Bioinformatics comparison of codon usage of genes encoding phosphate transporter in terms of salt tolerance, day length, temperature and pollination in different plants

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Abstract

In order to study and compare the phosphate transporter gene codon usage and it's respond to the traits like salt tolerance, day length, Pollination and temperature in different plants, 100 isoform from 10 plants are extracted from NCBI website and then analyzed with Gene Infinity and Minitab 16 software. The result shows that the highest codon usage similarity (81.95%) was for *wheat* and *oryza* (annual, self-polinated and Psychrophilic) from *Poaceae* family. The result for *poaceae* family shows that the highest mean abundance was for codons that have U or G at the end. In this study *Cucurbita maxima* (salt tolerance, annual and cross pollinated) have the lowest codon usage similarity (70.37%) in compare with other plants in this study. The highest difference between families was for *Fabaceae* (77.64%) but they are divided in one group at the cluster. So the results show that the families that have lowest distance have the highest codon usage similarity in terms of salt tolerance, day length, Pollination and temperature. It is conceivable that a direct relationship would exist between preferred codons and division of plant families.

Key words: Phosphate transporter, Codon usage, Isoform

Introduction

Phosphorus is one of the essential elements for plant growth and Regulate and controlled by genes in plants such as PHR, SIZ1, PHF1, PHO1, PHO2 and etc (Calderon- Vazquez et al., 2011, Scarth and Law,1983). Phosphate transporter gene (PHT) is one of the most important plant genes that are involved in Phosphorus absorption. The proteins of Phosphate transporter family contain 520 to 550 amino acids within 12 transmembrane regions (Calderon- Vazquez et al 2011; Koyama et al., 2001). In the transmembrane region of 6 and 7, there is a central cytoplasmic region ring. In this cytoplasmic there is a places that can be phosphorylated or
bind to sugar molecules (Smith et al., 2000; Davies et al., 2002). Phosphate transporter protein family belongs to number 9 from a large family of proteins that facilitates the transition elements (Davies et al., 2002). On the other salt tolerance, day length, Pollination and temperature traits are controlled by Genetic and non-genetic factors (Koyama et al, 2011; Keim et al 1973; Law et al 1978; Welsh et al 1973). For example, response to day length is controlled by Ppd1, Ppd and Ppd3 gene in Wheat (Pugsley 1965 and 1966). VRN genes are Responsible for vernalization in plants that involved in flowering time and Pollination. The amount of phosphate transport through the membrane and the plasma membrane completely depends on the rate of transcription that encoded phosphate transporter genes. In this regard, it has been found that phosphate transporter encode genes easily control the entry of P (Smith et al., 2003). Also checking of the relationship between genes and their network operation is potentially important. We can discuss about relationship between them and explore the interactions by codon usage of different coding genes and thereby to identify gene networks. Various factors such as high gene expression, C+G combination, mutation, natural selection and RNA Stability are responsible of codon usage in among different species and even between different genes (Ermolaeva et al., 2001; and Wain-Hobson et al., 1981). Also codon usage show detailed information about the changes that have led to evoluing different species. According to recent research, selection and mutation is caused by codon usage.

Material and Method

At the first, open reading frame (ORF) sequences of more than 100 different isoforms of phosphate transporter was taken from NCBI (http://www.ncbi.nlm.nih.gov/). The relative synonymous codon usage (RSCU) values of each codon were calculated by website Gene infinity http://www.geneinfinity.org/sms/sms_codonusage.html. For statistical analysis we usage software Minitab 16 and finally dendrogram of similarities and differences with Minitab software makes conceivable.

Result and Discussion

Codon usage is the selective and nonrandom use of synonymous codons by a plant to encode the amino acids in the genes for its proteins. The plants in this study were compared with some traits such as salt tolerance, day length, Pollination, temperature traits and family by codon usage similarity (table 1). In this table the plants are separately characterized by Temperatures, Pollination, Growth Period, Day Length, Resistance to salty and some other characteristics.
The results in Table 2 show that the members of a family are most similar to each other by codon usage. The result showed that the codon usage of all amino acids for *poaceae* family is for a codon that its Terminal nucleotide has C and G (Table 2). For plants such as maize, codon usage frequency for last nucleotide of amino acid that possesses a and T respectively, was close to zero. Amino acids with 6 codon (Leu, Ser and Arg) in wheat, maize, rice and barley that are belong to grasses family have most similar in comparison with three other plants in this study. In this term the terminal nucleotide for this family most ends by C or G. So it can be concluded that most plants compared are encoded with the same codon usage for phosphate transporter genes, and this similarity was greatest in the same family plants.
Observations from cluster analysis show that the greatest similarity belongs to any family of plants (fig 1). Wheat, maize, rice and barley plants that are belong to grasses family were separated with 61.49% similarity to other families. In this group, barley and rice with 81.95% have most similar in codon usage than other members of this family. Both of these plants are annual, cross pollinated and psychrophilic but in terms of salt tolerance barley belong to salt tolerant plants and and rice belong to salt sensitive plants. Cucurbita Maxima that is salt tolerance, annual and cross pollinated plant have the lowest codon usage similarity (70.37%) in compare with all the plants in this study. Observations showed that tomato and potato plants have most of codon usage 86.67% similarity in compare with other plants in this group. Tomato and potato are belong to solanaceae, self-polinated and dicotyledon family, Perhaps it’s the reason for the similarity of these two plants. Legumes and soybean are closest family to tomato and potato with 82.61% similarity in codon usage cluster (fig 1).

The highest difference between families was for Legumes and soybean (77.64%) but they are divided in one group at the cluster. Soybean is belong to salt sensitive, short day plants and self-pollinated plants while alfalfa studied in this research is belong to salt tolerance, long day and cross-pollinated plants and one reason for the decline of codon preference similarity between these two plants may due to the difference in these traits. In the end it can be concluded that families that have the lowest distance have the highest codon usage similarity in cluster analysis and it suggest that the highest distance within families in terms of these traits in this study is higher, the similarity distance of codon usage between these traits becomes greater. It is conceivable that a direct relationship would exist between preferred codons and division of plant families. Codon usage is related to carrier genetic (DNA) and functional (protein) information. Thus, these unique coding strategies make studies on molecular evolution challenging (Granatham et al., 1986). Evolution of codon usage seems to be correlated with evolutionary history of protein genes. Mutational bias does not seem to play a role in the evolution of moss coding sequences.

References:


