



GLOBAL JOURNAL OF SCIENCE FRONTIER RESEARCH  
Volume 11 Issue 9 Version 1.0 December 2011  
Type: Double Blind Peer Reviewed International Research Journal  
Publisher: Global Journals Inc. (USA)  
Online ISSN : 2249-4626 & Print ISSN: 0975-5896

# Evolution of the Universe and Biological Organisms Progressively Involves More Information from the Mathematical World

By Monendra Grover

*Amity University, Uttar Pradesh, New Delhi, India*

**Abstract** - Three kinds of worlds have been proposed by Roger Penrose, the physical world, the mental world and the mathematical world. The mathematical world may contain relations which do not exist in physical world. It is proposed in this paper that as the evolution of the universe and the biosphere progresses more and more relations from the mathematical world are needed to explain the universe and the biosphere. Specifically, the example from the membrane transporter systems in the prokaryotes and eukaryotes has been taken. It is observed that the membrane transporter systems in the eukaryotes are more complex than in prokaryotes and more and more relations from the mathematical world would be needed to explain these systems in eukaryotes as compared to prokaryotes. This is consistent with the hypothesis proposed in this paper since eukaryotes are considered more advanced than prokaryotes.



*Strictly as per the compliance and regulations of :*



# Evolution of the Universe and Biological Organisms Progressively Involves More Information from the Mathematical World

Monendra Grover

**Abstract** - Three kinds of worlds have been proposed by Roger Penrose, the physical world, the mental world and the mathematical world. The mathematical world may contain relations which do not exist in physical world. It is proposed in this paper that as the evolution of the universe and the biosphere progresses more and more relations from the mathematical world are needed to explain the universe and the biosphere. Specifically, the example from the membrane transporter systems in the prokaryotes and eukaryotes has been taken. It is observed that the membrane transporter systems in the eukaryotes are more complex than in prokaryotes and more and more relations from the mathematical world would be needed to explain these systems in eukaryotes as compared to prokaryotes. This is consistent with the hypothesis proposed in this paper since eukaryotes are considered more advanced than prokaryotes.

Penrose has proposed three kinds of worlds (Penrose, 1994). The first world proposed is the world of our conscious perceptions. This world contains the mental images of the objects existing in the 'physical world' (see later). In this world our perceptions intermingle with our thoughts and our decisions.

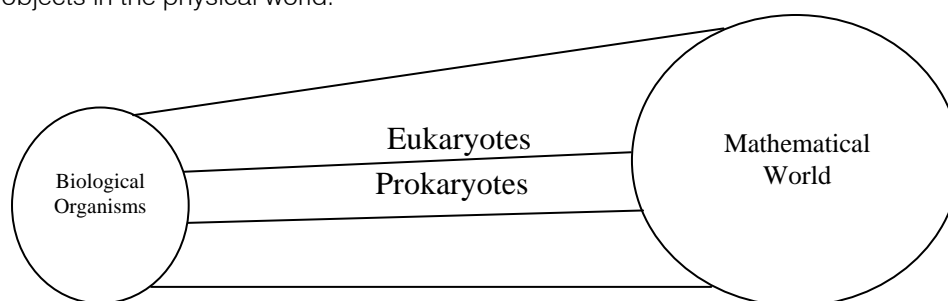
The second world has been proposed to be the physical world. It contains actual physical objects. The third world proposed is the Platonic world of mathematical forms. Besides, number, mathematical relationships etc., it has been proposed to consist of simulations of the objects in the physical world.

As the universe is evolving the mathematical relations needed to explain them are becoming more complex. Similarly as the biological organisms evolve the mathematical relations used to describe them are also becoming more complex. In the mathematical world a large number of relationships exist which may not be reflected in the physical world. It can be possibly inferred from the evolution of the universe and the biological organisms that representation of the mathematical world in the physical world is increasing with the increasing complexity of the universe and the biosphere.

## *The mathematical relations in the biological world*

The mathematical relations in the biological world get more complex as the biological organisms evolve and utilize more from the mathematical world (Fig.1).

