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RESEARCH ARTICLE

THE GENOME SIZE AND THE TWO BASIC ELECTRON, PROTON DEPENDENT METABOLIC REACTION SYSTEMS OF OBTAINING OF ATP

***Ambaga, M.**

New Medicine Medical Institute, Ulanbator, Mongolia

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Abbreviation:

Q-plastoquinol,
PC-plastocyanin.

ABSTRACT

It was became clear that during last 4 billion years, owing to the bioevolution link existed between the two basic electron, proton dependent metabolic reaction systems of obtaining of ATP had been formed the various capacity of ATP based regulation of expansion in the number of genes in the case of the human gene and also in the case of Archea genome and Bacteria genome. We are developing the idea that the evolution based difficulty as the limitation of expansion in the number of genes because of slow developed systems of ADP + Pi + H^+ + nH + memb.space, and the unsifficient of membrane redox potentials three - state line system in case of prokaryotes had been solved by appearance of powerful energy delivering systems as "Donators + membrane redox potentials three - state line system + O_2 + ADP + Pi + H^+ + nH + memb. space = (ATP + heat energy) + H_2O + nH + matrix + CO_2" (Ambaga and Tumen-Ulzii, 2015), conditioning the high capacity of ATP based increase of Genome Size . It can be say that during evolution development of living cells the shift from one cell to multicells had been accompanied with their metabolic system improvement as first slow developed system as ADP + Pi + H^+ + nH + memb.space had converted to second powerful energy delivering system as "Donators + membrane redox potentials three - state line system + O_2 + ADP + Pi + H^+ + nH + memb.space = (ATP + heat energy) + H_2O + nH + matrix + CO_2" (Ambaga and Tumen-Ulzii, 2015), which led to appearance of high capacity of ATP based increase of Genome Size. In such way the appearance of second more powerful energy accumulating systems as "Donators (glucose, aminoacids, fatty acids) + membrane redox potentials three - state line system + acceptor as O_2 + ADP + Pi + H^+ + nH + memb.space = (ATP + heat energy) + H_2O + nH + matrix + CO_2" had conditioned the increase the gene size, number of genes, linear gene structures in Human organism in comparision to Archea genome and Bacteria genome.

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INTRODUCTION

It would be interesting establish that what bioevolution based forces had been conditioned the big Genome Size, many number of genes, big average gene size in the Human organism. Meanwhile prokaryotes show no tendency to evolve greater complexity by this reason that bioenergetic potentials for prokaryotic cell genome was not enough to decide the ATP based increase of Genome Size. This explanation demonstrated that prokaryotes had not so powerfull bioenergetic potentials as the membrane - redox potentials three - state line system dependent - full 9 stepped cycle of proton conductance. From "Donators + membrane redox potentials three - state line system + O_2 + ADP + Pi + H^+ + nH + memb.space = (ATP + heat energy) + H_2O + nH + matrix + CO_2" (Ambaga and Tumen-Ulzii, 2015) equation members, prokaryotes had only the slow developed systems as ADP + Pi + H^+ + nH + memb.space, but had not the membrane redox potentials three - state line system. It should be said that evolution based biological mechanism of ATP based increase of Genome Size had been connected with these processes as shift from the slow developed bioenergy accumulating regulations of early evolution times in the form as "Donators + ADP + Pi + H^+ + nH + memb.space = ATP + nH + O_2 formation and the shortage of membrane redox potentials three - state line system "to more powerful energy accumulating systems as "Donators (glucose, aminoacids, fatty acids) + membrane redox potentials three - state line system + acceptor as O_2 + ADP + Pi + H^+ + nH + memb.space = (ATP + heat energy) + H_2O + nH + matrix + CO_2" . It would be more interesting establish the relationship between the formation of the membrane - redox potentials three - state line system dependent - full 9 stepped cycle of proton conductance and the appearance of the evolution based biological mechanism of ATP based increase of Genome Size.

****Corresponding author:*** **Ambaga, M.**
New Medicine Medical Institute, Ulanbator, Mongolia.

RESULTS AND CONCLUSION

If we would compare *E.coli* genome and Human genome, both have distinguished by the number of chromosome and the gene size, also by the number of genes, circular and lineaer gene structures depending on the various capacity of ATP based change of Genome Size, various expansion potential in the number of genes.

Genome Size (base pairs) for *E.coli* genome is 4.6 Mb and for Human genome-3.2 Gb.

The number of genes for *E.coli* genome is 4,288 and for Human genome-20,000. The average gene size for *E.coli* genome is 700 bp and for Human genome-27,000 bp.

