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Archaea: an all-out study

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Abstract: Archaea are strange but unique beings that have evolutionary relationships with bacteria and eukaryotes and have many unique properties of genotypes and phenotypes that indicate their own evolutionary status. In addition to its presence in the human body, it plays a key role in the ecological cycle of the planet. The metabolic strategies and physiological adaptation of archaea to extreme environments are great. Accurate and Responsive Mechanisms to ensure that Taxis patterns provide the needs of the cell, or the need for Bioremediation strategies that control environmental activities, develops important features in the global ecosystem to develop tools that have great economic and health benefits for Includes human beings. This research emphasizes recent progress in recognizing archaea mechanisms and highlights new insights on structural, environmental and habitat studies.

Keywords: Archaea, Taxis, Bioremediation

1. Introduction

Archaea, most of which had initially been isolated from difficult, harsh and abnormal environments, were called extremophiles playing a key role in vital processes such as carbon and nitrogen cycles (Falkowski et al., 2008, Martínez-Espinosa et al., 2011) in line with human health and modern biotechnology development. Molecular, genomic and phylogenetic data strengthen Woese's definition of archaea as the third domain of life in addition to Bacteria and Eukaryotes (Woese et al., 1990). Archaea not only exist in diverse environments, but also they can be abundant. Their predominance in marine plankton, including oceans, points to a crucial and still very poor role in the biogeochemical cycles of our planet (Keenan et al., 2001, Rothschild and Mancinelli, 2001). Evidence suggests that archaea are typically older than eukaryotes and bacteria; but, their growth rate is slower than that of eukaryotes and bacteria during evolutionary periods. However, no clear reasons have been found for the slow evolutionary rate of archaea compared to eukaryotes and bacteria, which may be related to their lives in anomalous environments (Martens-Habbena and Stahl, 2011). Although nowadays, our knowledge with regard to this group of organisms has been increased, compared to bacteria and eukaryotes, most basic processes in archaea have not been adequately characterized. For example, while cell surfaces play a key role in cell biology of archaea, inadequate information has been remained concerning their composition, biosynthesis and function (Zaremba-Niedzwiedzka et al., 2017). The similarities of archaea to bacteria and eukaryotes have been characterized such that it is clearly evident according to the cell wall and membrane that both bacteria and archaea have a cell wall. While bacteria cell walls contain peptidoglycan compounds, archaea cell walls have either pseudopeptidoglycan or protein-based cell walls (Sleytr et al., 2014). Archaea is composed of N-Acetyltalosaminuronic acid, instead of N-Acetylmuramic acid (MurNAc). Moreover, N-Acetylglucosamine (GlcNAc) and N-Acetyltalosaminuronic acid exist instead of β-(4-1) and β-(3-1) (Klingl, 2014). The cytoplasm of both bacteria and archaea consists of a cytoplasmic membrane composed primarily of glycerol phosphate phospholipids that the lipid composition of these membranes is distinct and specific for each of these organisms (Jain et al., 2014). The bacteria membrane is composed of glycerol and fatty acid attached together through an ester bond; while, archaea lack fatty acids, instead they have isoprene creating much tolerance in archaea membrane. Chirality (inversion) is specific to glycerol in archaea which is in the form of sn-Glycerol-1-phosphate; while, it is sn-Glycerol-3-phosphate in bacteria and eukaryotes (Pohlschröder et al., 2005, Summons et al., 1988). However, archaea are also significantly similar to bacteria in many respects, such as size and organization of chromosomes, the presence of polycistronic transcription units and utilization of Shine–Dalgarno sequences for the initiation of translation (Bell and Jackson, 2001, Lecompte et al., 2002, Londei, 2005).