Here we take the example of fundamental differences in the membrane transport of prokaryotes and eukaryotes membrane transport systems play important roles in cellular activities and metabolism. Transporters function in several important cellular functions such as environmental sensing and cell communication, excretion of toxic compounds,



**Fig.1 :** The mathematical relations in the biological world get more complex as the biological organisms evolve and utilize more from the mathematical world.

maintenance of ion homeostasis and in acquisition of organic nutrients (Saier, 1999). The energy sources in the membrane transporters are chemiosmotic energy in the form of sodium ion or proton electrochemical

gradients, phosphoenolpyruvate and adenosine triphosphate. Various transporter systems also differ in their membrane topology, substrate specificities and energy coupling mechanism and substrate specificities (Saier, 2000).

**Author :** Amity Institute of Biotechnology, Amity University, Uttar Pradesh, New Delhi-110012, India.  
**E-mail :** monendra\_grover@yahoo.com

Efforts have been made to classify the transporters. In this direction the transporter classification system attempts to classify membrane transporter systems according to their mode of transport, substrate specificity, molecular phylogeny and energy coupling mechanisms (Saier, 2000, Saier, 1999, Busch and Saier, 2002, Busch and Saier, 2004). Since transport mode and energy coupling have relatively stable characteristics, they serve as the primary basis of classification of transporters.

There are four major classes of solute transporters in the transport classification system. These are channels, primary (active transporters), secondary transporters and group translocators. Transporters of unknown mechanism or function constitute a distinct class. Channels are energy independent and transport water, specific type of ions, or hydrophilic (small) molecules down an electrical gradient or concentration channels have lower stereospecificity and higher rate of transport than other classes. Primary active transporters couple the transport process to a ATP hydrolysis. Secondary transporters utilize an ion or solute electrochemical gradient. Group translocators modify their substrates during the transport process. Each transporter class is further classified into individual families and subfamilies depending on function, phylogeny, and/or substrate specificity (Saier, 1999). Since the advent of genomic sequencing technologies, the complete sequences of a large number of organisms have been published covering a wide range of species from archaea to human. A large number of additional genome sequencing projects are also currently in progress around the world. An intensive look at transport processes is vital to the understanding of the metabolic capacity in sequenced organisms.

In a study (Ren and Paulsen, 2005) a total of 40,678 transport proteins from 141 species spanning 9 eukaryota, 17 Archaea and 115 eubacteria were predicted. These were classified into 134 families which included 13 unclassified families, 2 phosphotransferase systems and 32 channel protein families. These families are variable in size: some of these families are very large superfamilies with large number members such as the ABC superfamily, which is widely distributed in eukaryota, archaea and eubacteria. Some are small families with only a few members. The distribution of transporter families varies significantly across various phyla. 42 families specific to eukaryotes exist, these are mostly ion channel families existing exclusively in multicellular organisms such as *Homo sapiens*, *Arabidopsis thaliana* and *Drosophila melanogaster*. These channels are involved in important cellular responses such as maintenance of homeostasis in a multicellular environment, signal transduction and cell communication.

There are 38 transporter families (Ren and Paulsen, 2005) which are specific to prokaryotes, out of these 22 families are specific to eubacteria and 16 occur

