GENE CLONING AND BIOINFORMATICS ANALYSIS OF *ZmPRR37-1*

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Background

The photoperiod process of plants is very complex, involving the regulatory responses of many genes. As an indispensable component of biological clock regulation, the *PRRs* gene family forms an interrelated transcriptional feedback loop with other genes. It plays a very important role in the growth and development of crops.

Methods

In this experiment, the gene cloning and bioinformatics analysis of *PRR37-1* gene in *PRRs* family were carried out. Two kinds of materials, tropical maize inbred line CML288 and temperate maize inbred line Huangzao4, were used in the experiment. The *PRR37-1* genes of the two materials were cloned by primer design.

Results (up to 4 figures and tables can be included)

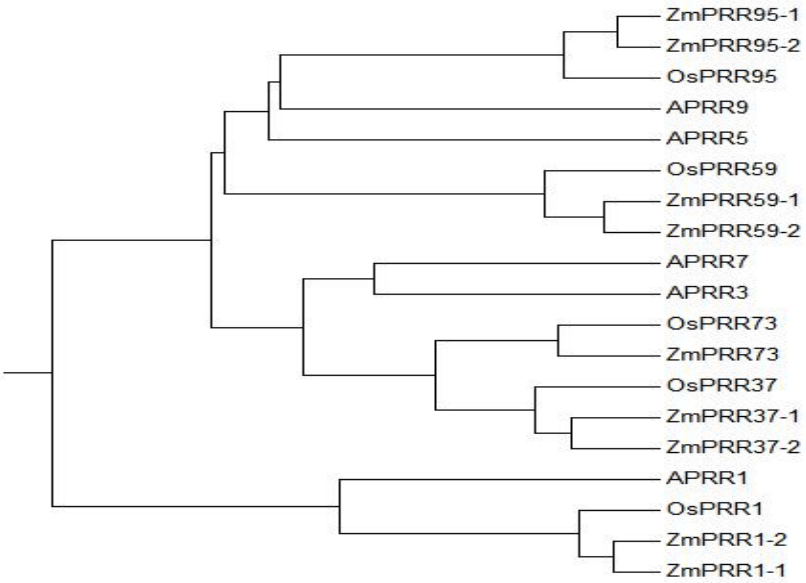

Figure 1 Phylogenetic tree of *PRR37-1* protein

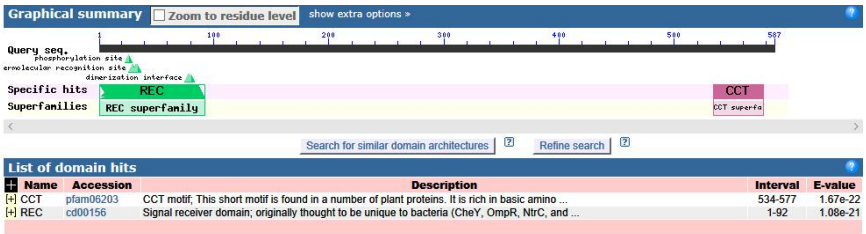

Figure 2 Conserved domain of *PRR37-1* protein CML288 material

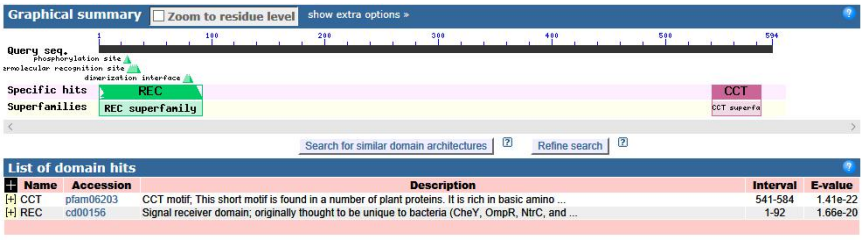

Figure 3 Conserved domain of *PRR37-1* protein Huangzao4 material

Conclusion

The gene sequence alignment results show that the two materials outside the show and the introns have the very big difference, and the gene encoding bioinformatics analysis of amino acids in n-terminal REC conservative area there are four amino acid differences, explain the differences between the tropical and temperate maize photoperiod sensitivity is likely to be related to the gene segments.Bioinformatics analysis showed that *PRR37-1* and *PRR37-1* were significantly different from each other. Subcellular localization prediction analysis showed that the two proteins were located in the nucleus and were consistent with the functional location of *PRR37-1* protein. By predicting the signal peptide, it was found that the signal peptide shear site of *PRR37-1* gene was located between amino acid 34 and amino acid 35. The transmembrane prediction analysis showed that *PRR37-1* protein had no transmembrane domain, and the transmembrane prediction showed that *PRR37-1* was not a transmembrane protein.

Funding

The study of *PRRs* family genes is not only conducive to a deep understanding of the mechanism of biological clock, but also of great significance to reveal the photoperiod regulatory network of plant flowering at the molecular level.

References

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