2.Central Metabolism

Living organisms utilize nutrients both to produce the required energy for biosynthesis and other endergonic processes. The degradative metabolic pathways by which the precursors are produced for cell components are known as catabolic pathways; whereas, the biosynthetic processes are referred to as anabolic reactions (Danson, 1988, Danson, 1993). The exact nature of the catabolic and anabolic pathways is dependent on the starting nutrients and the intended cell components; the metabolic linkage between them is provided by the pathways of central metabolism, the reactions which are used as the main routes to energy generation. Therefore, this is an evident and important statement that central metabolism is vital to all activities within a cell. Moreover, due to the high importance, these pathways are found in all living organisms so that the precise details vary between organisms but the basic pattern include the majority of species (Morris et al., 1985). Glucose metabolism is performed in two groups of archaea, including extreme halophiles and thermophiles, with little variation in the pathway of Enter-doudoroff cycles. In glucose catabolism, an intermediate (2-keto-3-deoxy-6-phosphogluconate) or its phosphate-free form is produced and the rest of the steps are similar to those in E-D pathway in bacteria. As a result, glucose is oxidized to gluconate and then dehydrated to 2-keto-3- deoxygluconate, which in turn is phosphorylated to 2-keto-3-deoxy-6-phosphogluconate. A modified version of Entner–Doudoroff pathway is found in other species of Halobacterium, Haloferax and Halococcus, that may be common for halophiles (Rawal et al., 1988, Severina et al., 1991). No route for glucose catabolism other than the modified Entner-Doudoroff pathway has been reported in halophiles. However, Tomlinson et al. have reported that pyruvate production from glucose does not need any ATP (Tomlinson and Hochstein, 1972b). Acid catabolic reactions in archaea are performed through citric acid cycle. Macromolecules' monomers in archaea are composed of intermediates like those of the pathways of bacteria metabolism (Tomlinson and Hochstein, 1972a, Tomlinson and Hochstein, 1972b). In ATP synthesis, extreme thermophiles have a-type cytochrome. Considering the location of this carrier in the metabolic membrane, organotrophy is initiated with electron reduction from the reduced substance to the electron-transport chain and is eventually transmitted to oxygen and sulfur and reduces them. The electron movement in electron transport chain (ETC) results in proton motive force formation around the membrane, which drives the synthesis of ATP via ATPase enzyme (Deppenmeier and CMLS, 2002, Gottschalk and Thauer, 2001, MÜLLER et al., 1988, Schlegel and Müller, 2013, Thauer et al., 2008). In methanogenic bacteria, and lithotrophic thermoacidophiles, Co_2 absorption occurs through the Acetyl-CoA pathway with little modification. Obligate thermophile like thermoproteus and sulfolobus, CO_2 absorbance is done via the reverse Krebs cycle (also known as the reverse tricarboxylic acid cycle), which are also similar to green sulfur-like bacteria in this regard. Halobacterium carbon dioxide is obtained through the Calvin cycle(Berg et al., 2010).

Taxis in archaea

In comparison with the well-explored bacterial chemical systems, studies on archaea chemotaxis are limited. Studies have shown that several euryarchaeota display tactic behavior and respond to acetate, some amino acids or light. However, the majority of these studies seem not yet to have been accompanied with genetic or biochemical research (Migas et al., 1989, Sment and Konisky, 1989). Most of our understanding of archaea taxis has been gleaned from studies of *Halobacterium salinarum* model organism. This microbe can perform aerobic respiration, and arginine fermentation and use light as an energy source (Gonzalez et al., 2009). The organism requires pumps bacteriorhodopsin (BR) and halorhodopsin (HR) that which have a role in ion exchange (Oesterhelt and Tittor, 1989). As a result, the mentioned different growth strategies, *H. salinarum* can react to different stimuli such as light, oxygen, amino acids and sensitive membrane potential (Kokoeva and Oesterhelt, 2000, Kokoeva et al., 2002, Seidel et al., 1995, Spudich et al., 1988, Yao and Spudich, 1992). *H. salinarum* contains 18 different MCP homologs named Halobacterial transducer proteins (Htrs), which possess their own sensing domain and interact with other receptor proteins (Koch et al., 2008). HtrI and HtrII have phototaxic reaction ((Spudich et al., 1988, Yao and Spudich, 1992). Htr8 and Htr10 (HemAT) require oxygen for absorption and phobic reactions ((Brooun et al., 1998, Hou et al., 2000). Htr14 (MpcT) can detect changes in membrane potential (Koch and Oesterhelt, 2005); while, Htr11 (Car) has cytosolic activity (Storch et al., 1999). Htr3 (BasT) is responsible for detection of branched chain and sulfur-containing amino acids and Htr5 (CosT) mediates osmolytes compatibility (Kokoeva and Oesterhelt, 2000, Kokoeva et al., 2002). Phototaxis offers boundless experimental possibilities. In compariosn with chemical stimuli, a light stimulus can be instantly switched on and off, allowing for formation of a dynamic range, duration of the stimulus as well as its intensity. This phototaxtic response has been studied and is considered as one of the applications in biology programs (Nutsch et al., 2003, Streif et al., 2010).