It was became clear that during last 4 billion years owing to the bioevolution link, which existed between the two basic electron, proton dependent metabolic reaction systems of obtaining of ATP had been formed the various capacity of ATP based change of expansion in the number of genes in the case human gene and also in the case Archea genome, Bacteria genome. We are developing the idea that the evolution based difficulty as the limitation of expansion in the number of genes because of slow developed systems of ADP + Pi + H^+ + nH + memb.space, and the unsifficient of membrane redox potentials three - state line system in case of prokaryotes had been solved by appearance of powerful energy delivering systems as "Donators + membrane redox potentials three - state line system + O_2 + ADP + Pi + H^+ + nH + memb.space = (ATP + heat energy) + H_2O + nH + matrix + CO_2" (Ambaga and Tumen -Ulzii, 2015), conditioning the high capacity of ATP based increase of Genome Size. The endosymbiosis process was one of favourable preconditions to develop the powerful energy delivering systems as "Donators + membrane redox potentials three - state line system + O_2 + ADP + Pi + H^+ + nH + memb.space = (ATP + heat energy) + H_2O + nH + matrix + CO_2" (Ambaga and Tumen-Ulzii, 2015) and the high organized bioenergetic membranes, followed by mitochondria based distribution of DNA. It can be say that during evolution development of living cells the shift from one cell to multicells had been accompanied with their metabolic system improvement as first slow developed systems as ADP + Pi + H^+ + nH + memb.space had converted to powerful energy delivering systems as "Donators + membrane redox potentials three - state line system + O_2 + ADP + Pi + H^+ + nH + memb.space = (ATP + heat energy) + H_2O + nH + matrix + CO_2" (Ambaga and Tumen-Ulzii, 2015) with high capacity of ATP based increase of Genome Size. In the early period of 4 billion years of bioevolution development had been formed the first reaction system of obtaining of ATP in the form of the slow developed bioenergy accumulating system (2 billion years ago) "Donator molecules + ADP + Pi + H^+ + nH + memb.space = ATP + nH + O_2 formation with shortage of membrane redox potentials three - state line system in the example of *E.coli* with relatively small Genome Size as 4.6 Mb and little number of genes as 4,288, small gene size as 700 bp. In the last period of 4 billion years of bioevolution development had been formed the second reaction system of obtaining of ATP in the form of more powerful energy accumulating systems as "Donator molecules (glucose, aminoacids, fatty acids) + membrane redox potentials three - state line system + acceptor as O_2 + ADP + Pi + H^+ + nH + memb.space = (ATP + heat energy) + H_2O + nH + matrix + CO_2" (Ambaga and Tumen-Ulzii, 2015), which led to big Genome Size as 3.2 Gb, many number of genes as 20,000, big average gene size as 27,000 bp in the Human example. We are proposed that transferring from first electron, proton dependent reaction system of obtaining of ATP as "Donator molecules + ADP + Pi + H^+ + nH + memb.space = ATP + nH + O_2 formation with shortage of membrane redox potentials three - state line system to second more powerful energy accumulating systems as "Donators (glucose, aminoacids, fatty acids) + membrane redox potentials three - state line system + acceptor as O_2 + ADP + Pi + H^+ + nH + memb.space = (ATP + heat energy) + H_2O + nH + matrix + CO_2" was bioevolution based forces, condiniong the increase of gene size, number of genes and appearance of linear gene structures in Human organism in comparision to Archea genome and Bacteria genome.

We came to conclusion that small Genome Size as 4.6 Mb and little number of genes as 4,288, small gene size as 700 bp determined in the Archea genome and Bacteria genome had been paralleled with the first electron, proton dependent reaction system of obtaining of ATP as "Donator molecules + ADP + Pi + H^+ + nH + memb.space = ATP + nH + O_2 formation with shortage of membrane redox potentials three - state line system. Meanwhile , big Genome Size as 3.2 Gb, many number of genes as 20,000, big average gene size as 27,000 bp revealed in the Human genome had been paralleled with the second more powerful energy accumulating systems as "Donators (glucose, aminoacids, fatty acids) + membrane redox potentials three - state line system + acceptor as O_2 + ADP + Pi + H^+ + nH + memb.space = (ATP + heat energy) + H_2O + nH + matrix + CO_2". Without this mitochondria - based energy accumulating systems as "Donators (glucose, aminoacids, fatty acids) + membrane redox potentials three - state line system + acceptor as O_2 + ADP + Pi + H^+ + nH + memb.space = (ATP + heat energy) + H_2O + nH + matrix + CO_2", life on Earth today would be nothing more than a sludge of simple microbes because of shortage of ATP based increase of Genome Size. But prokaryotes show no tendency to evolve greater complexity by this reason that bioenergetic potentials for prokaryotic cell genome was not enough to decide this problems (Nick Lane and William Martin, 2010).

This explanation demonstrated that prokaryotes had not so powerfull bioenergetic potentials as the membrane - redox potentials three - state line system dependent - full 9 stepped cycle of proton conductance. Purines are biologically synthesized as nucleotides and in particular as ribotides, A key regulatory step is the production of 5-phospho-α-D-ribosyl 1-pyrophosphate (PRPP) by ribose phosphate pyrophosphokinase, The first committed step is the reaction of PRPP, glutamine and water to 5'-phosphoribosylamine (PRA), glutamate, and pyrophosphate - catalyzed by amido phosphoribosyltransferase, which is activated by PRPP PRA + Glycine + ATP → GAR + ADP + Pi GAR + fTHF → fGAR + THF fGAR + L-Glutamine + ATP → fGAM + L-Glutamate + ADP + Pi fGAM + ATP → AIR + ADP + Pi + H_2O CAIR + L-Aspartate + ATP → SAICAR + ADP + Pi

Molecular oxygen, generated in the reaction medium, located in the system as "Donator molecules as water molecules + ADP + Pi + H^+ + nH + memb.space = ATP + nH + O_2 formation with shortage of membrane redox potentials three - state line system have been transferred to metabolic reaction medium located in the system as "Donator molecules (glucose, aminoacids, fatty acids) + membrane redox potentials

three - state line system + acceptor as O_2 + ADP + Pi + H^+ + nH + memb.space = (ATP + heat energy) + H_2O + nH + matrix + CO_2" (Ambaga and Tumen-Ulzii, 2015) during respiration, which served the more important role to develop the ATP based increase of Genome Size.

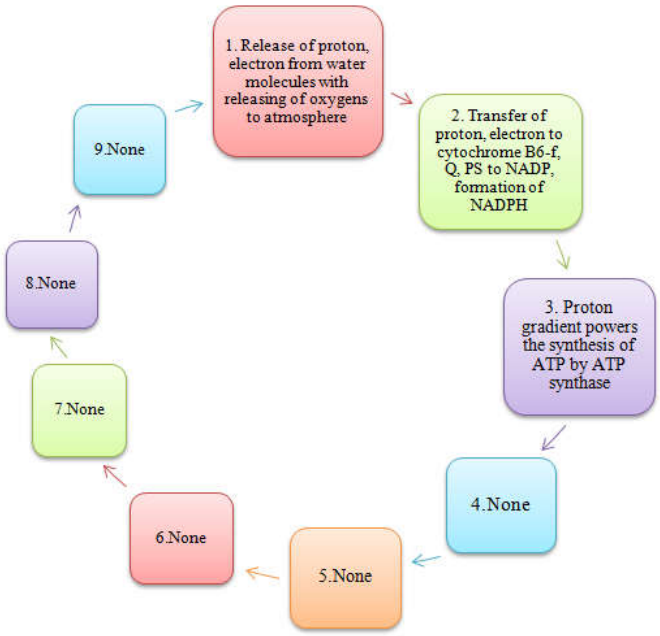

Figure 1. Electron, proton dependent first reaction system of obtaining of ATP

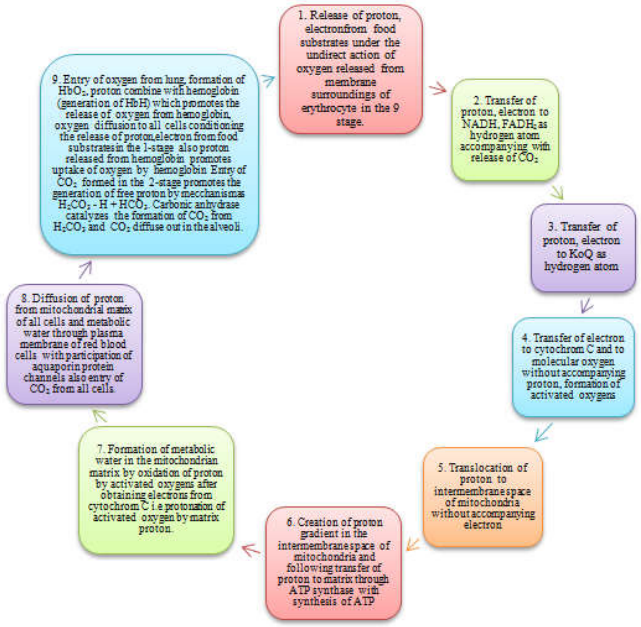

Figure 2. Electron, proton dependent second reaction system of obtaining of ATP

A living processes in our planet had been formed and developed in the basis of the bioevolutional link formed between the two basic electron, proton dependent metabolic reaction systems of obtaining of ATP during last 4 billion years, conditioning the ATP based increase of Genome Size.

