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MCDB 187AL

Background and Introduction

Introduction •

Clearly state the:

– Background that explains the problem:

Maintaining oak ecosystems (Sork et al. 2016) is economically valuable.

It is a natural resource for hardwood lumber (Luppold and Bumgardner 2013)

in hunting and range lands (Standiford and Howitt 1993; Kroeger et al. 2010) and

as a source of nutrition (Dahlgren et al. 1997; Herman et al. 2003).

Thirdly, oaks

are an important means of stabilizing the habitats of aquatic and terrestrial

animals (Dosskey et al. 1997; Kroeger et al. 2010).

Fourthly, oaks are used to beautify modern civilized areas and

As food by native cultures (Pavlik et al. 1991; Anderson 2005).

And thus, the maintenance of oak ecosystems is essential.

Oaks are planted by selective harvesting and their natural

reproduction, however the c

– Problem being investigated:

Annotate genome that we may perform epigenetic experiments on Quercus lobata.

– Reasons for conducting the research:

Since Management and maintenance of oak ecosystems is a high

Priority (see Background That Explains the Problem), it is essential to ensure they are optimally doing this.

Annotating their genome will allow us to perform epigenetic

Experiments on the Valley Oak genome to determine if this

Is the case.

• Summarize relevant research to provide context:

The Pelligrini Lab and others have:

• State how your work differs from published work:

Work differs by:

• Identify the questions you are answering

• Explain what other findings, if any, you are challenging or extending

• Briefly describe the experiment, hypothesis(es), research question(s); general experimental design or method

Study Intro papers of Valley Oak

CITE AUTHORS IN YOUR BACKGROUND:

Read Publications on Valley Oak made by the professor

­­Have a well-annotated genome to do experiments on how the Valley Oak is responding

To climate changes in the environment (for instance climate change and the effect on the Valley

Oak epigenome. To perform these epigenetic experiments, we need a well annotated genome.

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