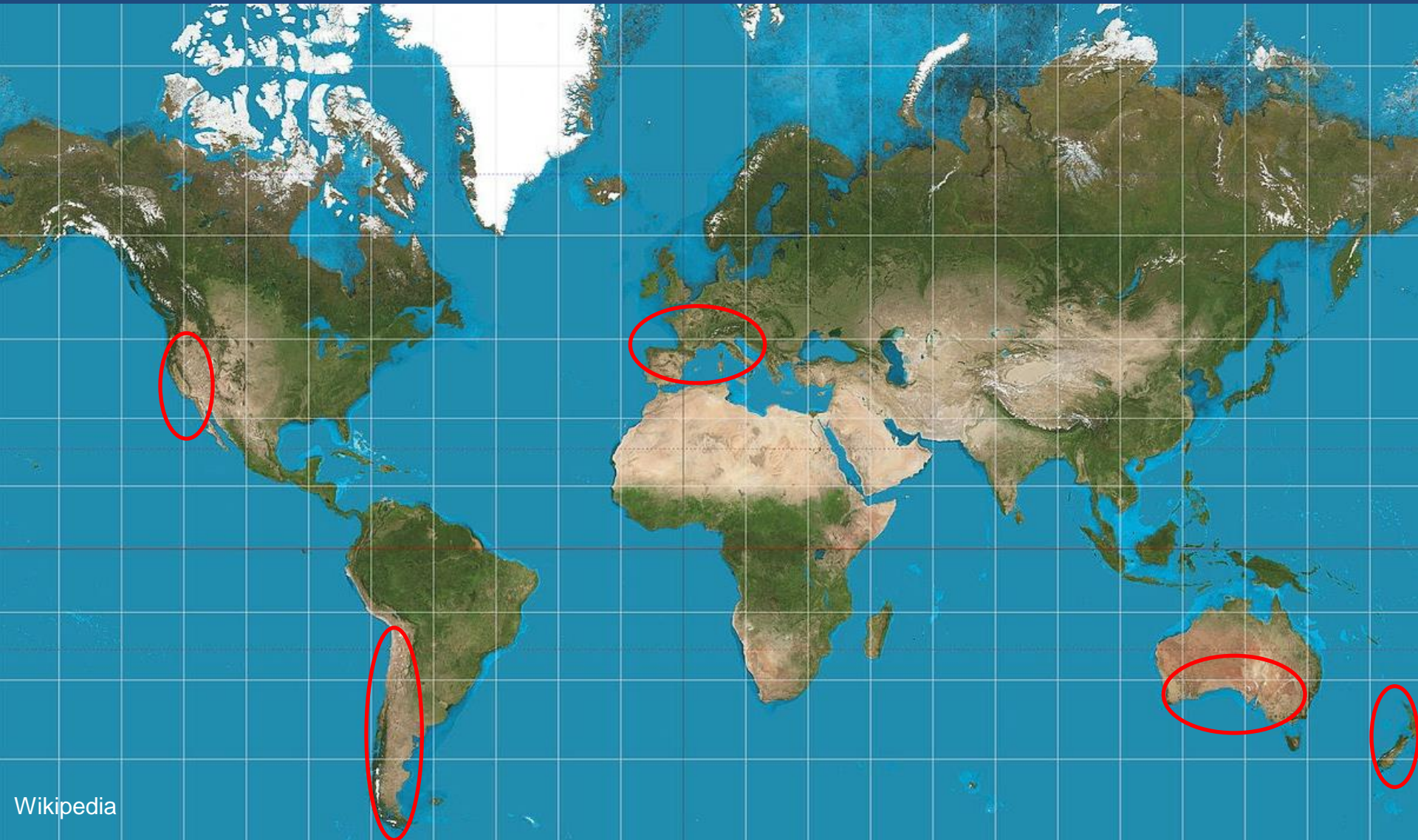


# Shifting distributions of pitch canker lesion lengths in Monterey pine as a result of systemic acquired resistance

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# Monterey pine



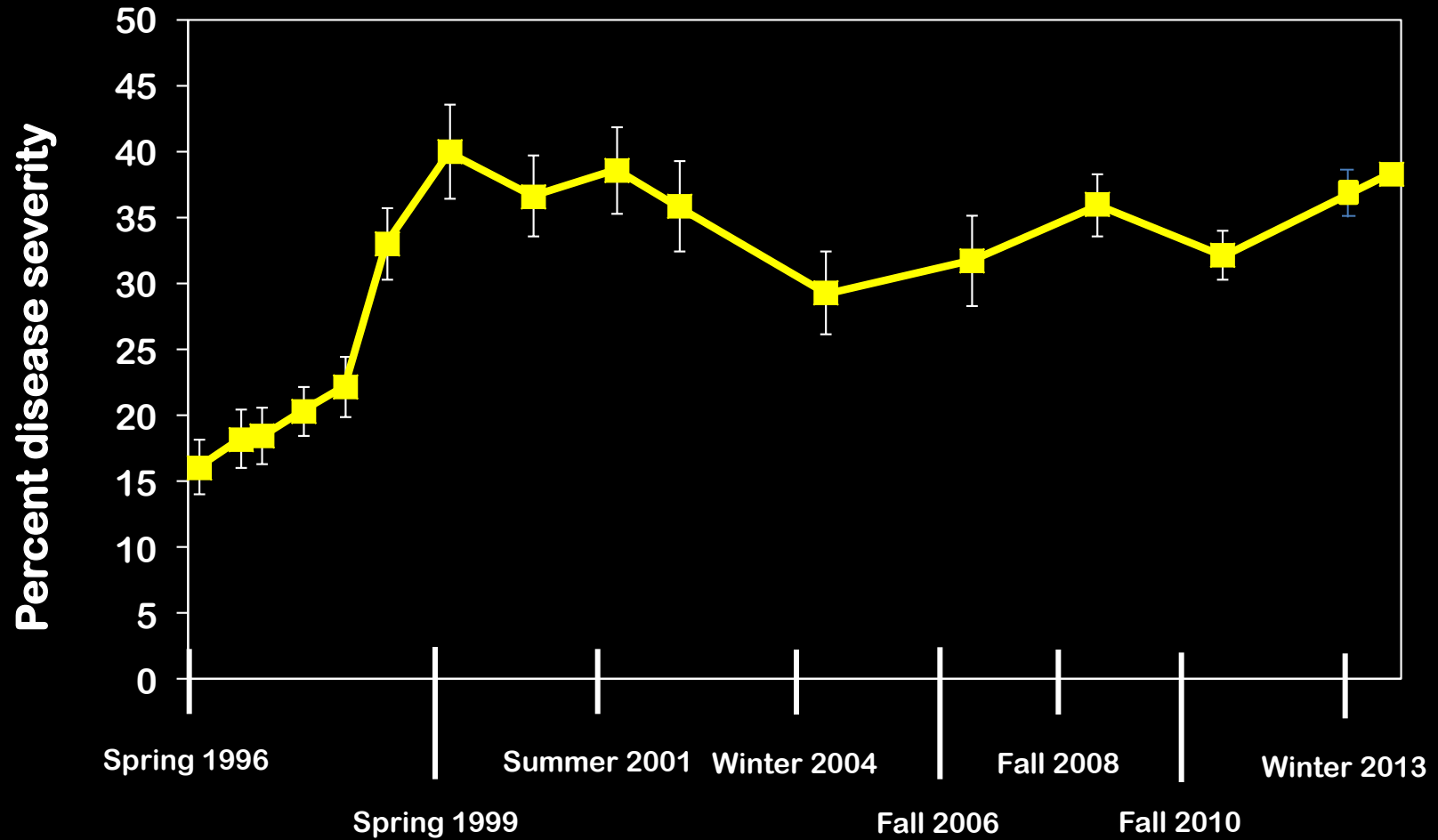
# Pitch canker

- Causal organism: *Fusarium circinatum*
- Introduced to CA from SE US (Mexican origin?)
- Resinous cankers on branches and trunks
- Trunk/soilborne infections can kill trees



