

Population Genetic Studies of Tanoak: An Overview of Current Knowledge and Its Applications to Conservation and Restoration

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Host Population Genetics and SOD

- Conservation and Restoration
 - Should we conserve the species?
 - If yes, successful conservation and restoration depend on a knowledge of the underlying genetic resource (degree of variation and geographic organization)
 - Thousands of genotypes in the landscape. Not all can be screened, so focus on populations
 - Molecular genetics can indicate regions of differentiation and high diversity.

Current Knowledge

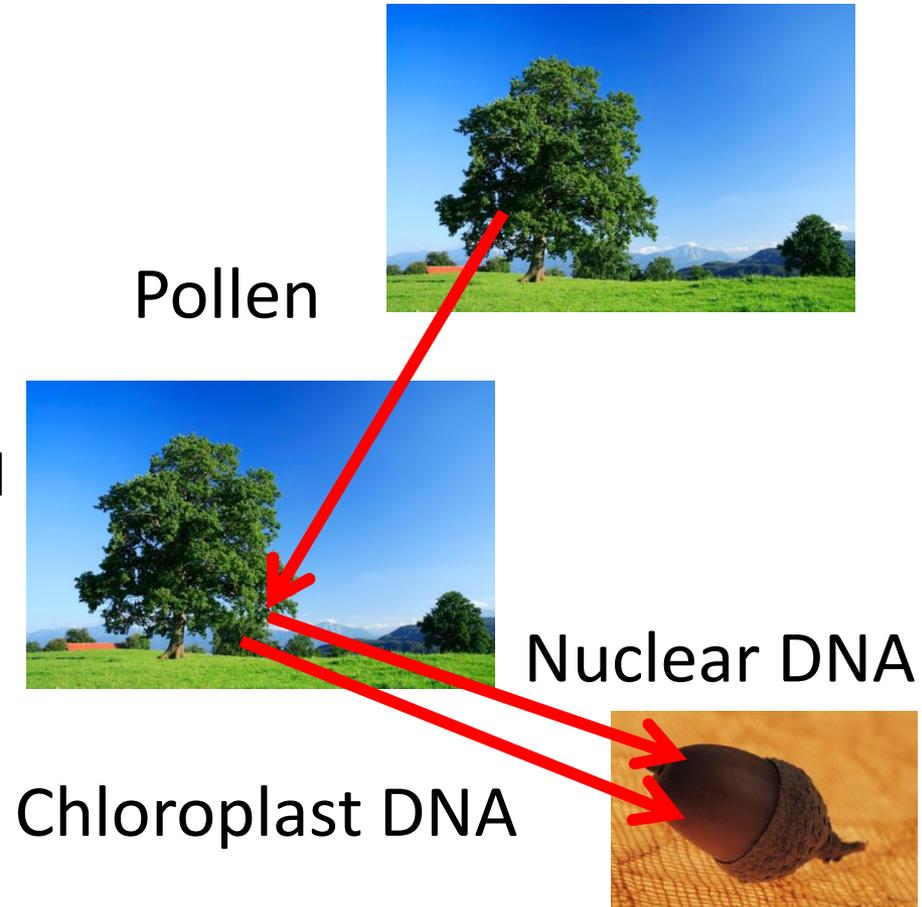
- Partition of neutral genetic diversity
- Contribution of clonality to stand genetic diversity
- Pollination and outcrossing

