We are IntechOpen, the world's leading publisher of Open Access books Built by scientists, for scientists

6,300

Open access books available

172,000

International authors and editors

190M

Downloads

Our authors are among the

154

Countries delivered to

TOP 1%

most cited scientists

12.2%

Contributors from top 500 universities

WEB OF SCIENCE™

Selection of our books indexed in the Book Citation Index
in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?
Contact book.department@intechopen.com

Numbers displayed above are based on latest data collected.
For more information visit www.intechopen.com

L- Myo-Inositol 1-Phosphate Synthase (MIPS) in Chickpea: Gene Duplication and Functional Divergence

Manoj Majee and Harmeet Kaur

*National Institute of Plant Genome Research, Aruna Asaf Ali Marg, New Delhi
India*

1. Introduction

Gene duplication is one of the key driving forces in the evolution of genes and important features of genomic architecture of living organisms including plants. Moreover, much of the plant diversity may have arisen largely due to duplication, followed by divergence and adaptive specialization of the pre existing genes (Ohno,1970; Zhang, 2003; Flagel & Wendel,2009). Current impetus on genomic sequence data provides substantial evidence for the profusion of duplicated genes in all organisms surveyed. Functional divergence after gene duplication can possibly result in two alternative evolutionary fates: i) neofunctionalization where one copy acquires an entirely new function whereas the other copy maintains the original function. ii) Subfunctionalization, in which each copy adopts part of the task of their parental gene (Ohno,1970; Nowak et al., 1997; Jenesen,1976; Orgel,1977;Hughes,1994). However, subfunctionalization is reported as a more prevalent outcome than neofunctionalization in nature. In any case, functional divergence of such paralogous proteins is found to be the key force shaping molecular network in organisms (Ohno, 1970). Recent studies also suggest that duplicate genes diverge mostly through the partitioning of gene expression as in subfunctionalization (Force et al.,1999; Wagner,2000; Gu et al.,2002). In addition, subfunctionalization can also take place at the protein function level leading to functional specialization, when one of the duplicated genes becomes better at performing one of the original functions of the progenitor gene (Hughes, 1994; Gu et al.,2002; Conant &Wolfe, 2008; Hughes, 1999; Zhang et al., 2002).

Myo-inositol-1-phosphate synthase (MIPS;EC5.5.1.4) is an evolutionary conserved enzyme which catalyzes the rate limiting step in well conserved inositol biosynthetic pathway and is extremely widespread in living organisms including plants (Loewus & Murthy, 2000; Majumder et al., 2003). The evolution of MIPS gene/ protein among the prokaryotes seems to be more divergent and complex than amongst the eukaryotes, however they preserve a conserve core catalytic domain among the MIPS proteins (Majumder et al., 2003).

Many of the plant species are known to contain more than one copy of gene encoding MIPS and are hypothesized to arise through gene duplication. Expression studies of multiple gene encoding MIPS have revealed the possibility of specialized role for individual enzyme isoforms. Previously, two genes encoding MIPS have been identified and characterized from chickpea by Kaur *et al.* A comparative study of two divergent genes (*CaMIPS1* & *CaMIPS2*)

reveals features of both functional redundancy and diversification (Kaur et al., 2008). This chapter explores how a possible gene duplication of MIPS gene in chickpea lead to a functional diversification that perhaps contributed adaptive evolution to the plant.

2. Gene duplication and functional divergence of MIPS in chickpea

2.1 Evolution and diversification of MIPS

The inositols are the nine isomeric forms of cyclohexane hexitols and *myo*-inositol is the most abundant and physiologically favored molecule in the biological system.

The biosynthesis of *myo*-inositol has been acknowledged as an evolutionary conserved pathway and its importance across biological organisms from different domains of life has been recognized for long time. The first and rate limiting step of this pathway is catalyzed by an evolutionary conserved enzyme named as MIPS.