Bioremediation via archaea

Bioremediation is the use of microorganisms for degradation or removal of contaminants. Most bioremediation research have focused on the processes performed by the domain bacteria; however, the specified archaea play an important role in many situations. In extreme conditions, such as halophilic or acidophilic environments, archaea are well suited for bioremediation. Archaea play a role in halophilic hydrocarbon degradation, acidophilic hydrocarbon degradation, hydrocarbon degradation in impenetrable environments such as soils and oceans, metal refining, and acid mine drainage (Hazen et al., 2016, Lefebvre and Moletta, 2006, SINGH et al.).

Pathogenic potential of archaea

Currently, research reveals that archaea are able to survive in the human body. However, the efforts made to prove the pathogenic potential of archaea in humans have not been successful by 2011 (Relman et al., 2000). Pathogenesis depends on host cell entry, growth, proliferation, use of host system tools and host immune system. Archaea will follow this pattern if they behave as pathogens (Eckburg et al., 2003). Microbiologists often do not prioritize archaea in clinical practices, because these organisms have been known as exotic extremophiles that have strange molecular machinery. Since archaea have been known to be methanogens associated with the human gut for several decades, human clinical studies may reveal new aspects of archaea–human interactions. Therefore, today SrRNA16 genes can be used to fully identify pathogenic factors in humans (Walters et al., 2011). By investigating the human colon content, researchers assigned about 0.8% of the genes to archaea which are in methanogen form (Fricke et al., 2006, Qin et al., 2010). Thus, these gene transmissions have made them resistant and present in the human colon. *M. smithii, M. Stadtmanae, Methanomassiliicoccus luminyensis* and *Candidatus Methanomethylophilus* alvus are examples of these organisms that are mostly found in the patients with intestinal inflammation ((Bang et al., 2014, Lecours et al., 2014). Intestinal methanogens play a role in human obesity and chronic constipation (Samuel and Gordon, 2006, Turnbaugh et al., 2006). Archaea have also been detected to play a role in the formation of dental plaques (Brusa et al., 1987) and are found on the surface of human skin (al., 2012, Oh et al., 2014).

Conclusion

The study of archaea has confirmed the initial predictions by Woese suggesting that archaea will exhibit a phenotypic diversity at least comparable to that of bacteria and that archaea will be characterized by unique features at the molecular level. In addition, it was revealed that archaea play a special role in bioremediation and are present in human host. Given the extreme climate nature of many archaea, the gradual survival strategies of these microorganisms seem considerable.

Reference

Bang C, Weidenbach K, Gutsmann T, Heine H, Schmitz RA 2014. The intestinal archaea Methanosphaera stadtmanae and Methanobrevibacter smithii activate human dendritic cells. PloS one, 9(6):e99411.

Bell SD, Jackson SP 2001. Mechanism and regulation of transcription in archaea. Curr Opin Microbiol, 4(2):208-13.

Berg IA, Kockelkorn D, Ramos-Vera WH, Say RF, Zarzycki J, Hügler M, Alber BE, Fuchs G 2010. Autotrophic carbon fixation in archaea. Nat Rev Microbiol, 8(6):447-60.

Brooun A, Bell J, Freitas T, Larsen RW, Alam M 1998. An archaeal aerotaxis transducer combines subunit I core structures of eukaryotic cytochrome c oxidase and eubacterial methyl-accepting chemotaxis proteins. J bacteriol, 180(7):1642-6.

Brusa T, Conca R, Ferrara A, Ferrari A, Pecchioni A 1987. The presence of methanobacteria in human subgingival plaque. J Clin Periodontol., 14(8):470-1.

Danson MJ 1988. Archaebacteria: the comparative enzymology of their central metabolic pathways. Adv Microb Physiol, 29: 165-231. Academic Press.

Danson MJ 1993. Central metabolism of the archaea. InNew Comprehensive Biochemistry, 26:1-24. Elsevier.

Deppenmeier U 2002. Redox-driven proton translocation in methanogenic Archaea. Cell Mol Life Sci, 59(9):1513-33.

Eckburg PB, Lepp PW, Relman DA 2003. Archaea and their potential role in human disease. Infect Immun, 71(2):591-6.

Falkowski PG, Fenchel T, Delong EF 2008. The microbial engines that drive Earth's biogeochemical cycles. Science, 320(5879):1034-9.