Current Knowledge

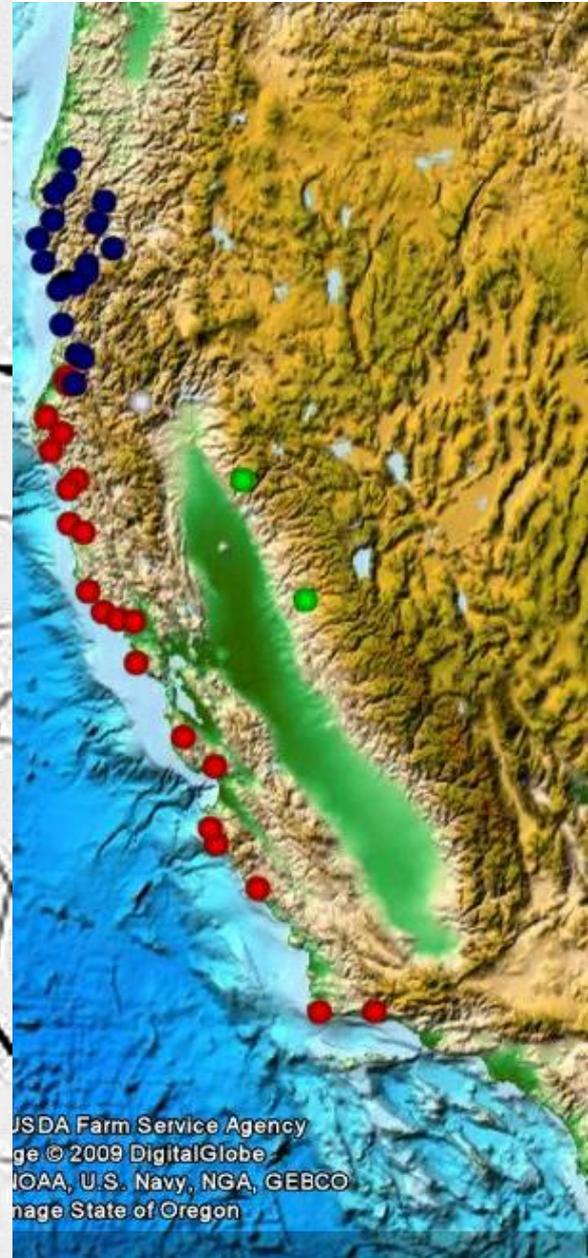
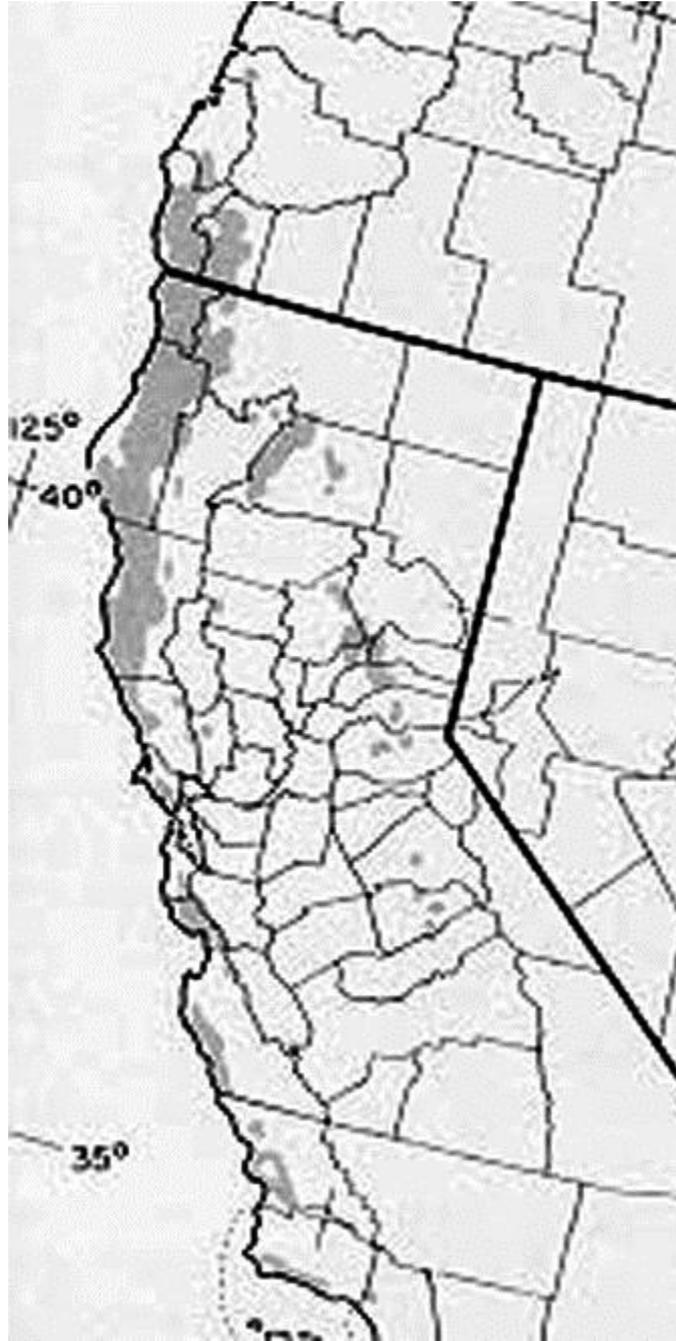
- Partition of neutral genetic diversity
 - Range-wide
- Contribution of clonality to stand genetic diversity
 - Within a Stand
- Pollination and outcrossing
 - Within a tree