MIPS particularly catalyzes the conversion of glucose 6- phosphate (Glc6P) to *myo* inositol 1- phosphate (Ins1P) through an internal oxidoreduction reaction involving NAD^+ . Subsequently inositol 1- phosphate is dephosphorylated to produce free inositol by Mg^{2+} dependent *myo*- inositol 1- phosphate phosphatase (IMP: EC 3.1.3.25) (Loewus & Loewus, 1983; Loewus, 1990). This free *myo* inositol occupies the central position in inositol metabolism since this free inositol can be channellized to various metabolic routes and produce different inositol derivatives (Fig-1) (Loewus & Murthy, 2000; Loewus, 1990).

Fig. 1. Inositol biosynthesis and its consumption in other pathway.

This free inositol and its derivatives have acquired diverse functions over the course of evolution. As for example, inositol containing phospholipids are the important constituents of many archaea. Few thermophilic archaea also use inositol phosphodiester as thermo protective solutes. Then with the emergence and diversification of eukaryotes, function of

inositol and its derivatives proliferated dramatically. So far, inositol and its derivatives have been shown to be involved in growth regulation, membrane biogenesis, hormone regulation, signal transduction, pathogen resistance and stress adaptation in higher plants (Loewus & Murthy, 2000; Stevenson et al., 2000; Michell, 2008).

Since the usage and distribution of inositol and inositol derivatives are reported in all domains of life, it is imperative to contain MIPS enzyme in diverse organisms such as archaea, eubacteria, parasites, animals, higher plants and many others. Few higher plants and algae are reported to have both cytosolic and chloroplastic isoforms of MIPS. However, the biochemical and enzymatic properties of these two forms do not differ significantly between each other. Recent studies suggest that rice chloroplastic MIPS is coded by *OsINO1-1* gene located on chromosome 3 (RayChaudhuri et al. 1997; Ray et al., 2010).

The structural gene coding (*INO1*) for this ancient enzyme was first identified and cloned in *Saccharomyces cerevisiae* (Donahue & Henry, 1981). Subsequently more than 80 *INO1* genes were reported from various sources including both prokaryotes and eukaryotes.

Evolution and diversification of MIPS has been highlighted by Majumder et al. (2003) and a clear difference between prokaryotic and eukaryotic MIPS protein sequences was observed when compared among each other. The MIPS protein sequences of prokaryotes are quite divergent among themselves and significantly distinct than any other known eukaryotic sequences. In contrast, the eukaryotic MIPS sequences show remarkable similarities among each other. A phylogenetic tree constructed to include few representative MIPS sequences from diverse organisms present an overall evolutionary divergence of this enzyme in the biological kingdom. The higher plants constitute one close subgroup, while the higher animals, protozoa, fungi form the other subgroups in the eukaryotic cluster (Fig-2). In *Archeoglobus*, MIPS shows more sequences similarity to the eukaryotic MIPS than the other known prokaryotic ones and thereby all eukaryotic MIPS seems to have evolved from one common stock, probably from the fusion of an archaebacterial and eubacterial MIPS genes (Fig-2 & 3).

Four stretches of amino acid residues (GWGGNG, LWTANTERY, NGSPQNTFVPGL and SYNHLGNNDG) are found to be conserved in MIPS proteins of all eukaryotes and among them; SYNHLGNNDG is identified as highly conserved. Interestingly among higher plants, MIPS enzyme shows greater conservation in addition to these four domains (Fig-3). Many of the plant species also possess multiple genes encoding MIPS and are thought to arise through gene duplication in course of time.

Subsequent analysis of crystal structures of various MIPS proteins provide ample evidence towards the presence of conserved “core structure” in all MIPS proteins throughout evolution. Moreover, some of the important amino acid residues are identified in the active site of the yeast MIPS and are shown to be highly conserved in all eukaryotic MIPS. These amino acids are considered to be the part of a “eukaryotic core structure” which has remained largely the same during evolution, despite the divergence in rest of the sequences over time (Fig-3) (Stein & Geiger, 2002; Norman et al., 2002).

Crystal structure analysis of MIPS from *Saccharomyces cerevisiae* also revealed that each monomer of the homo-tetrameric MIPS has three functionally important structural domains namely the NAD binding Rossmann fold, the catalytic binding site and the core domain. This study also exemplifies a case of induced fit model for binding of the substrate with the catalytic domain of the enzyme. (Stein & Geiger, 2002)

Fig. 2. A phylogenetic tree of few representative MIPS amino acid sequences from various domains of living organisms. Neighbour-Joining algorithm was used to construct tree from the distance matrix using Clustal X. Thousand rounds of bootstrapping were performed to ensure the validity of the tree.

CaMIPS1	-----MFIENFKVDSPNVKYTETEIQSVYNYETTEL VHENRN GTYQWIVKPKTVKYEFK
CaMIPS2	-----MFIESFKVESPNVKYTDTEIQSVYSYETTEL VHENRNNTYQWVVKPKTIKYEFK
OsMIPS	-----MFIESFRVESPHVRYGAAEIESDYQYDTTEL VHESHDGASRWIVRPKSVRYNFR
HsMIPS	-----MEAAAQFFVESPDVVYGPEAIEAQYEYRTTRVSREG----GVLKVHPTSTRFTFR
ScMIPS	MTEDNIAPITSVKVVTDKCTYKDNE LLTKYSYENAVVTKTAS---GRFDVTPTVQDYVFK
PfMIPS	-----
MtMIPS	-----MSEHQ S
AfMIPS	-----
CaMIPS1	TDTHVP-KLGVM LVGWGGNNGSTLTGGVIANREGISWATKDNIQQANYFGSLTQASATRV
CaMIPS2	TQTHVP-KLGVM LVGWGGNNGSTLTGGVIANREGISWATKDKIQQSNYFGSLTQASAIRV
OsMIPS	TTTTVP-KLGVM LVGWGGNNGSTLTAGVIANREGISWATKDKVQQANYYGSLTQASTIRV
HsMIPS	TARQVP-RLGVM LVGWGGNNGSTLTA AVLANRLRLSWPTRSGRKEANYYGSLTQAGTVSL
ScMIPS	LDLKKPEKLGIMLI GLGGNNGSTLVASVLANKHNVEFQTKEGVKQPNYFGSMTQCSTLKL
PfMIPS	-----MVRVAIIGQGYVASIFAVGLERIKE-----GELGYYG-----
MtMIPS	LPAP EASTEVRVAIVGVNCASSLVQGVEYYN-----ADDTSTVPG-----
AfMIPS	-----MKVWL VGAYGIVSTTAMVGARAIERGIAPKIGLVSELPHFEG-----
	: . *
CaMIPS1	GSFQ-GEEIYAPFKSLLPMVNPDDIVFGGWDISDMNLADAMARA-RVFDIDLQQLRPYM
CaMIPS2	GSFQ-GEEIYAPFKSLLPMVNPEDIVWGGWDINN MNLADAMGRA-RVFDIDLQQLRPYM
OsMIPS	GSYN-GEEIYAPFKSLLPMVNPDDL VFGGWDISNMNLADAMTRA-KVLDIDLQQLRPYM
