

# Exploring upstream open reading frames (uORFs) in kiwifruit

Alexandra Kate Gibbon

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# Chapter 1

## 1.1 abstract

```
bookdown::serve_book()
```



## Chapter 2

# Literature reveiw

### 2.1 Background

Genetic regulation can occur at a multitude of points throughout the process of transcription of a gene all the way through to post-translational modification of the resulting protein [Ai et al., 2022]. In the past it was thought that most regions of the genetic code that did not directly encode a protein product did not play an important role in the biology of the organism [Brar and Weissman, 2015]. It is now well known that many non-coding regions play instrumentally important regulatory roles. This includes both long and short non coding RNAs and small transient peptides. In recent years it has become clear that these regulatory elements may prove useful in developing tools or for exploitation in order to produce novel traits in living organisms. This task is becoming increasingly important in the wake of the climate crises.

### 2.2 Climate change and crops

The changing climate is a growing concern for food production. It affects both plants included in many peoples staple diet as well as high value crops that many countries rely on economically. The warming climate has lead to increased incidence of extreme weather events such as drought and floods and is also playing a major role in the spread of pathogens across larger geographical ranges. Adding to these is issues is the risk that warming tempretures will stop certain plants from meeting vernilisation requirements, which ultimately prevents them from forming seeds and fruit.

## 2.3 Kiwifruit

Kiwifruit are one of the most economically important crops in the New Zealand export market. They represent 32% of New Zealand's horticultural export revenue.

## 2.4 Upstream open reading frames

Upstream open reading frames (uORFs) are small open reading frames located upstream of the main open reading frame (mORF) in the 5' untranslated region (5' UTR) of messenger RNA (mRNA). They belong to a larger group known as small open reading frames (sORFs), which can be present across the entire mRNA molecule. These features can play several roles in regulation of both the mRNA in cis and other molecules in trans.



## Chapter 3

# Methods

### 3.1 Molecular cloning

Three types were used in the course of this project

#### 3.1.1 Golden gate cloning

#### 3.1.2 Gateway cloning

#### 3.1.3 Restriction enzyme cloning



## Chapter 4

# Results



## Chapter 5

## Discussion



## Chapter 6

# Blocks

### 6.1 Equations

Here is an equation.

$$f(k) = \binom{n}{k} p^k (1-p)^{n-k} \quad (6.1)$$

You may refer to using `\@ref{eq:binom}`, like see Equation (6.1).

### 6.2 Theorems and proofs

Labeled theorems can be referenced in text using `\@ref{thm:tri}`, for example, check out this smart theorem 6.1.

**Theorem 6.1.** *For a right triangle, if  $c$  denotes the length of the hypotenuse and  $a$  and  $b$  denote the lengths of the **other** two sides, we have*

$$a^2 + b^2 = c^2$$

Read more here <https://bookdown.org/yihui/bookdown/markdown-extensions-by-bookdown.html>.

### 6.3 Callout blocks

The R Markdown Cookbook provides more help on how to use custom blocks to design your own callouts: <https://bookdown.org/yihui/rmarkdown-cookbook/custom-blocks.html>





## Chapter 7

## Conclusion



# Bibliography

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Gloria A. Brar and Jonathan S. Weissman. Ribosome profiling reveals the what, when, where and how of protein synthesis. *Nature Reviews. Molecular Cell Biology*, 16(11):651–664, November 2015. ISSN 1471-0080. doi: 10.1038/nrm4069.