Genomes

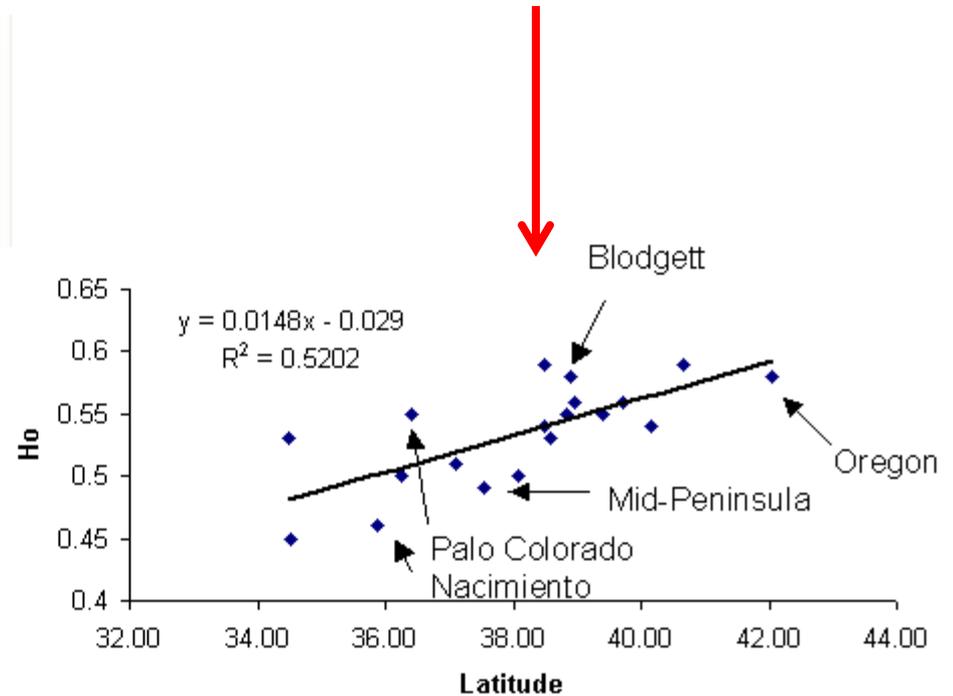
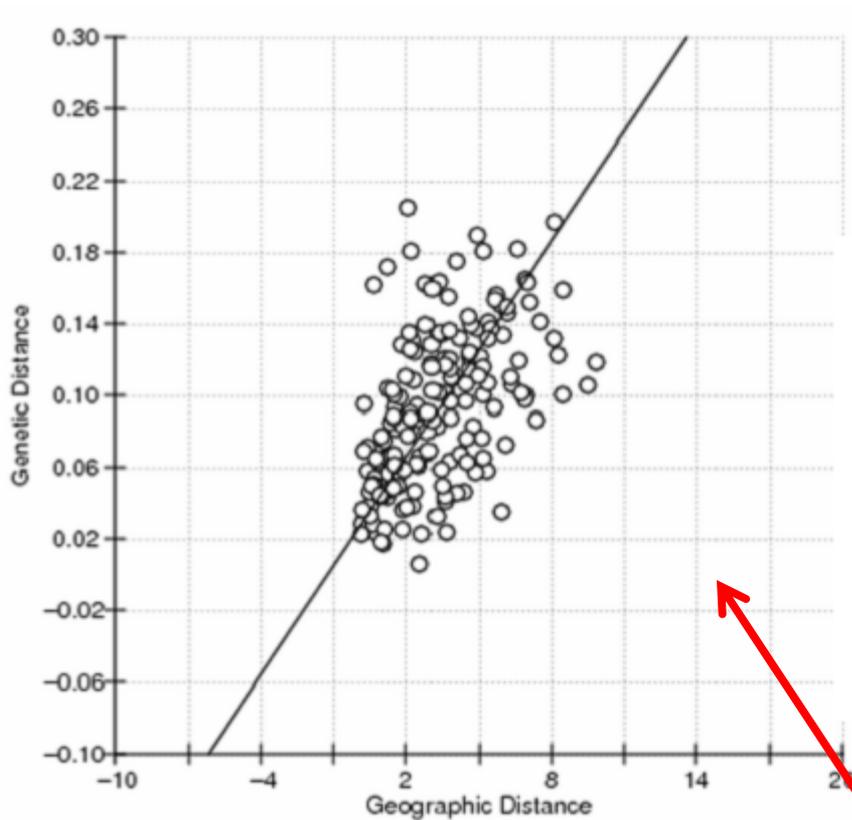
- Genetic resources can be assessed using regions of DNA on which natural selection does not act (neutral), or on genes (selective)
- DNA is present in the nucleus and in cellular organelles such as chloroplasts
- Chloroplast DNA inherited maternally through seed dispersal (clonal)- good indication of ancient fragmentation of the species' range
- Nuclear DNA inherited biparentally through pollen and seed dispersal- more recent processes