HsMIPS	GLDAEGQEVFVPFSAVLPMVAPNDLVFDGWDISSLNLA EAMRRA-KVLDWGLQEQLWPHM
ScMIPS	GIDAEGNDVYAPFNSLLPMVSPNDFVVGWDINNADLYEAMQRS-QVLEYDLQQLRKAKM
PfMIPS	-----IPLANELPIKVEDIKIVASYDV DKTIGLPLSEI-VQRYWKGNVPESLQE
MtMIPS	-----LMHVREFGPYHVRDVKFVAAFDVDAKKVGF DLSDA-IFASENNTIKIADVA
AfMIPS	-----IEKYAPSFSEFFGGHEIRLLSNAYEAAKEHWELNRHFDREILEAVKSDL
	* . .
CaMIPS1	ESMVPLPGIYDPDFIAANQGD RANNVIKGTKR-----EQINQIIKDIKEFK EANKV
CaMIPS2	ESMVPLPGIYDPDFIAANQGD RANNVINGTKK-----EQLQQIIKDIKEFK EASKI
OsMIPS	ESMVPLPGIYDPDVIAANQGS RANNVIKGTKK-----EQMEQIIKDIREFK ESKSV
HsMIPS	EALRPRPSVYIPEFIAANQSARADN LIPGSRA-----QQL EQIRRDIRD FRSSAGL
ScMIPS	SLVKPLPSIYYPDFIAANQDERANNCINLDEKGNVTTRGK WTHLQRIRRD IQNFKEENAL
PfMIPS	VFVRKGIHLGSLRNLP IEATGLEDEMT-----LKEAIERLVEEWKEKKVD
MtMIPS	PTNVIVQRGPTLDGIGK-----YYADTIELSDAE PV
AfMIPS	EGIVARKGTALNCGSGIKELGDIKTLEGEGLS-----LAEMVSRIEEDIKSFAD
	: .
CaMIPS1	DRVVVLWLTANTERYSNLVVGLNDTMENLFAAVDRNE-SEISPSTLFAIACVTENVPFING
CaMIPS2	DKVVVLWLTANTERYSNVVVGLNDTMENLLASVDKNE-AEISPSTLYALACVLENVPFING
OsMIPS	DKVVVLWLTANTERYSNVCVGLNDTMENLLASVDKNE-AEISPSTLYAIACVM EGIPFING
HsMIPS	DKVIVLWLTANTERFCEVIPGLNDTAENLLRTIELG--LEVSPSTLFAVASILEGCAFLNG
ScMIPS	DKVIVLWLTANTERYVEVSPGVNDTMENLLQSIKNDH-EEIAPSTIFAAASILEGVPYING
PfMIPS	VIINVPTTEAFTPF GKLEELEKA IKDNNKERLTATQ-AYAYAAAQYAKE--VGGA AFVNA
MtMIPS	DVVQALKEAKVDVLVS YLPVGSEE-----ADKFYAQCAIDAGVAFVNA
AfMIPS	DETVVIN VASTEPLPNYSE EYHGSLEGFERMIDEDRKEYASASMLYAYAALKLGLPYANF
	. . : * . . : *
CaMIPS1	SP-QNTFVPGLIDLAIKRNTLIGGDDFK--SGQTKMKSVLVDFLVGAGIKPTSIVSYNHL
CaMIPS2	SP-QNTFVPGLIDLAIQRNSLIGGDDFK--SGQTKMKSVLVDFLVGAGIKPTSIVSYNHL
OsMIPS	SP-QNTFVPGLIDLAIKNNCLIGGDDFK--SGQTKMKSVLVDFLVGAGIKPTSIVSYNHL
HsMIPS	SP-QNTLVPGALELAWQHRV FVGDDFK--SGQTKVKSVLVD FLIGSGLKTMSIVSYNHL
ScMIPS	SP-QNTFVPGLVQLAEHEGTFIAGDDLK--SGQTKLKS VLAQFLVDAGIKPVSIASYNHL
PfMIPS	IPTLIANDPAFVELAKESNLVIFGDDGA--TGATPLTADILGH LAQRNRHVLDIVQFNIG
MtMIPS	LPVF IASDPVWAKKFTDAGVPIVGDDIKSQVGATITHRVLAKLFEDRGVQLDR TMQLNVG