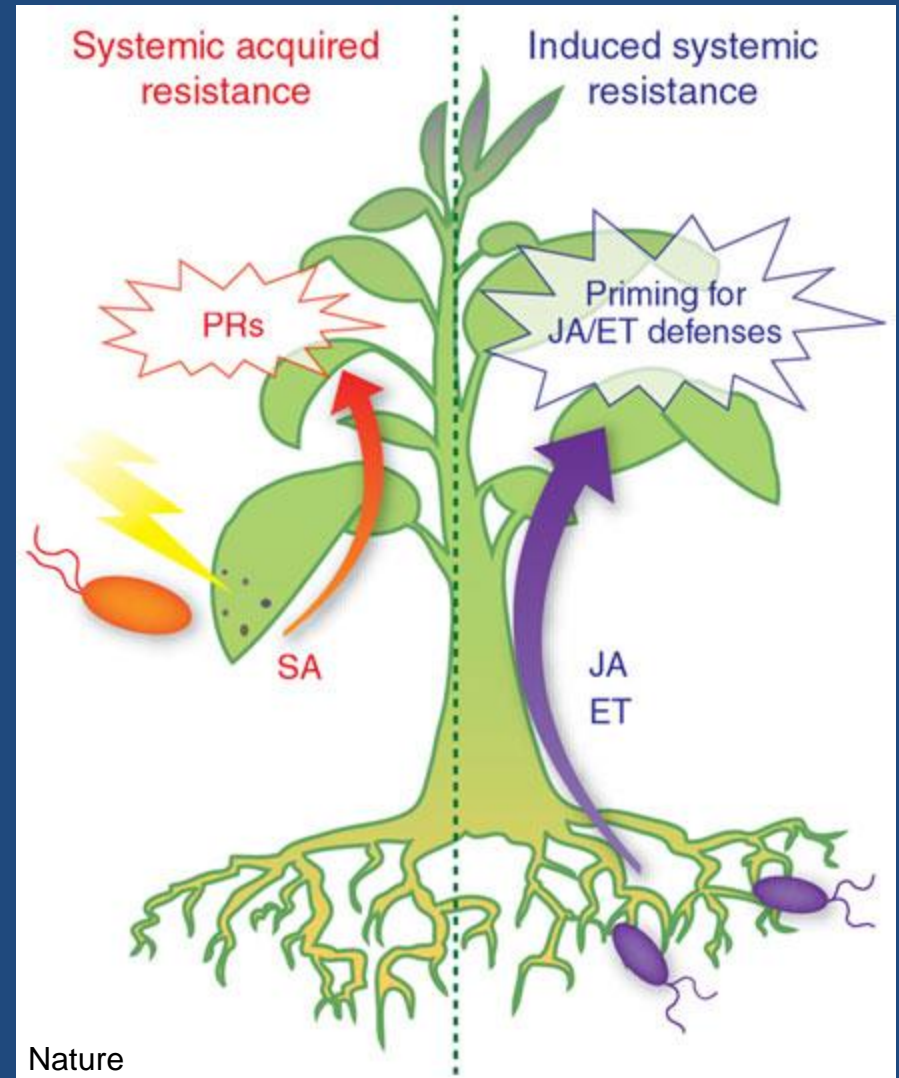


## Pitch canker disease progress over time

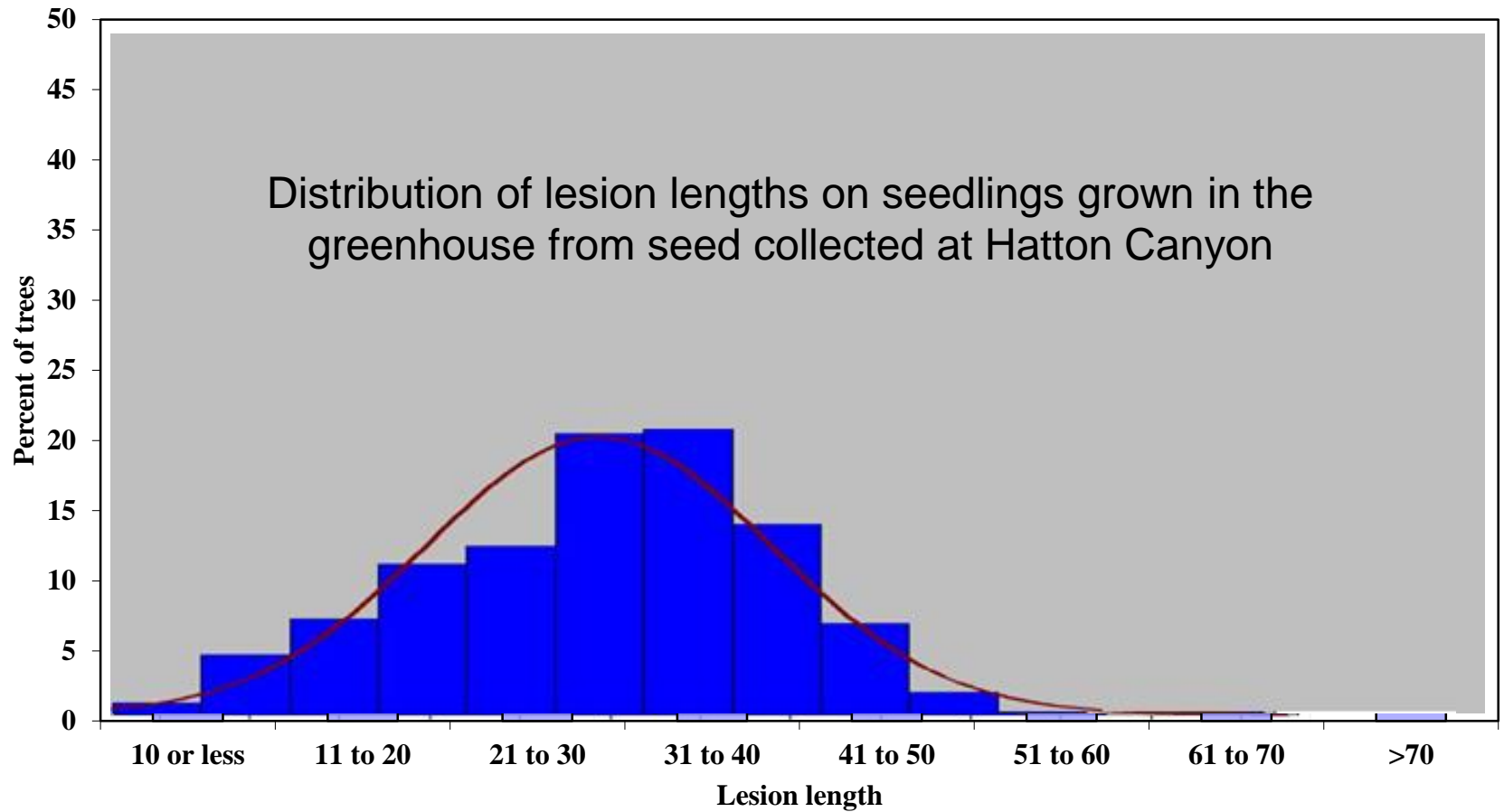


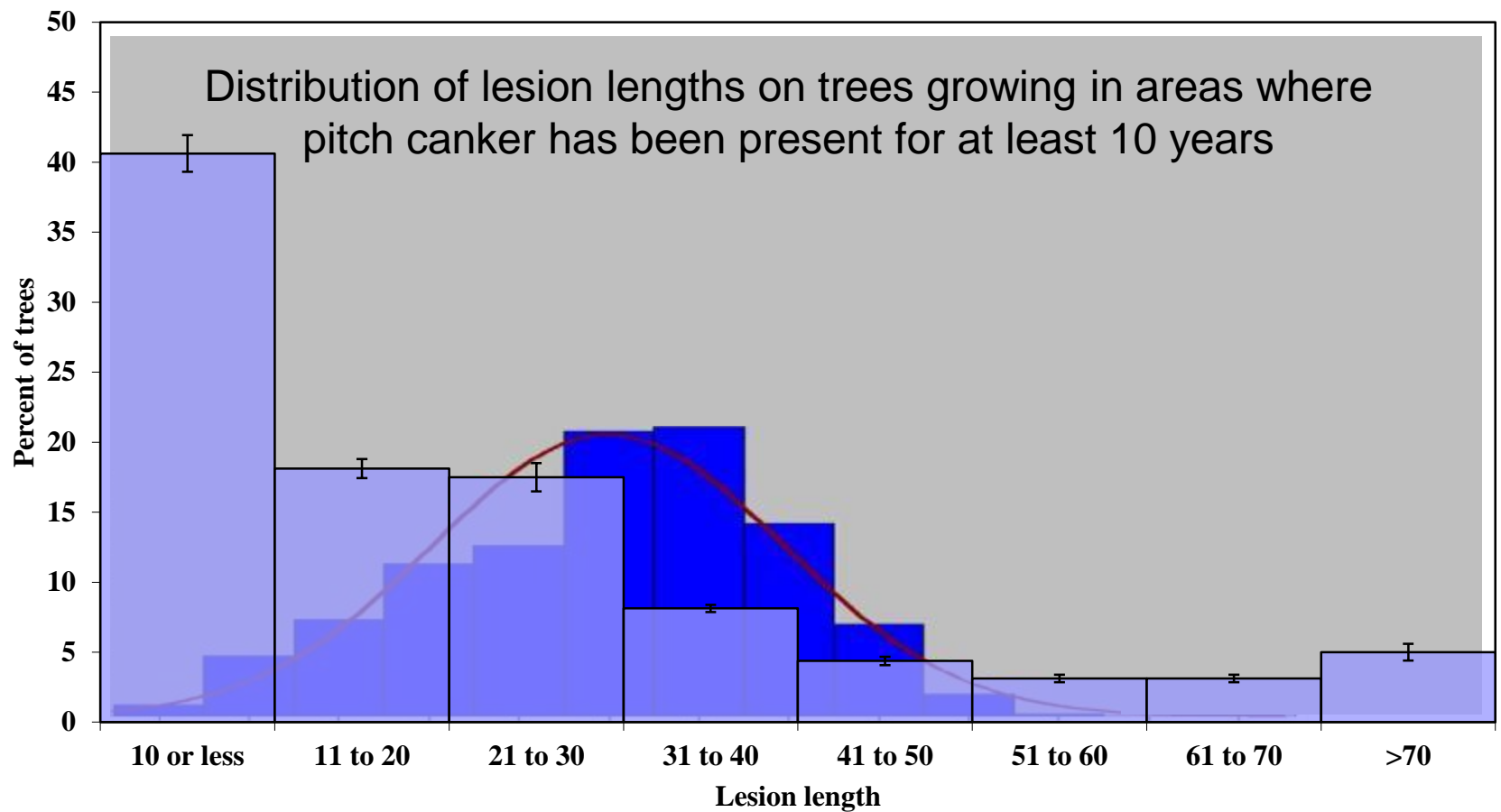
# Systemic acquired resistance

- Initial pathogen challenge leads to systemic acquired resistance (SAR) throughout plant
- Manifests in Monterey pine as reduced lesion lengths