- *L. densiflorus ssp. densiflorus*
- Chloroplast DNA
 - Four major (2 rare) haplotypes
 - Strong divergence between coastal and Sierran populations



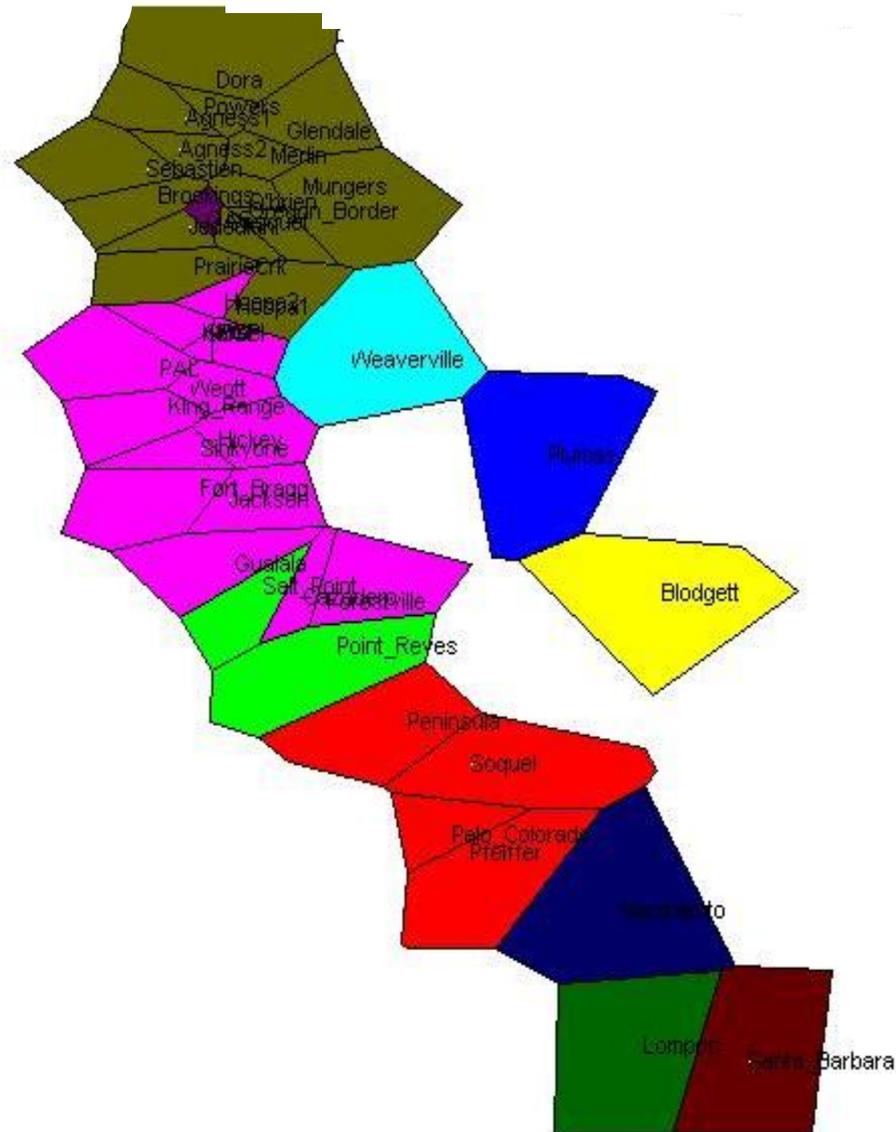
There is increasing genetic diversity with latitude