Fig. 3. Multiple sequence alignment of MIPS from prokaryotes and eukaryotes. Proposed common active site amino acid residues for the *Mycobacterium tuberculosis* and *Saccharomyces cerevisiae* MIPS sequence are highlighted in green color and four conserved domains of eukaryotes (GWGGNG, LWTANTERY, NGSPQNTFVPGL and SYNHLGNNDG) are highlighted in yellow color. 43 variant positions between CaMIPS1 and 2 have been highlighted in blue color.

2.2 MIPS from chickpea: A case of functional divergence

Chickpea is an annual self- pollinated diploid legume crop which is mostly grown in the arid and semi arid regions of the world. Long term evolution and adaptation to harsh conditions make chickpea rich in resistant genes for environmental stresses including drought and cold. Several classes of genes controlling potential resistance have been

identified through genomic and proteomic studies (Ahmaed et al., 2005; Mantri ,2007; Bhusan et al., 2007).

In this particular plant, inositol seems to play an important role in drought tolerance besides growth and development, since inositol content and MIPS transcript was found to be significantly increased under dehydration condition (Boominathan et al.,2004). Subsequently, chickpea is reported to have two MIPS coding genes (*CaMIPS1* and *CaMIPS2*) (Kaur et al. 2008) and both genes are revealed to have overall similar structure consisting of 9 introns and 10 exons (Fig-4). Sequence analysis of these two genes show high similarity (>85%) in their coding regions but their non-coding or 5' and 3' flanking regions are extremely divergent. Moreover length of each exon is similar between these two genes while the size of introns varies. Such findings suggest that these two MIPS genes most likely arose by ancestral gene duplication and have undergone considerable sequence divergence.

In spite of the remarkable resemblance in their coding sequences, some base substitutions occurs in exons leading to changes in 43 amino acids in protein sequences, however, maintaining four highly conserved functional domains and known active site amino acids of MIPS (Fig-3) (Majumder *et al.* 2003). Among these 43 amino acids, 19 amino acids differ considerably between *CaMIPS1* and *CaMIPS2* while rest of the amino acid substitutions are relatively insignificant, i.e. substitution between amino acids having similar physico chemical properties (Kaur et al., 2008).

Fig. 4. Diagrammatic representation of *CaMIPS1* and *CaMIPS2* genomic structure. Length of exon and intron indicated in bp. [Modified from Kaur et al., 2008]

Functional divergence after gene duplication can result in following alternative fates: One copy acquires a novel function (neofunctionalization) or one copy loses its function completely or each copy adopts part of the task of their parental gene (subfunctionalization) (Ohno, 1970; Nowak et al., 1997; Jenesen, 1976; Orgel,1977;Hughes,1994).

Functional complementation and in-vitro enzymatic properties were analyzed to check the fate of these two genes. First to check the functional identity of these two divergent genes, a complementation experiment was carried out in natural inositol auxotroph *Schizosaccharomyces pombe* PR109 which clearly demonstrates that both *CaMIPS1* and

CaMIPS2 indeed encode functional MIPS enzymes. Subsequently, the enzymatic properties of these two enzymes were examined since *CaMIPS1* and *CaMIPS2* polypeptides are reported to have some differences in their amino acid sequences. Both enzymes showed nearly same *K_m* values for Glc6P suggesting the similar substrate specificity. For both proteins, the optimum temperature for enzyme activity is at 35°C and optimum pH is 7.0 suggesting the similar biochemical characteristics (table1). Further the enzymatic activities of each protein under stress environment in *invitro* conditions were examined and the activities of these two enzyme proteins were shown to differ significantly in response to high temperature and salt concentration (Kaur et al., 2008). *CaMIPS1* activity is considerably affected at high temperature or in presence of increasing sodium chloride concentration while the *CaMIPS2* activity is less affected in similar conditions and thereby retaining higher activity than *CaMIPS1* (Fig-5). The amino acid substitutions in protein sequence as analyzed by sequence comparison and the higher enzyme activity in *CaMIPS2* under stress condition also indicates that it might be evolved during the course of time to function better under stress conditions. This differential activity towards high temperature and salt of these two enzymes could be supported by the bioinformatics analysis in respect to the available yeast MIPS crystal structure and salt tolerant *PcINO1* (MIPS coding gene from Salt tolerant *Porteresia coarctata*) protein sequence (Majee et al., 2004). Based on the bioinformatics study, *CaMIPS2* appears to be more stable towards destabilizing factors such as high temperature, salt, etc, thereby retains better functionality under such conditions (Kaur et al., 2008). Subsequently, growth pattern of *CaMIPS1* & *CaMIPS2* transformed *Schizosaccharomyces pombe* under stress conditions were analyzed and *CaMIPS2* transformed *S. pombe* cells were reported to grow or survive better than *CaMIPS1* transformants both at high temperature and salt environment (Fig-6) suggesting *CaMIPS2* gene product functions more efficiently under stress conditions due to its stress tolerant property and hence provide sufficient inositol to grow as compared to *CaMIPS1*.