both in Archaea and eubacteria. There are 41 transporters which exist across all the three domains of living kingdom. This implies that these may be very ancient families. Most of these were found in secondary transporter class. However these families function in the transport of a variety of substrates which includes various cations and anions, nucleotides, carboxylates, sugars, amino acids. 14 families are shared by eubacteria and eukaryota and 16 are shared by Eubacteria and Archaea. Between 2% and 16% of ORFs in prokaryotic and eukaryotes were predicted to encode membrane transport proteins. The eukaryotes, especially the multicellular eukaryotes, display the largest total number of transport proteins, such as *Drosophila* has 682 proteins, 3.7% of total proteins, *Arabidopsis* has 882, 3.5% of total proteins, *C.elegans* has 669 proteins, 4.1% of total proteins and humans have 841, 3.0% of total proteins. However with regard to percentage of total ORFs the transport proteins of eukaryotic species (9.5% plus or minus 2.9%) account for a relatively smaller number of proteins than Archaea (average 6.7 %, plus or minus 2.3%). Groups belonging to same phylogenetic group show variations in the quantity of transport proteins. Organisms with a larger genome size and thus more ORFs generally encode a greater number of transporters (Paulsen et al. 2000, Konstantinidis and Tiedje, 2004). Besides transporters, transcription factors, secondary metabolism genes and regulatory genes also appear to increase with genome size (Konstantinidis and Tiedje, 2004, Cases et al. 2003, Jordan et al. 2001). The following reasons could account for the increased number of transporters in organisms with increasing genome sizes: A. an increased number of distinct transporter families and B. Greater number of paralogs in certain transporter families due to higher degree of expansion or duplication. Prokaryotes display relatively linear relationship between the number of transporter families and the genome size. With the increase in genome size, the rate of increase in number of families per organism is about 8 times greater than average number of paralogs per family. However the expansion of transporter families can only be partially explained by the increase in genome size (Ren and Paulsen, 2005). One of the factors influencing the above mentioned expansion could be strain specific properties and lifestyles.

The single celled eukaryotes such as the yeast appear to show characteristics similar to those of prokaryotes, showing expansions in paralogs and transporter families. By contrast, in plants and animals, the large number of paralogs in certain transporters is a major factor for increase in transporters. For example the *Arabidopsis* genome encodes 92 paralogs of the MFS and 110 paralogs of the ABC superfamily.

These differences in the relative abundances of distinct transporter families and transporter paralogs reflect basic differences in the transporter needs or

priorities of these organisms (Ren and Paulsen, 2005). A strategy of specialization is possibly being followed by multicellular organisms, with many apparently redundant transporter paralogs. Many of the closely related paralogous transporters are possibly expressed only in certain subcellular localizations or specific tissues, or at specific developmental stages. Many of these transporters in multicellular organisms appear to be involved in signal transduction processes and cell-cell communication. By contrast, the single celled eukaryotes and prokaryotes, with large number of different families of transporters and relatively fewer paralogs appear to emphasize on a strategy of diversification. This is corroborated by the fact that one of the primary roles of membrane transport systems in these organisms is nutrient acquisition. A large diversity of transporter types presumably allows for a broader range of substrate utilization (Ren and Paulsen, 2005). Thus the mathematical relations needed to describe membrane transport in multicellular eukaryotes would be more complex since the transporters in these organisms serve a variety of functions mentioned above. This is in contrast to prokaryotes where the mathematical relations used to elucidate membrane transport would be simpler as most of these transporters though diverse are involved in nutrient transport only.

In the same study (Ren and Paulsen 2005) a wide range of variations have been observed in the relative usage of energy coupling mechanisms to drive transport processes among the eukaryotes and prokaryotes studied. In this study transporters were categorized into five major groups according to energy coupling mechanisms and transport mode: primary transporters, secondary transporters, ion channels, group translocators and unclassified. Primary and secondary transporters are universal, as these are present in all the organisms analyzed in this study. However their percentage among the total transporters varies widely: 12% to 78% for primary carriers and 17 to 80% for secondary carriers. In prokaryotes and unicellular eukaryotes, primary and secondary transporters are the dominant type of transporters. These type of carriers contribute more than 90% of total transporters in the above mentioned organisms. In higher eukaryotic organisms channel proteins make up 12% to 43% of the total transporter proteins.

In contrast to eukaryotes, prokaryotic organisms primarily use primary active transporters, large because of predominant usage of the ABC uptake systems, which are absent in eukaryotes (Dean and Allikmets, 2001). Organisms with the highest percentage of transporters usually belong to one of the following groups: A. The first group includes organisms that lack an electron transfer chain and a citrate cycle, and therefore proton motif force can be generated in these organisms through indirect means only such as substrate level phosphorylation followed by ATP

hydrolysis. ATP is their primary source of energy and is primarily responsible for driving nutrient uptake and maintaining ion homeostasis (Saier, 2000). B. The second group includes photosynthetic organisms with the ability to synthesize ATP via photosynthesis. C. The third group consists of Proteobacteria that have a significant expansion of the ABC superfamily (Konstantinidis and Tiedje, 2004).