Trees that are farther apart are more genetically different

Nuclear DNA Lineages

- Analysis of 900 samples from 43 populations
 - Assignment to 11 clusters (1 *echinoides*)
 - Clusters of single or few populations in central California and the Sierra/Klamath ranges
 - Two widespread groups of populations in northern California and Oregon
 - Striking breaks at Arcata and the San Francisco Bay



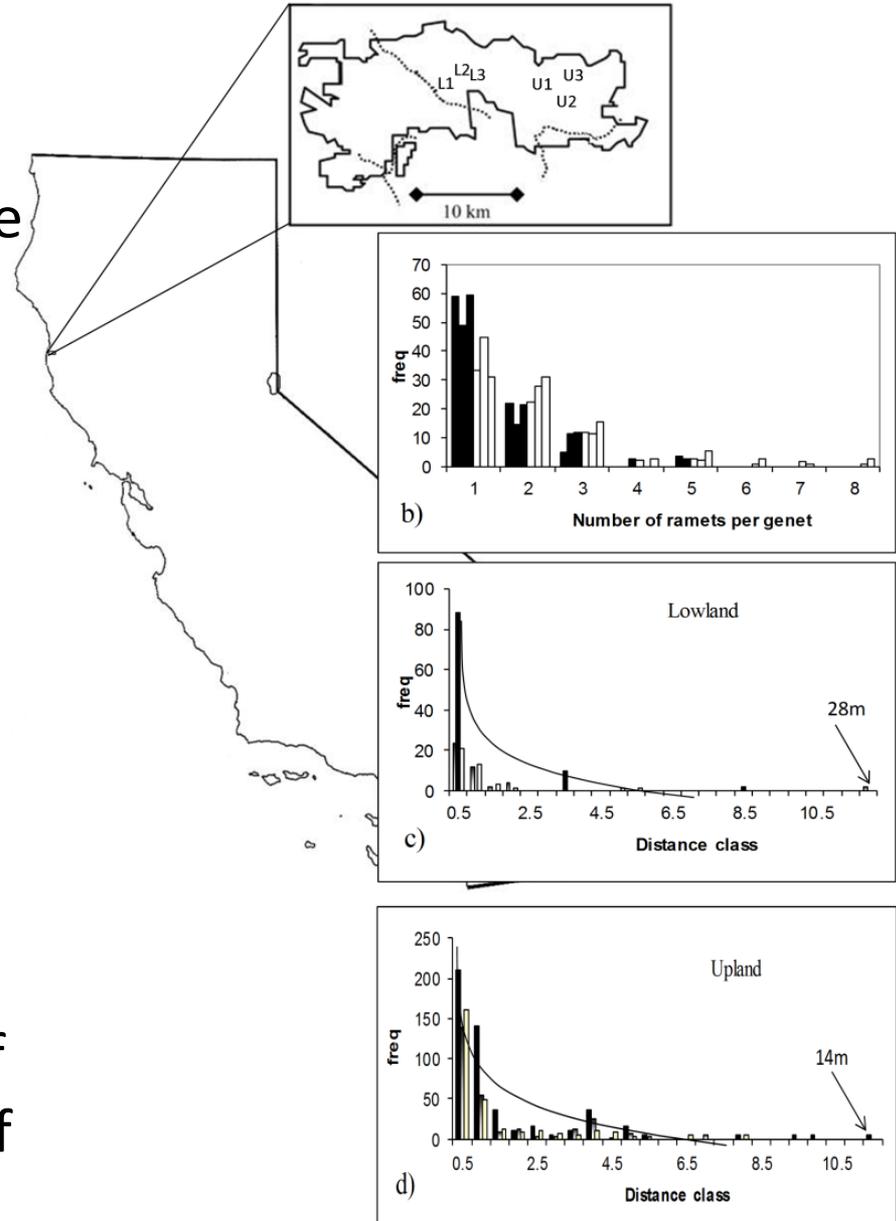
Conclusions- Range-wide analysis

- 1) Seed dispersal distances are very limited
 - An abrupt transition of chloroplast haplotypes near Arcata, shows that seeds have not dispersed to form mixed haplotype stands
- 2) Nuclear DNA indicates a number of discrete groups of populations.
 - These need to be accounted for in any plans for restoration and seed movement.
- 3) What about future climate?

Contribution of clonality to stand genetic diversity

- Tanoak reproduces by seed and resprouting
- How does resprouting contribute to genetic diversity?

- 1) In stands regenerated after fire, thinning of resprouts leads to few stems per clone.