Fig. 5. Effect of salt (A) & temperature (B) on *CaMIPS1* and *CaMIPS2* enzyme activity. [Modified from Kaur et al., 2008]

Characters	CaMIPS1	CaMIPS2
Km		
Gluc 6-P	2.63 mM	2.70 mM
NAD ⁺	0.181 mM	0.192 mM
Vmax		
Gluc 6-P	0.074 μmole min ⁻¹	0.075 μmole min ⁻¹
NAD ⁺	0.069 μmole min ⁻¹	0.070 μmole min ⁻¹
pH optima	7.5	7.5
Temp. optima	35°C	35°C

[Modified from Kaur et al., 2008]

Table 1. Biochemical characterization of recombinant CaMIPS1 and CaMIPS2 enzymes.

Fig. 6. Growth pattern of *Schizosaccharomyces pombe* transformed with CaMIPS1 and CaMIPS 2 at high temperature and salt environment. [Modified from Kaur et al., 2008]

Recent studies suggest that duplicate genes diverge mostly through the partitioning of gene expression as in subfunctionalization and thereby being expressed in a differential manner; redundant genes may acquire functional divergence (Force et al., 1999; Wagner, 2000; Gu et al., 2002). This hypothesis was examined on *CaMIPS1* and 2. *CaMIPS1* gene was shown to express in root, shoot, leaves, and flower in fairly equal abundance but no transcript was observed in seed, while *CaMIPS2* transcript was observed

in all examined tissues including seed. This result proposes that *CaMIPS1* and *CaMIPS2* genes are indeed differentially regulated in different organs to coordinate inositol metabolism with cellular growth as hypothesized previously (Loweus & Murthy,2000). Subsequently, expression pattern of these two genes are examined in various environmental stresses. Interestingly, *CaMIPS2* was shown to be induced at different level in various environmental stresses while level of *CaMIPS1* transcript was found to be unaltered by such stresses (Fig-7). This differential expression is also supported by the divergence of their upstream regulatory sequences.

Fig. 7. Expression analysis of *CaMIPS1* and *CaMIPS2* through real time PCR analysis under various stresses. [Modified from Kaur et al., 2008]

3. Conclusion

Gene duplication, followed by sequence divergence leads to functional divergence of the paralogous proteins, is a major force for adaptation of living organisms. Without gene duplication, the plasticity of genome or organism in adapting to changing environment would be very limited. Chickpea plants are know to be evolved and diversified considerably over time and acquired subsequently various potential genes for their adaptation to environmental stresses. It seems that this drought tolerant legume plant requires more inositol for their adaptation particularly under drought condition and hence acquired *CaMIPS2* over time. Collectively, our results exemplified that *CaMIPS1* and *CaMIPS2* are differentially expressed in chickpea to play discrete though overlapping roles in plant;

however *CaMIPS2* is likely to be evolved through gene duplication, followed by adaptive changes in its sequences to function better under environmental stresses and thereby play a key role in environmental stress adaptation along with other aspects of inositol metabolism in chickpea.

4. Acknowledgement

This work was supported by a grant from Department of Biotechnology (Next Generation Challenge Programme on Chickpea Genomics), Department of Science and Technology (Fast Track Scheme) , Government of India.

We also like to acknowledge the Research support from National Institute of Plant Genome Research, New Delhi. H.K. thanks the Council of Scientific and Industrial Research, Government of India, for Senior Research Fellowship.