Distribution of lesion lengths on seedlings grown in the greenhouse from seed collected at Hatton Canyon



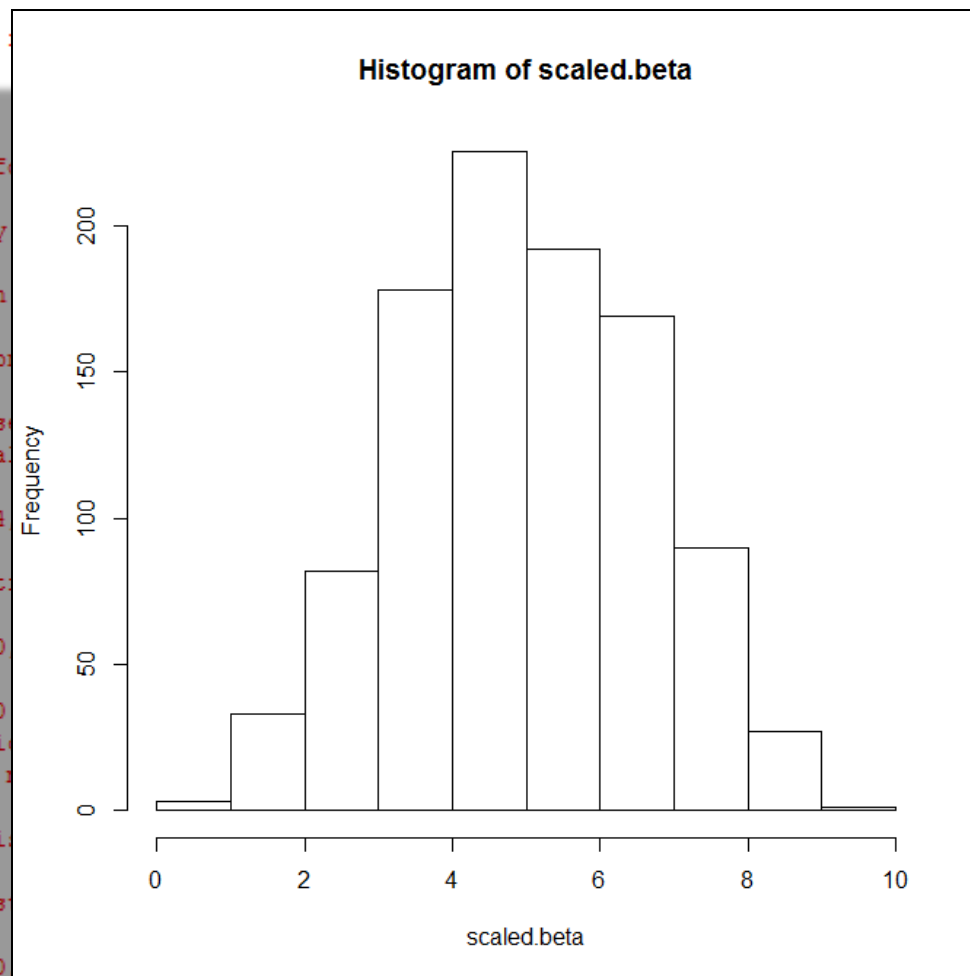


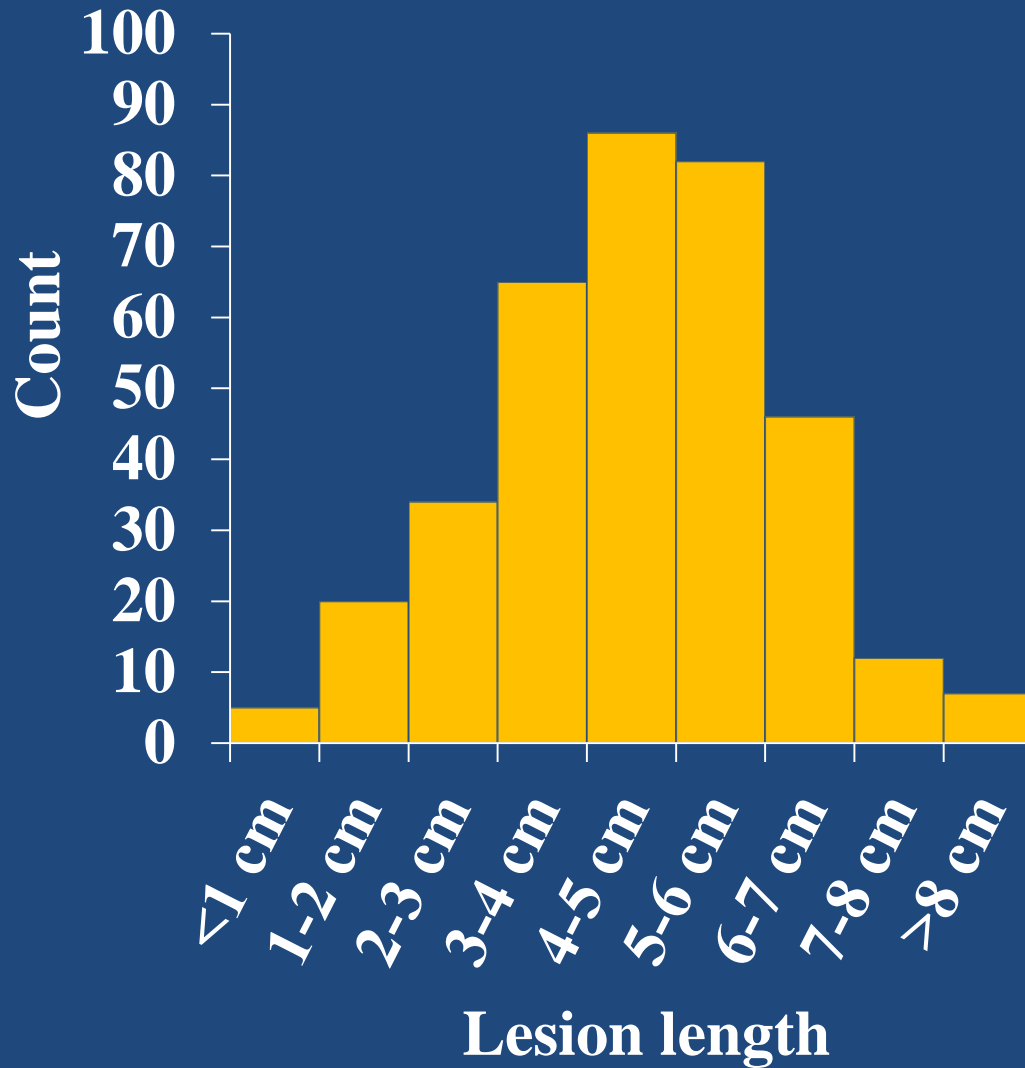
# Objective

- Develop model with three major components to explain observed shift in resistance:
  - 1) Representation of naïve seedling lesion length distribution



```
> test=character(last.run)
>
> # Generate for loop to
>
> #for(x in 1:last.run){
>
> # Generate data array f
>
> shifting.lesions<-array
>
> # Assign names for each
>
> colnames(shifting.lesion
>
> # Generate dummy data s
> # chosen to mimic Normal
>
> beta.dist<-rbeta(1000,4
>
> # Store basic beta dist
>
> shifting.lesions[1:1000
>
> # Data ranges between 0
> # rescale to a realisti
> # 10 cm is chosen as a
>
> scaled.beta<-10*beta.di
>
> # Store scaled beta dist