- 2) As many as 8 mature stems per clone
- 3) ~40% of a stand is clonal
- 4) Members of the clone are normally spatially close, but the average distance of extinction of clones is 6m, with a maximum of 28m recorded



Spatial structure of clonality

- Upland sites are drier with smaller stature trees
- These are likely to have undergone greater disturbance frequency than lowland sites
- Has disturbance frequency affected levels of clonality?
 - 1) Clonal diversity lower on upland sites (i.e. more stems per clone) but not significantly
 - 2) Average distance between clones greater on lowland sites
 - 3) No difference in genetic diversity

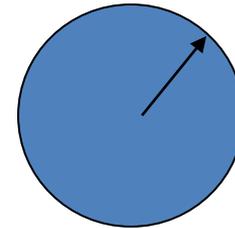
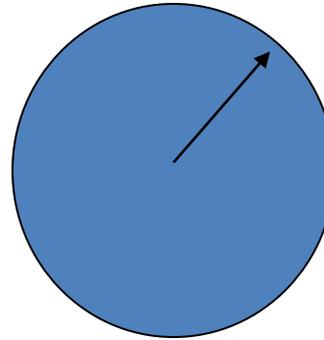
| | Clonal diversity | Clonal range max. (m) |
|----------------|------------------|-----------------------|
| Site 1L | 0.73 | 28.4 |
| Site 2L | 0.69 | 6.5 |
| Site 3L | 0.61 | 5.3 |
| Lowland | 0.68 | 13.4 |
| Site 1U | 0.43 | 14.0 |
| Site 2U | 0.59 | 8.2 |
| Site 3U | 0.61 | 10.2 |
| Upland | 0.54 | 10.8 |

How far do genes move by seed/pollen and clonal dispersal?