5. References

- Ahmad, F.; Gaur, P. M. & Croser, J. (2005) Chickpea (*Cicer arietinum* L.) In genetic resources, Chromosome Engineering and Crop Improvement. Grain legumes Edited by Singh R, Jauhar P. vol1,pp 187-217, CRC Press. USA
- Bhusan, D.; Pandey, A.; Choudhary, M.K.; Datta, A.; Chakraborty, S. & Chakraborty, N. (2007) Comparative proteomics analysis of differentially expressed proteins in chickpea extracellular matrix during dehydration stress. *Molecular & Cellular Proteomics*, vol 6:1868-1884.
- Boominathan, P.; Shukla, R.; Kumar, A.; Manna, D.; Negi, D.; Verma, P.K. & Chattopadhyay, D. (2004) Long term transcript accumulation during the development of dehydration adaptation in *Cicer arietinum*. *Plant Physiology*, vol 135: 1608-1620
- Conant, G.C. & Wolfe, K.H. (2008) Turning a hobby into a job: How duplicated genes find new functions. *Nature Review Genetics*, vol 9: 938-950
- Donahue, T.F. & Henry, S.A. (1981) *Myo*-inositol 1- phosphate synthase. Characteristics of the enzyme and identification of its structural gene in yeast. *Journal of Biological Chemistry*, vol 256: 7077-7085
- Flagel, L.E. & Wendel, J.F. (2009) Gene duplication and evolutionary novelty in plants. *New Phytologist*, vol 183: 557-564.
- Force, A.; Lynch, M.; Pickett, F.B.; Amroes A.; Yan, Y.-L. & Postlethwait, J. (1999) Preservation of duplicate genes by complementary, degenerative mutations. *Genetics*, vol 151, 1531-1545
- Gu, Z.; Nicolae, Lu, H.-S. & Li, H.W. (2002) Rapid divergence in expression between duplicate genes inferred from microarray data. *Trends in Genetics*, vol 18, 609-613
- Hughes, A.L. (1994) The evolution of functionally novel proteins after gene duplication. *Proceedings of the Royal Society, Lond Ser. B* 256: 119- 124
- Hughes, A.L. (1999) *Adaptive Evolution of genes and genomes*, Oxford University press.
- Jensen, R.A. (1976) Enzyme recruitment in the evolution of new function. *Annual Review of Microbiology*, vol 30, 409-425
- Kaur, H.; Shukla, R.; Yadav, G.; Chattopadhyay, D. & Majee, M. (2008) Two divergent genes encoding L -*myo* inositol 1 phosphate synthase1 (*CaMIPS1*) and 2 (*CaMIPS2*) are differentially expressed in chickpea. *Plant, Cell & Environment*, vol 31, 1701-1716

