

# Comparative Functional analysis of *ovate* gene in the solanaceous species

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## Introduction

*Solanaceae* is the third most economically important plant taxa worldwide, having high agricultural utility. It is comprised of more than 3000 species, including fruit-bearing vegetables, ornamental plants, plants with edible leaves and medicinal plants. There is a high level of conservation ( $2n=24$ ) among major species, that make it an excellent model for understanding fruit and tuber



development and plant defense. *Ovate* as a major quantitative trait locus (QTL) control pear-shaped fruit development in both tomato and eggplant. It encodes a previously uncharacterized class of regulatory genes important for plant development and functions as a plant-growth suppressor.

Nowadays comparative and functional genomics apply new idea and advanced technique for research of multiple gene traits. The research on QTL gene will promote cultivation and exploitation of wild solanaceous species and further improve other economically important crops. Functional comparison of orthologous genes in closely related solanaceous species could be extended to other crops.

## Material and method

Eggplant and tobacco wild-type plants, eggplant 77P17 BAC, tobacco genome database, *ovate* gene sequences from tomato BAC19 and potato, pepper, petunia *ovate* orthologous sequences are collected.

In the beginning bioinformatics methods were used, then we did southern hybridization, molecular clone, PCR, RACE experiments and so on. We applied statistical and phylogenetic analysis experiments results to obtain better evolutionary relationship in solanaceous species at last.

## Results I

**Obtain *ovate* orthologous sequences from tobacco and identify two copies**



Fig 1. Tomato *ovate* DNA blast tobacco genome database, find *ovate* orthologous sequences and assemble two contigs

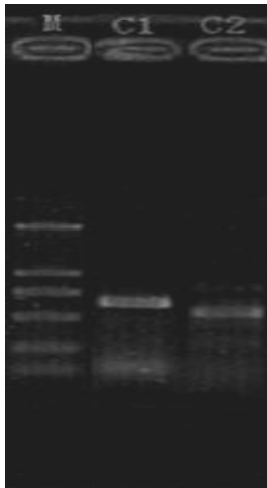


Fig 2. Two pairs of gene special primers PCR amplify tobacco genome DNA, identify two copies

## Results II

### Obtain *ovate* orthologous sequences from eggplant

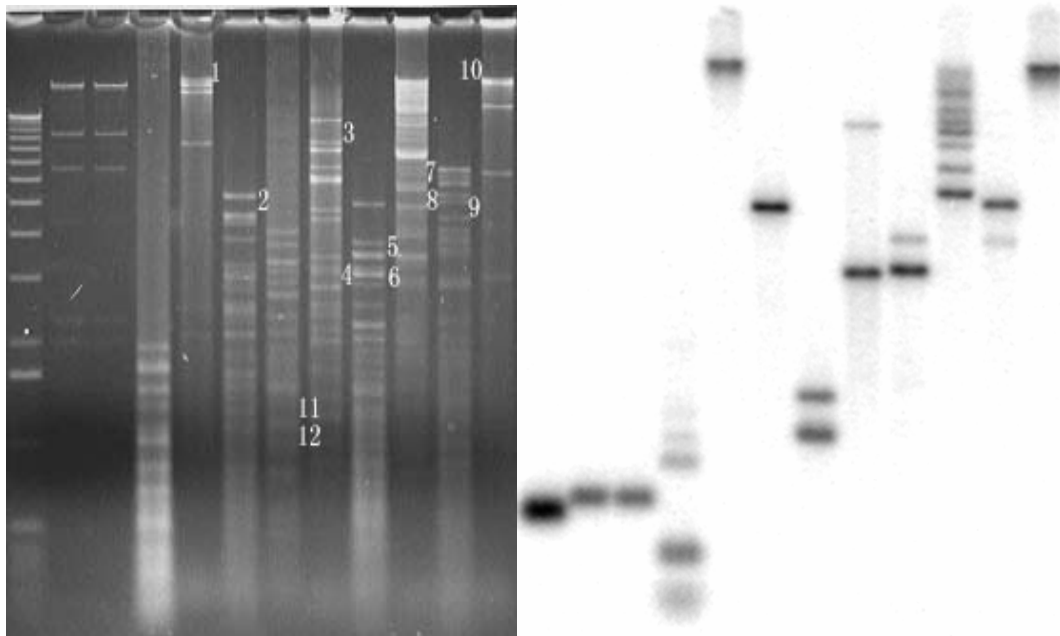


Fig 3. Tomato *ovate* DNA probe southern hybridize eggplant 77P17 BAC, find *ovate* orthologous sequences