Dispersal by seed,
pollen and sprouting

Lowland

Upland



Axial distance of seed/pollen gene dispersal

69m

46m

Axial distance of clonal gene dispersal

1.7m

2.1m

- 1) On lowland sites neighborhoods of related individuals extend over ~70m
- 2) Stand density and tree size affect the size of these neighborhoods

Restoration implications

- 1) Within stands, maximum genetic diversity with minimum risk of planting mal-adapted genotypes would favour seed collections from non-clonal and unrelated individuals from as short a distance as possible from the site to be restored
- 2) A diverse array of individuals should be used as seed trees.
 - 1) On lowland sites: a minimum of-
 - 20m between trees to avoid clone-mates
 - 70m to obtain seed from unrelated individuals
 - 2) On upland sites: a minimum of-
 - 15m likely to avoid clone-mates
 - 50m to obtain seed from unrelated individuals

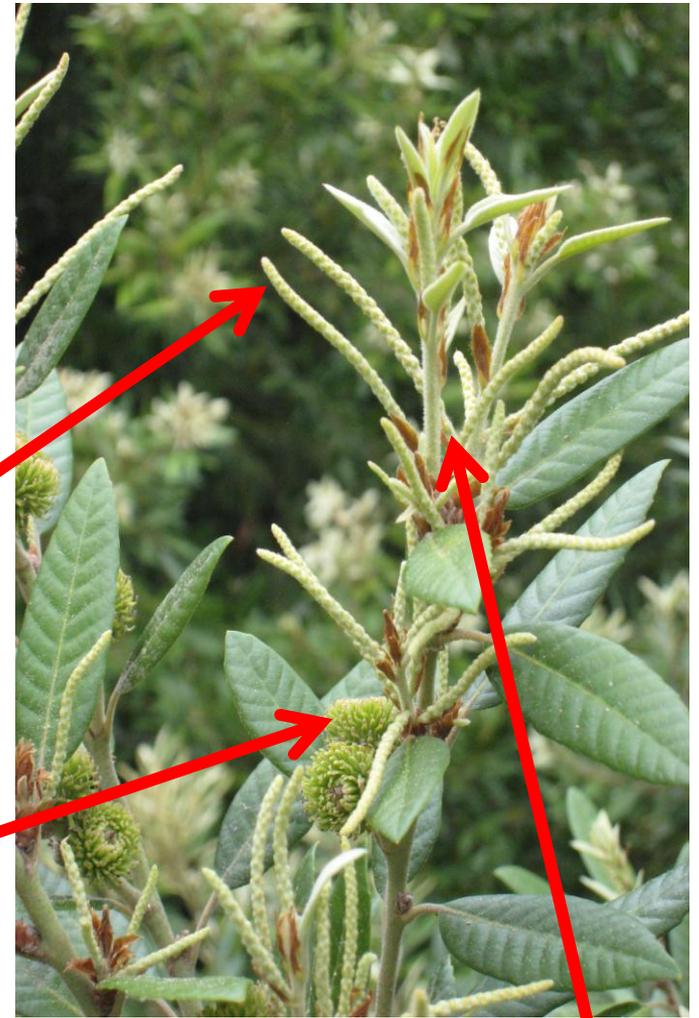
Pollination Mechanism



Inflorescence
in wedding
veil

Current
year
ament

1-yr old
maturing
acorn



Female flowers
as spikes at
base of ament

| | Bagged inflorescences | Un-bagged inflorescences |
|------------------------------------------------------------------------------------|--------------------------|-----------------------------|
| Proportion of inflorescences in which acorns showed signs of expansion | 0.32 | 0.81 |
| Proportion of successful pollinations per pistil | 0.14 | 0.65 |

Mating System

| | San Mateo | | O'Brien | |
|--------------------------|-----------|----------|---------|----------|
| | seed | seedling | seed | seedling |
| Outcrossing | 0.88 | 0.91 | ? | 0.95 |
| Breeding among relatives | 0.08 | 0.07 | ? | 0.04 |
| Pollen donors | 7 | 5 | ? | 8 |

Conclusions- within tree

- Insect pollinators are important for maximum seed production, but some wind pollination is likely to contribute to seed production and low levels of selfing may occur