

# Bioprospecting the regional diversity of Australian wine microbiota



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## Introduction

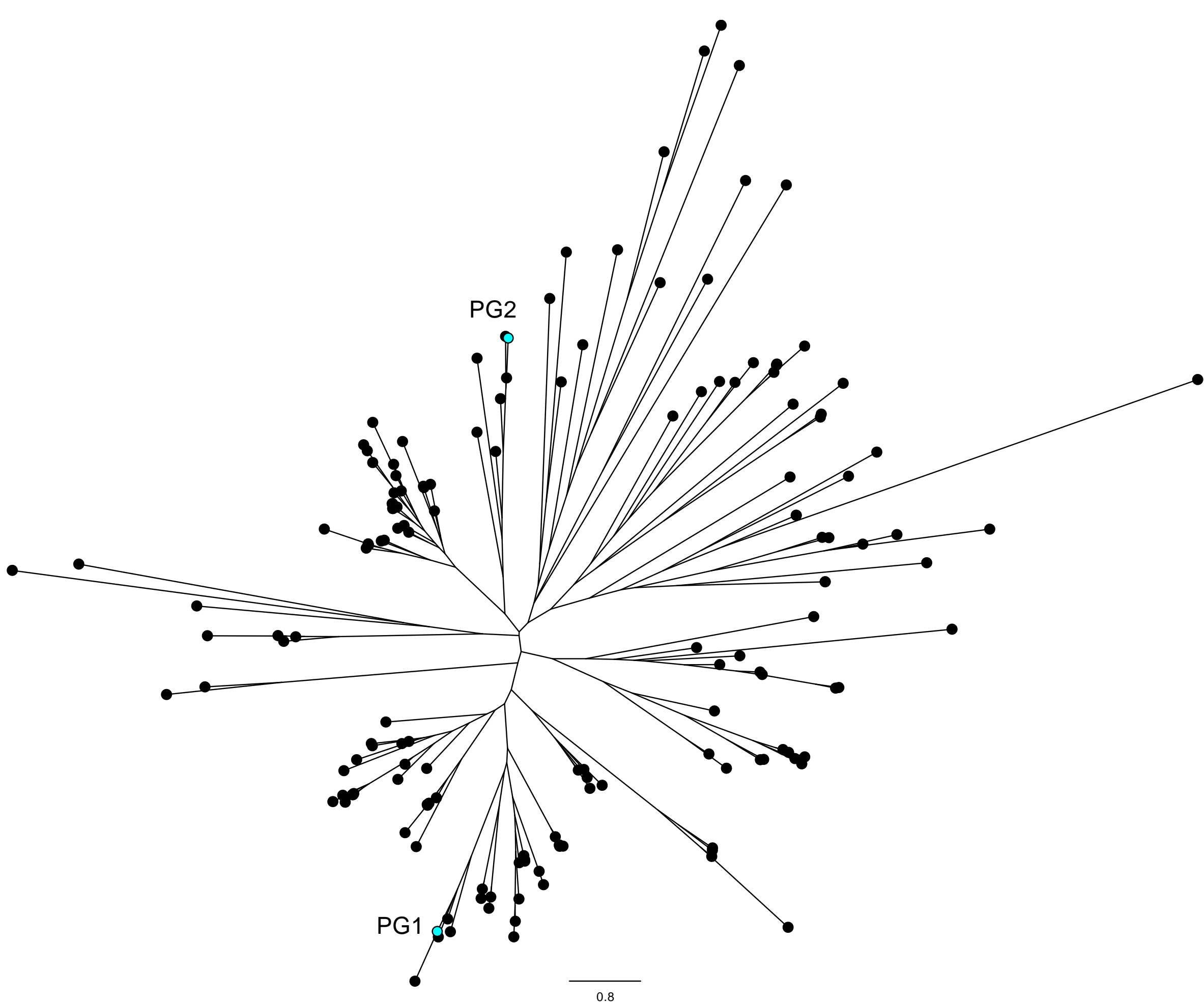
Many enzymes are inhibited by the conditions of winemaking, especially wine pH. The microbiota native to wine-grapes have demonstrated influence on winemaking and the enzymes they produce are expected to be better adapted to winemaking conditions. However, the majority of these microorganisms cannot be isolated and grown outside of their native environment and culture-based methods for investigating them are therefore limited.