>
> shifting.lesions[1:1000
>
> # Set up a graph array to show three different graphs in one graphic
>
> #par(mfrow=c(2,2))
>
> # Make histogram of scaled beta distribution
>
> hist(scaled.beta)
```





**Susceptibility  
phenotypes normally  
distributed in naïve  
seedlings grown in  
growth chamber from  
seed collected in a  
native Monterey pine  
stand**

# Objective

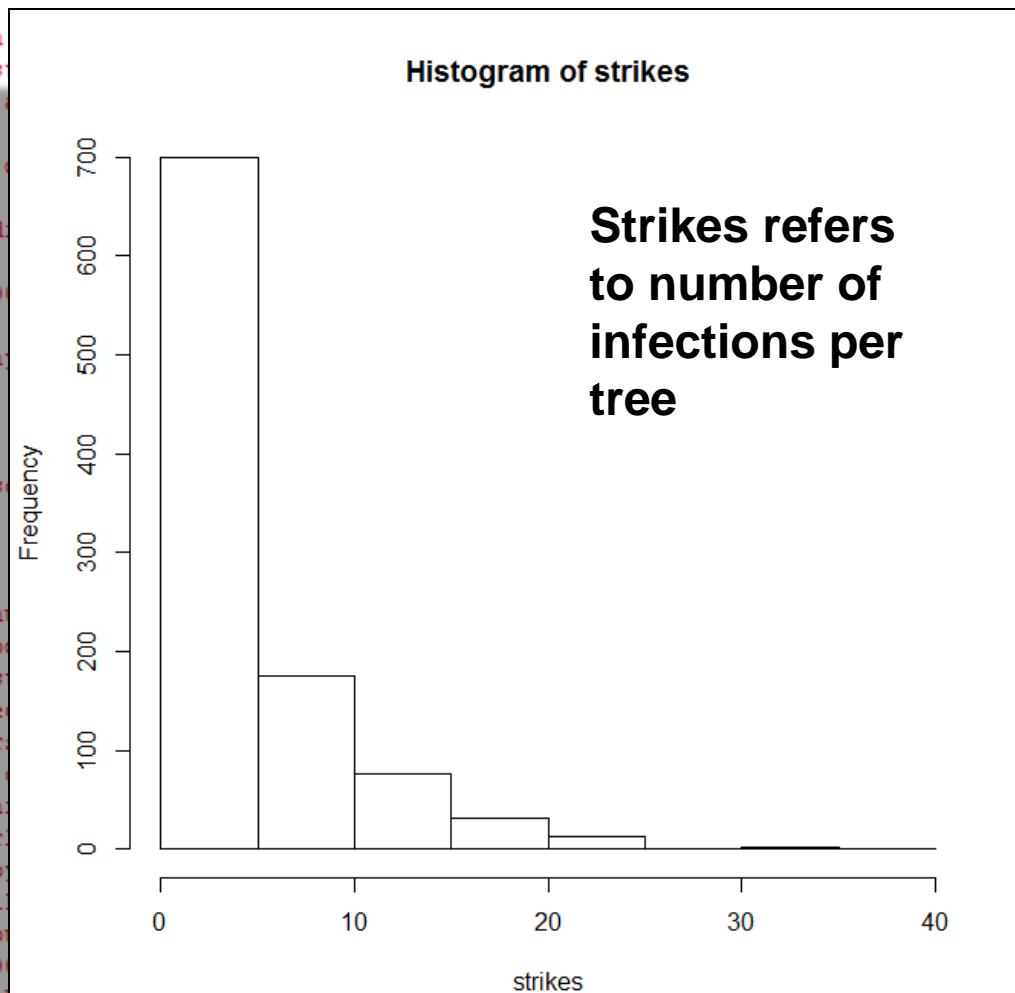
- Develop model with three major components to explain observed shift in resistance:
  - 1) Representation of naïve seedling lesion length distribution
  - 2) Stochastic contagious contact distribution between hosts and pathogen



```

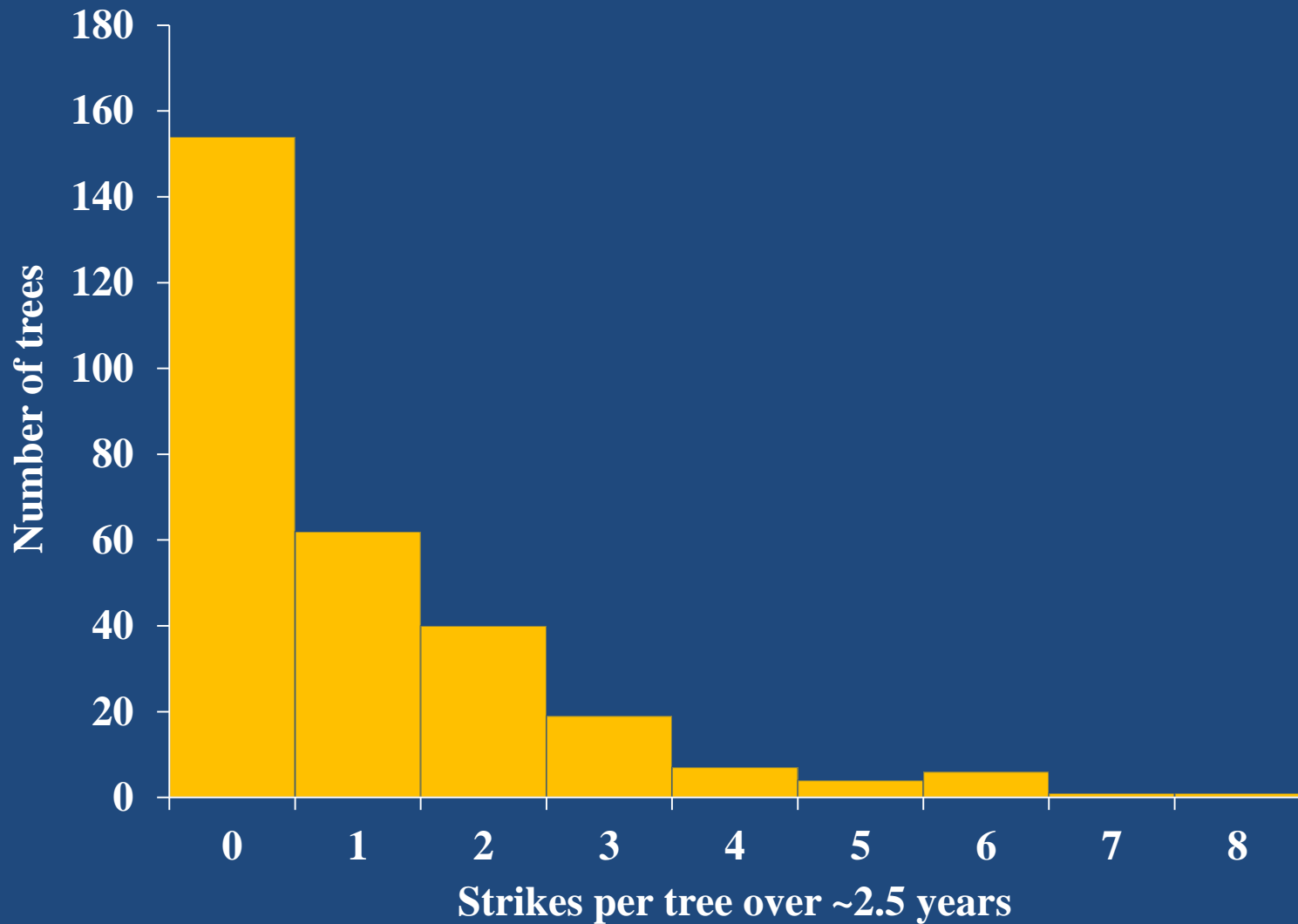
>
> # Data ranges between
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>
> scaled.beta<-10*beta.
>
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>
> # Set up a graph array
>
> #par(mfrow=c(2,2))
>
> # Make histogram of s
>
> hist(scaled.beta)
>
> # Generate data for n
> # suitable time perio
> # and ask, how many s
> # Based on data colle
> # per tree in 10 year
> # strikes tend to be
> # per tree over 5 year
> # on proximity to earl
> # model the outcome b
> # final tally of strik
> # appropriate distrib
> # generate another 10
> # available in R in w
>
> # "size" is an inverse measure of aggregation; i.e. small values indicate high patchiness
> # or high tendency of new strikes to occur close to old ones. Note that this is an
> # example of what Meentemeyer et al called an implicit spatial model; the spatial
> # arrangement of strikes over trees is implied but not modeled explicitly.
>
> strikes<-rnbinom(1000,mu=5,size=1)
> hist(strikes)
>