- Loewus, F.A. & Loewus, M.W. (1983) *Myo*- inositol: its biosynthesis and metabolism. *Annual Review of Plant Physiology*, vol 34,137-161
- Loewus, F.A. & Murthy, P.N. (2000) *Myo*- inositol metabolism in plants. *Plant Science*, vol 150, 1-19
- Loewus, F.A. (1990) *Inositol biosynthesis*. In *Inositol metabolism in plants* (Morre D.J., Boss W.F. & Loewus F.A .eds). pp13-19, New York, Wiley-Liss., USA
- Majee, M.; Maitra, S.; Dastidar, K.G.; Pattnaik, S.; Chatterjee, A.; Hait, N.C.; Das, K.P. & Majumder, A.L. (2004) A novel salt tolerant L *myo*- inositol -1-phosphate synthase from *Porteresia coarctata* (Roxb) Tateoka, a halophytic wild rice. *Journal of Biological Chemistry*, vol 279, 28539-28552
- Majumder, A.L.; Chatterjee, A.; Dastidar, K.G. & Majee, M. (2003) Diversification and evolution of L- *myo*-inositol 1 phosphate synthase. *FEBS Letter* ,vol 533, 3-10.
- Mantri, N.L.; Ford, R.; Coram, T.E. & Pang, E.C. (2007) Transcriptional profiling of chickpea genes differentially regulated in response to high salinity, cold, and drought. *BMC genomics*, vol 8:303
- Michell, R.H. (2008) Inositol derivatives: evolution and functions. *Nature reviews Molecular Cell Biology* ,vol9, 151-161
- Norman, R.A.; McAlister, M.S.B.; Murray Rust, J.; Movahedzadeh, F.; Stoker, N.G. & McDonald, N.Q. (2002) Crystal structure of inositol 1 phosphate synthase from *Mycobacterium tuberculosis*, a key enzyme in phosphatidyl inositol synthesis. *Structure* ,vol10: 393-402
- Nowak, M.A.; Boerlijst, M.C.; Cooke, J, Smith, M.J. (1997) Evolution by genetic redundancy. *Nature*, vol 388,167-171
- Ohno, S. (1970) *Evolution by gene duplication*. Springer -Verlag. New York,, USA
- Orgel, L.E. (1977) Gene duplication and the origin of proteins with novel functions. *Journal of Theoretical Biology*, vol 67,773
- Ray, S.; Patra, B.; Das Chaterjee, A., Ganguli, A. & Majumder, A.L. (2010) Identification and organization of chloroplastic and cytosolic L-*myo*-inositol 1- phosphate synthase coding gene (s) in *Oryza sativa*: comparison with the wild halophytic rice, *Porteresia coarctata*. *Planta* 231:1211-1227
- RayChaudhuri, A.; Hait, N.C.; DasGupta, S.; Bhaduri, T.J.; Deb, R. & Majumder, A.L. (1997) L *myo*- inositol 1-phosphate synthase from plant sources (characteristics of the chloroplastic and cytosolic enzymes). *Plant Physiology* 115: 727-736
- Stein, A.J. & Geiger, J.H. (2002) The crystal structure and mechanism of L *myo* inositol 1 phosphate synthase. *Journal of Biological Chemistry* 277: 9484-9491.
- Stevenson, J.M.; Perera, I.Y.; Heilmann, I.; Persson, S. & Boss, W.F. (2000) Inositol signaling and Plant Growth. *Trends in Plant Science* 5: 252-258.
- Wagner, A. (2000) Decoupled evolution of coding region and mRNA expression patterns after gene duplication: Implication for the neutralist selectionist debate. *Proceedings of National Academy of Sciences USA*. vol 97: 6579-6584
- Zhang, J. (2003) Evolution by gene duplication; an update: *Trends in Ecology and evolution*, vol18, 292-298.
- Zhang, J.; Zhang, Y.P. & Rosenberg, H.F. (2002) Adaptive evolution of duplicated pancreatic ribonuclease gene in a leaf eating monkey. *Nature Genetics*, vol 30, 411-415

Gene Duplication

Edited by Prof. Felix Friedberg

ISBN 978-953-307-387-3

Hard cover, 400 pages

Publisher InTech

Published online 17, October, 2011

Published in print edition October, 2011

The book Gene Duplication consists of 21 chapters divided in 3 parts: General Aspects, A Look at Some Gene Families and Examining Bundles of Genes. The importance of the study of Gene Duplication stems from the realization that the dynamic process of duplication is the "sine qua non" underlying the evolution of all living matter. Genes may be altered before or after the duplication process thereby undergoing neofunctionalization, thus creating in time new organisms which populate the Earth.

How to reference

In order to correctly reference this scholarly work, feel free to copy and paste the following:

Manoj Majee and Harmeet Kaur (2011). L- Myo-Inositol 1-Phosphate Synthase (MIPS) in Chickpea: Gene Duplication and Functional Divergence, Gene Duplication, Prof. Felix Friedberg (Ed.), ISBN: 978-953-307-387-3, InTech, Available from: <http://www.intechopen.com/books/gene-duplication/l-myo-inositol-1-phosphate-synthase-mips-in-chickpea-gene-duplication-and-functional-divergence>

INTECH
open science | open minds

InTech Europe

University Campus STeP Ri
Slavka Krautzeka 83/A
51000 Rijeka, Croatia
Phone: +385 (51) 770 447
Fax: +385 (51) 686 166
www.intechopen.com

InTech China

Unit 405, Office Block, Hotel Equatorial Shanghai
No.65, Yan An Road (West), Shanghai, 200040, China
中国上海市延安西路65号上海国际贵都大饭店办公楼405单元
Phone: +86-21-62489820
Fax: +86-21-62489821

© 2011 The Author(s). Licensee IntechOpen. This is an open access article distributed under the terms of the [Creative Commons Attribution 3.0 License](https://creativecommons.org/licenses/by/3.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

IntechOpen

IntechOpen