## Aim

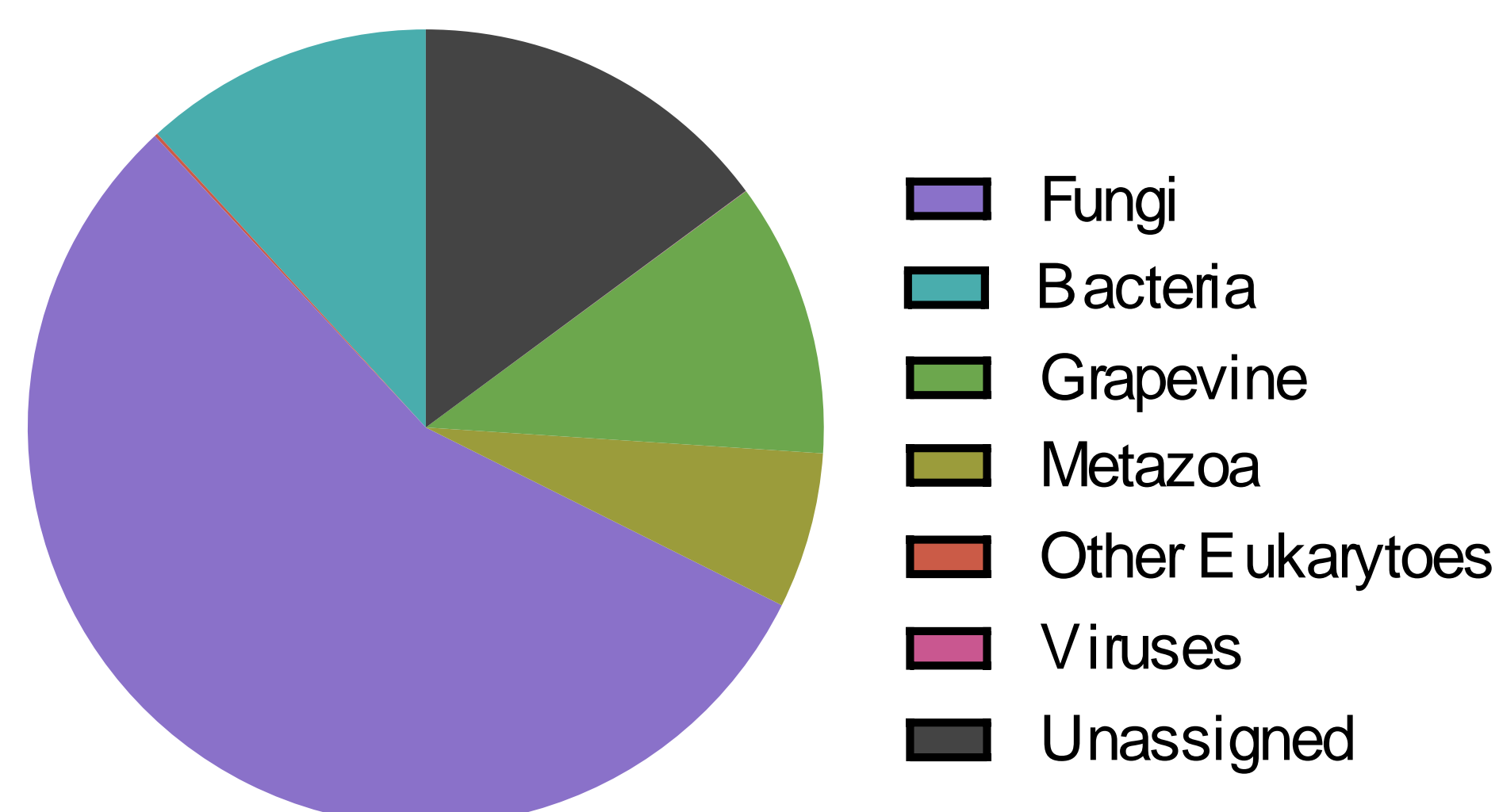
Identify and investigate microorganisms from wine-grape environments as a potential reservoir of enzymes adapted to the wine-grape environment