```





# Natural infection frequency





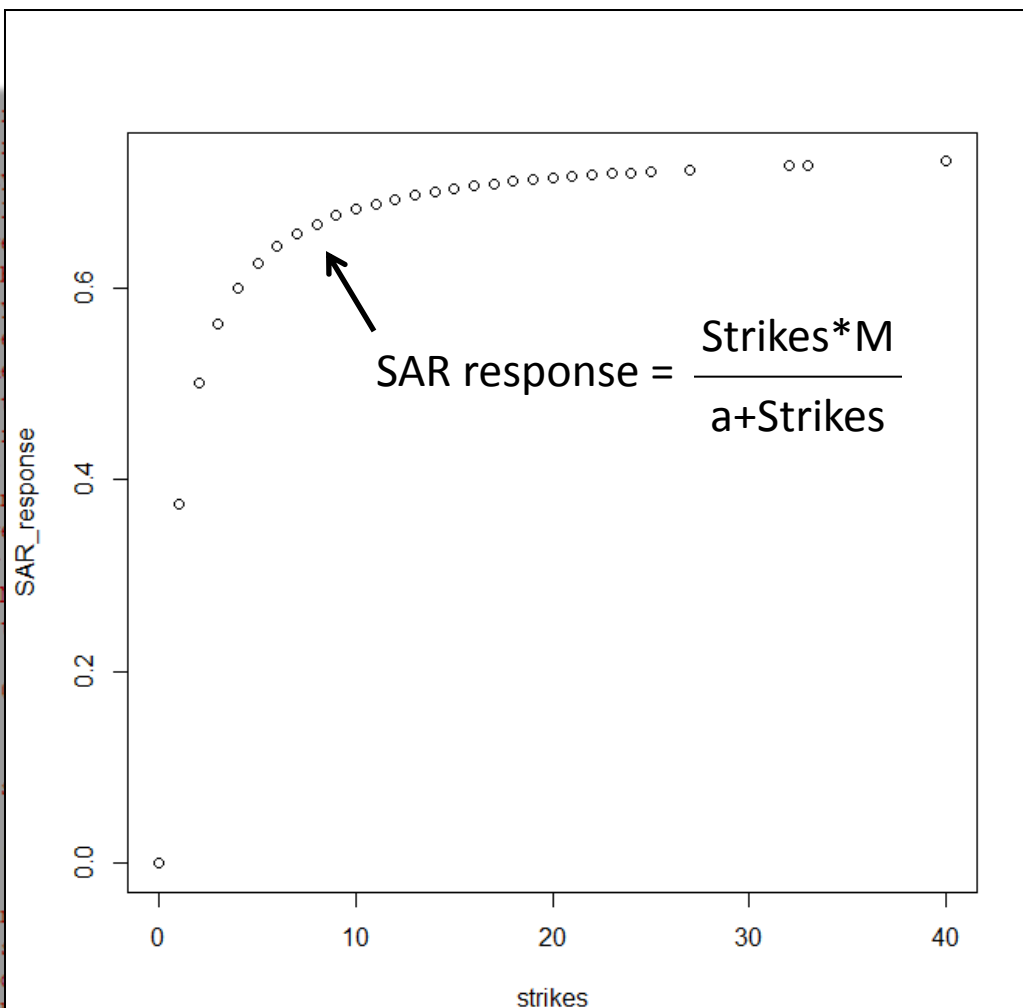
# Objective

- Develop model with three major components to explain observed shift in resistance:
  - 1) Representation of naïve seedling lesion length distribution
  - 2) Stochastic contagious contact distribution between hosts and pathogen
  - 3) Host phenotype response function that determines impact of disease on SAR

```

>
> hist(scaled.beta)
>
> # Generate data for
> # suitable time period
> # and ask, how many
> # Based on data collected
> # per tree in 10 years
> # strikes tend to increase
> # per tree over 5 years
> # on proximity to water
> # model the outcome of
> # final tally of strikes
> # appropriate distribution
> # generate another set of
> # available in R is the
> # "size" is an inverse
> # or high tendency
> # example of what I mean
> # arrangement of strikes
>
> strikes<-rnbinom(100, 1, 0.1)
> hist(strikes)
>
> # Store strikes data in a vector
>
> shifting.lesions[1,] = 1
>
> # Now we need a function to
> # To do this we assume a
> # proportionate reduction in
> # parameters: M, the maximum
> # number of strikes required to
> # of a, the more rapid/extreme the response of the plant to infection.
>
> M<-0.75 # Lesions can reduce only to 75% of their initial size
> a<-1 # One strike causes 50% reduction in lesion length on subsequent infections.
> SAR_response<-(strikes*M)/(a+strikes)
> plot(strikes,SAR_response)
>

```



# Quantitative effect of pitch canker infection on induction of resistance

- Trees grown in Davis, CA for 2-4 years from cuttings and seedlings (2009-2013 plantings)
- Trtmnts consist of varying numbers of initial inoculations (i.e, zero, one, five, 10, 20)

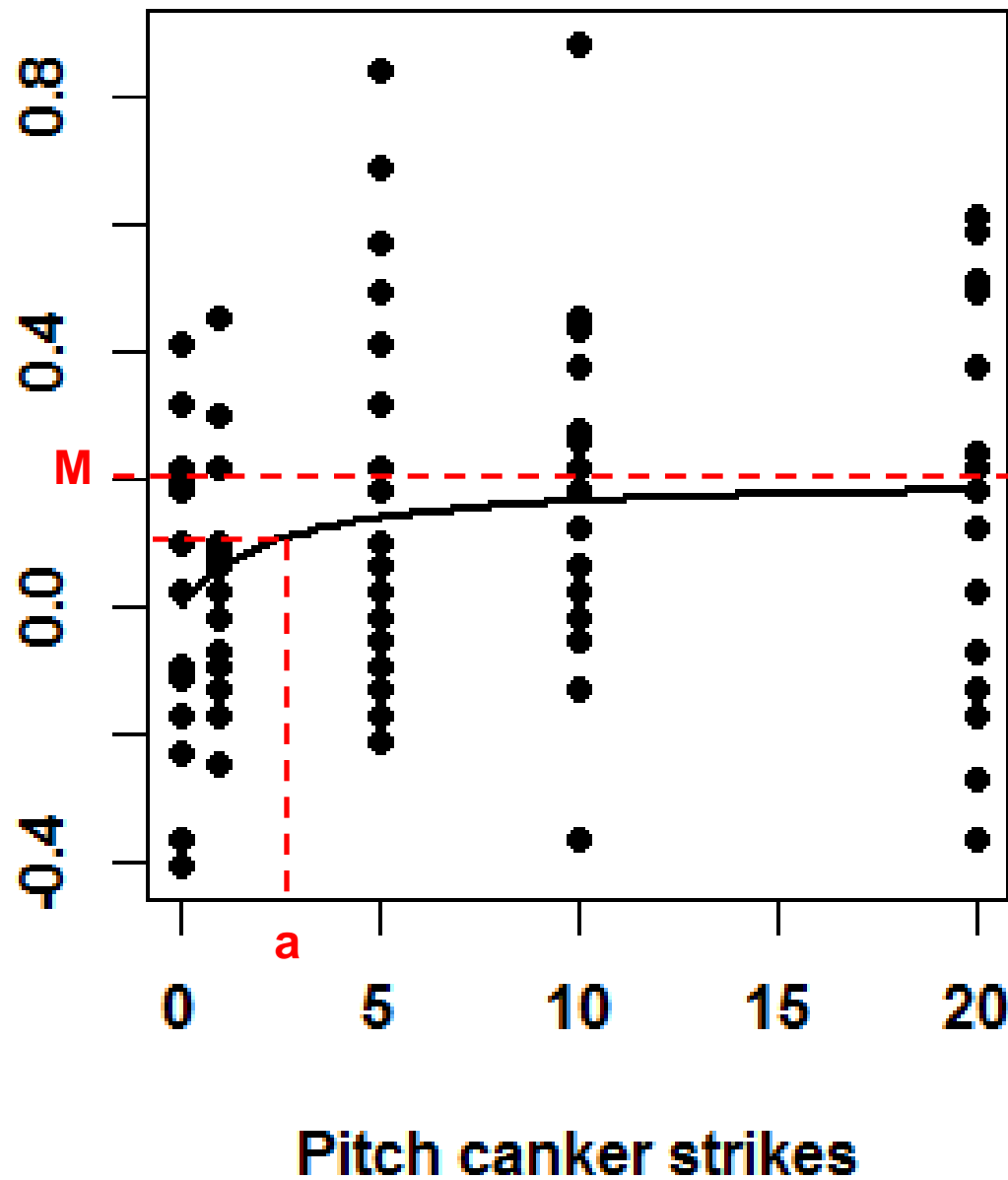




# Quantitative effect of pitch canker infection on induction of resistance

- Trees grown in Davis, CA for 2-4 years from cuttings and seedlings (2009-2013 plantings)
- Trtmnts consist of varying numbers of initial inoculations (i.e, zero, one, five, 10, 20)
- Each tree challenge inoculated with three infections after 8-10 weeks
- Relative contribution of each initial infection to induced resistance response measured

