

Building a genomic toolkit to protect the navel orange

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Year 1 of 1 (80% Complete)

Objectives

1. Produce complete sequence of the Washington navel orange genome.
2. Identify the location and sequence of genes in the completed genome.
3. Compare sequences of Cara Cara and Powell to Washington navel to uncover mutations linked with flesh color and maturity.

Problem and Significance

Navel oranges are the most widely produced citrus type in the state of California, representing nearly fifty percent of citrus bearing acreage in the state. Seedlessness is a key characteristic of navel oranges, but this trait requires navel varieties to be maintained by clonal propagation. As a result, all navels grown in California are descended from a single tree and are nearly genetically identical. This includes specialty varieties like the Cara Cara and late-season navels, both of which have increased in bearing acreage over the last decade. While clonal propagation of navels ensures that important quality characteristics are preserved for generations, it also increases their susceptibility to catastrophic events, including the introduction of exotic pests and pathogens. Recent advances in genome editing now make it possible to improve clonally propagated varieties like the navel. The research in this project was initiated to ensure that the UCR breeding program develops the tools required for genome editing in order to protect navels from both current and future challenges.

Benefit to Industry

Access to a complete genome sequence of the Washington navel orange will ensure that researchers have the tools necessary to safeguard the most commonly grown California citrus variety from future changes in environmental conditions, including novel diseases. With this resource, efforts to improve and protect the navel orange will no longer be limited to the identification of spontaneous budsports with desirable characteristics. Instead, directed measures to preserve the continued success of this variety in California can be pursued.

Progress Summary

The production of the Washington navel orange genome is complete. This so-called genome “assembly” is derived from the Parent Washington navel, and initial results indicate that the genome assembly is of high quality. This assessment is based on the total number and length of assembled fragments. The identification of the location and sequence of genes (Objective 2) is nearly complete. We are in the final stage which involves manually curating a subset of gene predictions.

Finally, we plan to sequence two additional navel varieties, Cara Cara and Powell, to pinpoint the genetic lesions that underlie their unique traits (Objective 3). Work on this objective has been delayed due to COVID-19 and will continue into the next fiscal year.

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