## Results

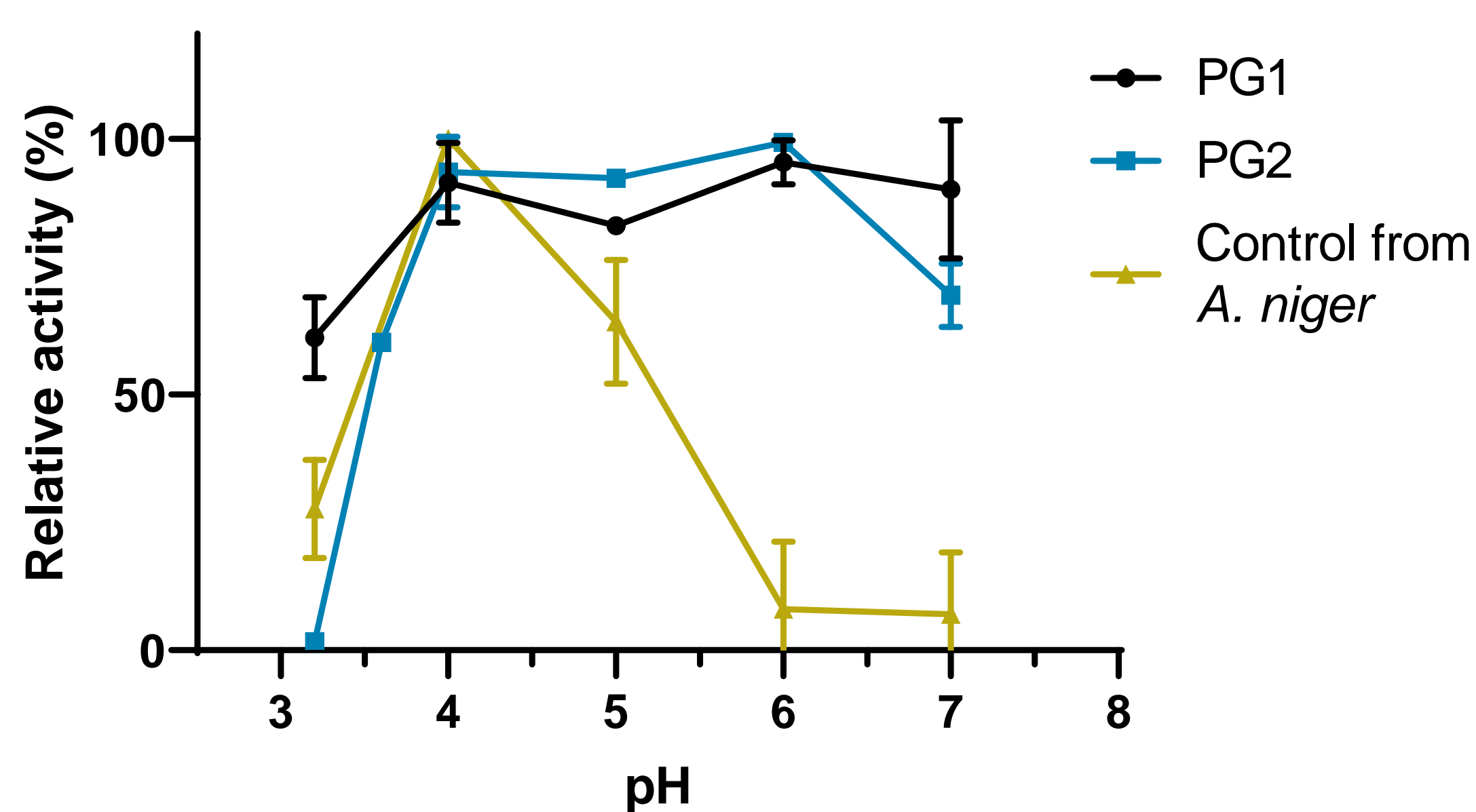
Sequence relation of 158 pectinases identified from Chardonnay must metagenome



Taxonomic assignment of Chardonnay must sequencing data



pH response of pectinases identified from Chardonnay must metagenome



## Conclusions

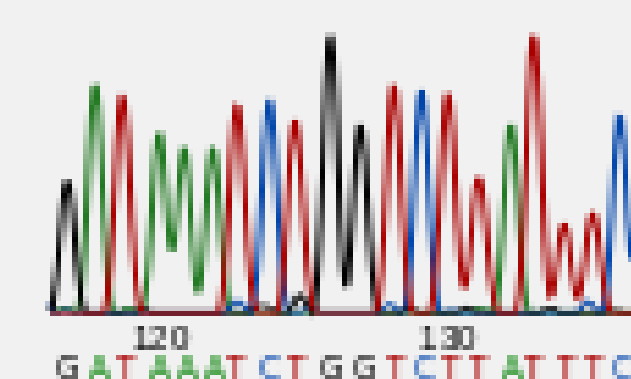
- A high proportion of fungal genomes were represented in Chardonnay must sequencing data.
- 158 pectinases were identified from the Chardonnay metagenome and found to be highly variable in sequence.
- PG1 is active at wine pH - a target for further testing in chemically defined grape juice.

## Methods



### 1. Extract microbial DNA from sample:

- Chardonnay must



### 2. Environmental DNA sequenced

```
Parse reads and remove duplicate sequences
def wr_duplicates(filename, newfile):
    f=open(filename)
    w=open(newfile, 'w')
    for line in f:
        line=line.rstrip()
        if line[0]!='@':
            if line not in l:
                w.write(line)
                l.append(line)
            else:
                w.write('*')
        else:
            w.write(line)
    return
```

### 3. Identify enzymes of interest (EOIs)



### 4. EOIs produced in *Pichia pastoris*



### 5. Characterisation of EOIs



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