The phosphotransferase system is only present in a subgroup of eubacteria, and completely lacking in Archaea and Eukaryota. Channel proteins contribute a relatively smaller percentage of transporters in the prokaryotic species analyzed in the study by Ren and Paulsen. The percentage of channel proteins, however, increases significantly in multicellular eukaryotes. In animals ion channels with communication functions such as in signal transduction or as sensors for external stimuli constitute this group. For example members of the GIC family (Nakanishi and Masu, 1994) and ligand-gated ion channel family (Hong, 1998) are activated by major inhibitory (GABA) and major excitatory (glutamate) neurotransmitters in the brain (Lujan et al. 2005). Some evidence shows that GIC type channels and ion gated channels are expressed predominantly during embryonic and postnatal brain development, while others are expressed predominantly in the postnatal brain (Lujan et al. 2005). In plants about one third of the channel proteins are aquaporins (water channels) (Johansson et al. 2001), a large majority of which show a cell specific expression in root (Javot and Murrel, 2002). The tissue specific expression in multicellular eukaryotes adds another level of complexity to the mathematical relations used to describe membrane transport in eukaryotes, as compared to prokaryotes.

## REFERENCES RÉFÉRENCES REFERENCIAS

1. Busch W, Saier MH Jr (2002) The transporter classification (TC) system, 2002. *Crit Rev Biochem Mol Biol* 37: 287–337.
2. Busch W, Saier MH (2004) The IUBMB-endorsed transporter classification system. *Mol Biotechnol* 27: 253–262.
3. Cases I, de Lorenzo V, Ouzounis CA (2003) Transcription regulation and environmental adaptation in bacteria. *Trends Microbiol* 11: 248.
4. Dean M, Allikmets R (2001) Complete characterization of the human ABC gene family. *J Bioenerg Biomembr* 33: 475–479.
5. Hong X (1998) Identification of major phylogenetic branches of inhibitory ligand-gated channel receptors. *J Mol Evol* 47: 323.
6. Javot H, Maurel C (2002) The role of aquaporins in root water uptake. *Ann Bot* 90: 301–313.
7. Johanson U, Karlsson M, Johansson I, Gustavsson S, Sjövall S, et al. (2001) The complete set of genes encoding major intrinsic proteins in *Arabidopsis* provides a framework for a new nomenclature for



major intrinsic proteins in plants. *Plant Physiol* 126: 1358–1369.

8. Jordan IK, Makarova KS, Spouge JL, Wolf YI, Koonin EV (2001) Lineage-specific gene expansions in bacterial and archaeal genomes. *Genome Res* 11: 555–565
9. Konstantinidis KT, Tiedje JM (2004) Trends between gene content and genome size in prokaryotic species with larger genomes. *Proc Natl Acad Sci U S A* 101: 3160–3165
10. Lujan R, Shigemoto R, Lopez-Bendito G (2005) Glutamate and GABA receptor signalling in the developing brain. *Neuroscience* 130: 567–580
11. Nakanishi S, Masu M (1994) Molecular diversity and functions of glutamate receptors. *Annu Rev Biophys Biomol Struct* 23: 319–348.
12. Penrose, R. (1994) *Shadows of the mind*, Oxford University Press
- Ren Q, Paulsen IT (2005) Comparative Analyses of Fundamental Differences in Membrane Transport Capabilities in Prokaryotes and Eukaryotes. *PLoS Comput Biol* 1(3): e27.
13. Saier MH Jr (1999) Classification of transmembrane transport systems in living organisms. In: VanWinkle L, editor. *Biomembrane transport*. San Diego : Academic Press. pp. 265–276.
14. Saier MH Jr (2000) A functional-phylogenetic classification system for transmembrane solute transporters. *Microbiol Mol Biol Rev* 64: 354–411.
15. Saier MH Jr (1999) A functional-phylogenetic system for the classification of transport proteins. *J Cell Biochem* 75(Suppl 32): 84–94.