



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 its response 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-pollinated 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 evolving 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.

Table 1: The different characteristics of plants examined in this study

Num	Plant	Seed	Family	Resistance to salty	Day length	Growth period	Pollination	Temprature
1	<i>Triticum aestivum</i>	Monocots	<i>Poaceae</i>	Semi resistant	Long-day	Annual	Self-pollinated	Psychrotropic
2	<i>Hordeum vulgare</i>	Monocots	<i>Poaceae</i>	Resistance	Long-day	Annual	Self-pollinated	Psychrotropic
3	<i>Oryza sativa</i>	Monocots	<i>Poaceae</i>	Sensitive	Short-day	Annual	Self-pollinated	Psychrotropic
4	<i>Glycine max</i>	Eudicots	<i>Fabaceae</i>	Sensitive	Short-day	Annual	Self-pollinated	
5	<i>Zea mays</i>	Monocots	<i>Poaceae</i>	Sensitive	Short-day	Annual	Other pollinated	Thermophile
6	<i>Arabidopsis thaliana</i>	Eudicots	<i>Brassicaceae</i>	Resistance		Annual		Psychrotropic
7	<i>Medicago truncatula</i>	Eudicots	<i>Fabaceae</i>	Resistance	Long-day	Annual	Other pollinated	Psychrotropic
8	<i>Cucurbita maxima</i>	Eudicots	<i>Cucurbitaceae</i>	Resistance		Annual	Other pollinated	Psychrotropic
9	<i>Solanum tuberosum</i>	Eudicots	<i>Solanaceae</i>	Sensitive	Gland (short-day) Flowering (Long-day)		Self-pollinated	Psychrotropic
10	<i>Lycopersicon esculentum</i>	Eudicots	<i>Solanaceae</i>	Semi resistant	Indifferent	perennial	Self-pollinated	Psychrotropic

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.

Table 2: Preferred codon for amino acid of plants examined in this study

	1	2	3	4	5	6	7	8	9	10
aa	<i>Triticum aestivum</i>	<i>Hordeum vulgare</i>	<i>Oryza sativa</i>	<i>Glycine max</i>	<i>Zea mays</i>	<i>Arabidopsis thaliana</i>	<i>Medicago truncatula</i>	<i>Cucurbita maxima</i>	<i>Solanum tuberosum</i>	<i>Lycopersicon esculentum</i>
Ala	GCC	GCC	GCC	GCA	GCC	GCT	GCT	GCG GCC	GCT	GCT
Cys	TGC	TGC	TGC	TGC	TGC	TGC	TGT	TGC	TGT	TGT
Asp	GAC	GAC	GAC	GAC	GAC	GAT	GAT	GAC	GAT	GAT
Glu	GAG	GAG	GAG	GAA	GAG	GAG	GAA	GAA	GAA	GAA
Phe	TTC	TTC	TCC	TCC	TCC	TCC	TTT	TCC	TCC	TCC
Gly	GGC	GGC	GGC	GGA	GGC	GGT	GGA	GGG	GGA	GGA
His	CAC	CAC	CAC	CAC	CAC	CAC	CAT	CAT	CAT	CAT
Lle	ATC	ATC	ATC	ATT	ATC	ATC	ATT	ATT	ATT	ATT
Lys	AAG	AAG	AAG	AAG	AAG	AAG	AAA	AAA	AAA	AAA

Leu	CTC	CTC	CTC	TTG	CTC	CTT	CTT	TTG	TTG	TTG
Met	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG
Asn	AAC	AAC	AAC	AAT	AAC	AAC	AAT	AAC	AAT	AAT
Pro	CCG	CCG	CCG	CCA	CCG	CCA	CCA	CCA	CCA	CCA
Gln	CAG	CAG	CAG	CAA	CAG	CAA	CAA	CAG	CAA	CAA
Arg	CGC	CGC	CGC	AGG	CGC	AGG	AGA	CGA	AGA	AGG CGT
Ser	TCC	TCC	TCC	TCA	TCC	TCT	TCT	TCC TCG	TCT	TCA
Thr	ACC	ACC	ACC	ACA	ACC	ACA	ACT	ACC	ACT	ACA
Val	GTG	GTG	GTC	GTT	GTC	GTT	GGT	GTG	GTT	GTT
Trp	TGG	TGG	TGG	TGG	TGG	TGG	TGG	TGG	TGG	TGG
Tyr	TAC	TAC	TAC	TAC	TAC	TAC	TAT	TAC	TAC	TAC
End	TAG	TAG	TGA	TGA	TAG	TAG	TGA	TGA	TGA	TGA

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 *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-pollinated 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).

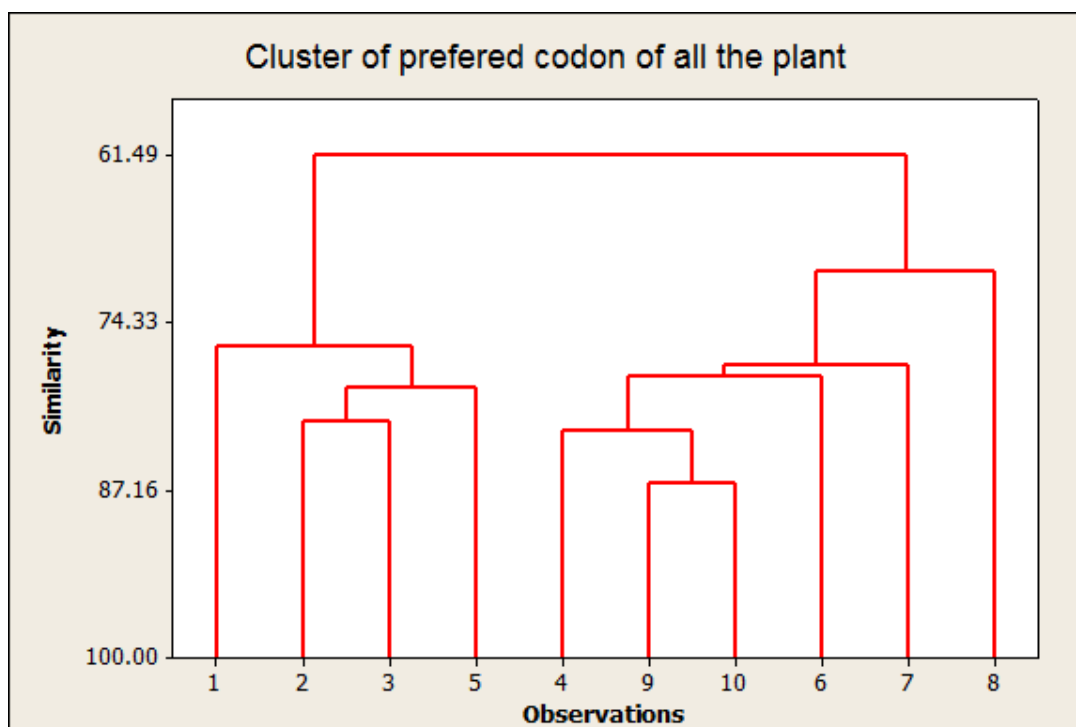


Figure 1. the cluster analysis of the plants: 1. *Triticum aestivum* 2. *Hordeum vulgare* 3. *Oryza sativa* 4. *Glycine max* 5. *Zea mays* 6. *Arabidopsis thaliana* 7. *Medicago truncatula* 8. *Cucurbita maxima* 9. *Solanum tuberosum* 10. *Lycopersicon esculentum*

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 (Grantham 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.

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