It can be say that during evolution development of living cells the shift from one cell to multicells had been accompanied with their metabolic system improvement as first slow developed systems as ADP + Pi + H^+ + nH + memb.space had converted to powerful energy delivering systems as "Donators + membrane redox potentials three - state line system + O_2 + ADP + Pi + H^+ + nH + memb.space = (ATP + heat energy) + H_2O + nH + matrix + CO_2" (Ambaga and Tumen-Ulzii, 2015), which led to appearance of high capacity of ATP based change of Genome Size.

REFERENCES

Allen, F., Nick Lane, William F. Martin 2013. Early bioenergetic evolution, Published 10 June 2013. DOI: 10.1098/rstb. 2013.0088

Ambaga M 2016. The Full Cycle of Proton and Electron Conductance inside the Human Body, Consisting of 9 Linked Stages. *Acad. J. Sci. Res.,* 4(6): 127-131.

Ambaga M 2017. The membrane - redox potentials three - state line system dependent - full 9 stepped cycle of proton conductance and the evolution based biological mechanism of early ageing, *World Journal of Scientific Research and Review,* vol 5, No2, pp.1-5.

Ambaga M 2017. The full 9 stepped cycle of proton conductance and the two basic electron, proton dependent metabolic reaction system of obtaining of ATP, *Applied Science and innovative Research,* vol.1, No 1, pp 63-68.

Ambaga M 2017. The membrane - redox potentials three - state line system dependent - full 9 stepped cycle of proton conductance is evolution power to the new route of multicellular life, *WJSRR,* vol 5, N 1, pp.1-5.

Ambaga M 2017. The metabolic fates of C, H, O atoms contained in food molecules in the full 9 stepped cycle of electron and proton conductance inside the human body, *International Journal of Current Research,* Vol 09, Issue, 01, pp 45091-45094.

Ambaga M, Tumen-Ulzii A 2016. Integrated NCM medicine with s-NCM new knowledge, *lambert Academic Publishing*

Ambaga M, Tumen-Ulzii A 2017. The integration of Tibetan Traditional Medicine and Modern Medicine, *lambert Academic Publishing*

Ambaga M. 2016. A new suggestion about existing of membrane - redoxy potential three state line system between donators and acceptors inside the living cells, *Asian Journal of Science and technology*, Vol.07, Issue, 07, pp.3157-3161.

Ambaga M. 2016. The buffering capacity of erythrocyte membrane surroundings in relation to free protons, formed in the Full Cycle of Proton and Electron Conductance inside the Human Body. *International Journal of Development Research,* Vol 06, Issue, 07, pp. 8458-8461.

Ambaga M. 2016. The Full Cycle of Proton and Electron Conductance inside the Human Body and triple

Ambaga M. 2016. The possibility to drive the membrane - redox potential, a three state line system dependent - full 9 stepped cycle of proton conductance inside human body to favorable direction during pathological situations, *International Journal of Current Research,* Vol, Issue, 11, November, pp 42456 -42459,

Ambaga M. 2017. The membrane - redox potentials three - state line system dependent - full 9 stepped cycle of proton conductance and the evolution based biological mechanism of obesity, *International Journal of Current Research,* February, Vol 09, Issue, 02, pp .46284-46284

Ambaga M. and Tumen-Ulzii A 2015. The life become dependent from the presence of electrons and protons, which were formed during events called big bang 15 billion years ago, electrons and protons sets the stage for formation of life in the universe.

Filipa L. Sousa, Thorsten Thiergart, Giddy Landan, Shijulal Nelson-Sathi, Inês A.C. Pereira, John F. Allen, Nick Lane, William F. Martin 2013. Early bioenergetic evolution, Published 10 June.DOI: 10.1098/rstb.2013.0088

Nick Lane and William Martin, 2010. The energetics of genome complexity, Nature, 467, 929-934, (21 October), doi:10. 1038/nature 09486, Published online, 20 October 2010

Nick Lane, and William F. Martin 2012. The origin of membrane bioenergetics *J.Cell*, http://dx.doi.org/10.1016/j. cell.2012.11.050.

Rlung, Mkhris, Badgan theory of Tibetian Traditional medicine, *International Journal of Current Research*, Vol 8, Issue 08, p.36391-36393.

Willey J.M, Sherwood L.M, Woolverton Ch.J, Prescotts Microbiology, eight edition.

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