Proportional lesion reduction



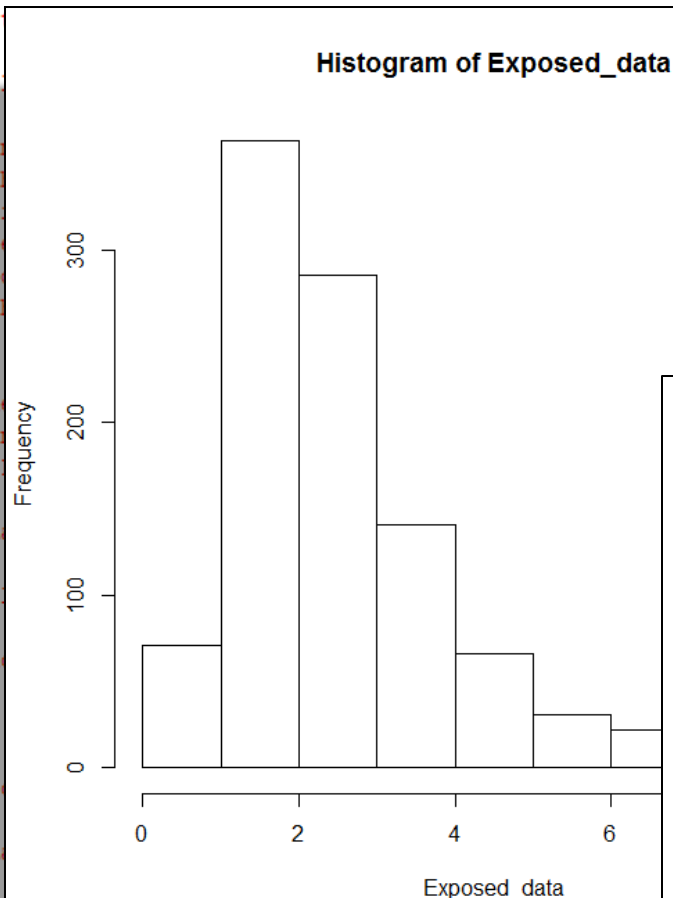
$$SAR = \frac{\text{Strikes} * 0.2}{2.33 + \text{Strikes}}$$



```

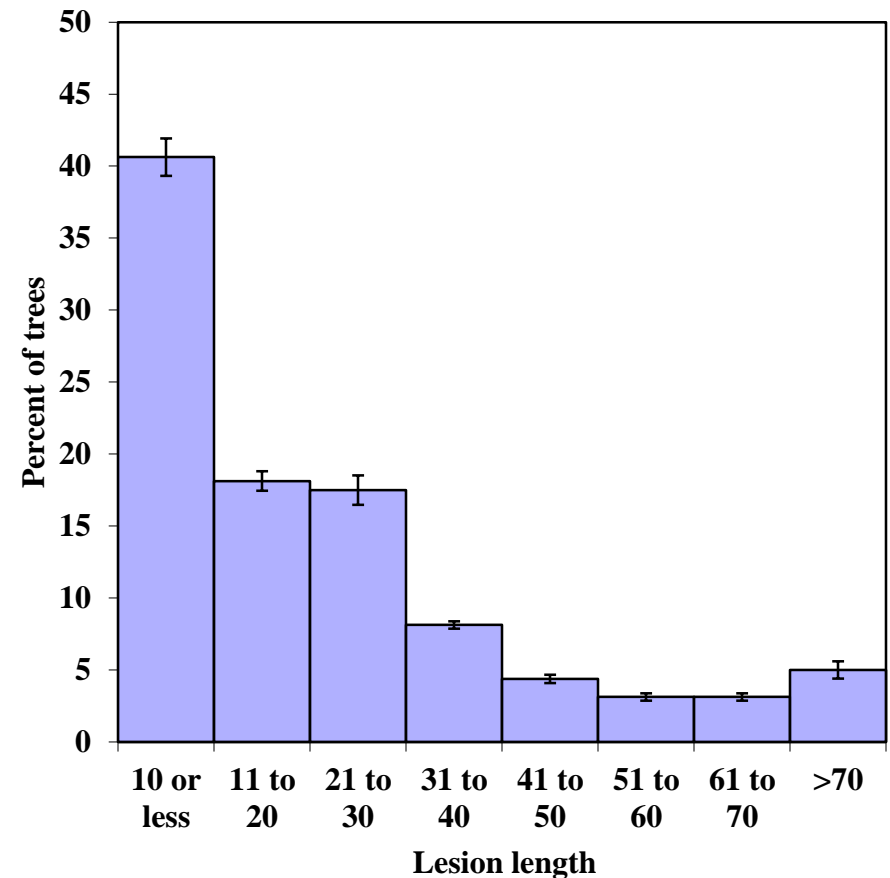
>
> # Store s
>
> shifting.
>
> # Now we
> # To do t
> # proport
> # paramet
> # number
> # of a, t
>
> M<-0.75 #
> a<-1 # On
> SAR_respo
> plot(stri
>
> # Store d
>
> shifting.
>
> # Introdu
>
> l_min<-1
>
> # Now cal
>
> Exposed_d
> for (tree
+ Exposed_d
+ scaled.beta[tree]-(SAR_response[tree]*scaled.beta[
+ }else{
+ scaled.beta[tree]}
+ }
>
> #Plot a histogram of the distribution of lesion len
>
> hist(Exposed_data)
>
> |

```



## Tying the pieces together:

Naïve seedling lesion length distribution multiplied by SAR response function yields shifted lesion length distribution.



## Effect of exposure to *F. circinatum* on distribution of lesion length phenotypes

- 760 seedlings planted in native stand on Monterey Peninsula in December 2012 from same seed source as naïve seedlings
- To be inoculated with *F. circinatum* after 2.5 and 5-10 years growth under natural exposure
- Susceptibility phenotypes of those growing in presence of natural inoculum expected to be shifted towards resistance







# Concluding remarks

**Potential for disease reduction  
in severely infected bishop pine  
at Point Reyes over time**





# Acknowledgements

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