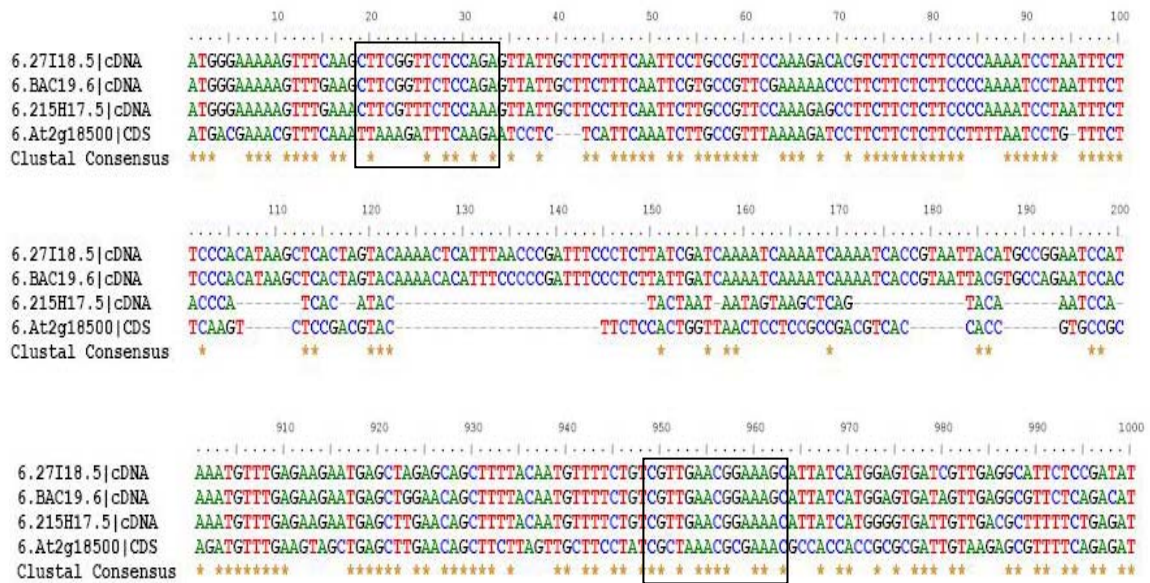


Fig 4. Multiple alignment of the known *ovate* homologous sequences and design a pair of degenerate primers

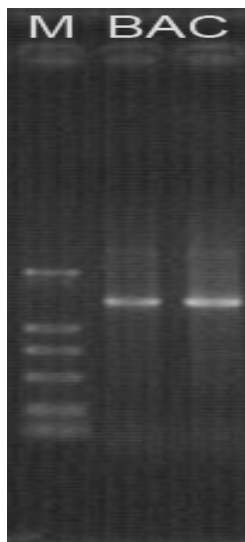


Fig 5. Degenerate primers PCR amplify eggplant 77P17 BAC, get *ovate* orthologous sequences

### Results III

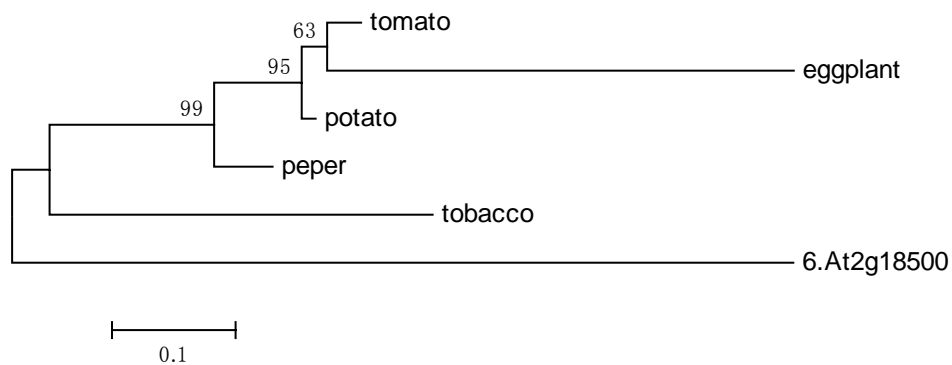


Fig 6. Phylogenetic trees of analyses of *ovate* orthologous sequences in six species