Fricke WF, Seedorf H, Henne A, Krüer M, Liesegang H, Hedderich R, Gottschalk G, Thauer RK 2006. The genome sequence of Methanosphaera stadtmanae reveals why this human intestinal archaeon is restricted to methanol and H2 for methane formation and ATP synthesis. J Bacteriol, 188(2):642-58.

Gonzalez O, Gronau S, Pfeiffer F, Mendoza E, Zimmer R, Oesterhelt D 2009. Systems analysis of bioenergetics and growth of the extreme halophile Halobacterium salinarum. PLoS Comput Biol, 5(4).

Gottschalk G, Thauer RK 2001. The Na+-translocating methyltransferase complex from methanogenic archaea. Biochimica et Biophysica Acta (BBA)-Bioenergetics, 1505(1):28-36.

Hazen TC, Prince RC, Mahmoudi N 2016. "Marine oil biodegradation, 2121-2129. ACS Publications.

Hou S, Larsen RW, Boudko D, Riley CW, Karatan E, Zimmer M, Ordal GW, Alam M 2000. Myoglobin-like aerotaxis transducers in Archaea and Bacteria. Nature, 403(6769):540-4.

Hulcr J, Latimer AM, Henley JB, Rountree NR, Fierer N, Lucky A, Lowman MD, Dunn RR 2012. A jungle in there: bacteria in belly buttons are highly diverse, but predictable. PloS one, 7(11).

Jain S, Caforio A, Driessen AJ 2014. Biosynthesis of archaeal membrane ether lipids. Front Microb, 5:641.

Keenan RJ, Freymann DM, Stroud RM, Walter P 2001. The signal recognition particle. Annu Rev Biochem, 70(1):755-75.

Klingl A 2014. S-layer and cytoplasmic membrane–exceptions from the typical archaeal cell wall with a focus on double membranes. Front Microb, 5:624.

Koch MK, Oesterhelt D 2005. MpcT is the transducer for membrane potential changes in Halobacterium salinarum. Mol Microbiol, 55(6):1681-94.

Koch MK, Staudinger WF, Siedler F, Oesterhelt D 2008. Physiological sites of deamidation and methyl esterification in sensory transducers of Halobacterium salinarum. J Mol Biol, 380(2):285-302.

Kokoeva MV, Oesterhelt D 2000. BasT, a membrane-bound transducer protein for amino acid detection in Halobacterium salinarum. Mol Microb, 35(3):647-56.

Kokoeva MV, Storch KF, Klein C, Oesterhelt D 2002. A novel mode of sensory transduction in archaea: binding protein-mediated chemotaxis towards osmoprotectants and amino acids. EMBO, 21(10):2312-22.

Lecompte O, Ripp R, Thierry JC, Moras D, Poch O 2002. Comparative analysis of ribosomal proteins in complete genomes: an example of reductive evolution at the domain scale. Nucleic Acids Res, 30(24):5382-90.

Lecours PB, Marsolais D, Cormier Y, Berberi M, Haché C, Bourdages R, Duchaine C 2014. Increased prevalence of

Methanosphaera stadtmanae in inflammatory bowel diseases. PLoS One, 9(2).

Lefebvre O, Moletta R 2006. Treatment of organic pollution in industrial saline wastewater: a literature review. Water research, 40(20):3671-82.

Londei P 2005. Evolution of translational initiation: new insights from the archaea. FEMS Microbiol Rev, 29(2):185-200.

Martens-Habbena W, Stahl DA 2011. Nitrogen metabolism and kinetics of ammonia-oxidizing archaea. Methods Enzymol, 496: 465-487. Academic Press.

Martínez-Espinosa RM, Cole JA, Richardson DJ, Watmough NJ 2011. Enzymology and ecology of the nitrogen cycle. Biochem Soc Trans, 39 (1): 175–178.

Migas J, Anderson KL, Cruden DL, Markovetz AJ 1989. Chemotaxis in Methanospirillum hungatei. Appl Environ Microbiol, 55(1):264.

Morris JG 1985. Anaerobic metabolism of glucose. Comprehensive biotechnology: the principles, applications and regulations of biotechnology in industry, agiculture and medicine, 1:357-78.

Müller V, Wınner C, Gottschalk G 1988. Electron-transport-driven sodium extrusion during methanogenesis from formaldehyde and molecular hydrogen by Methanosarcina barkeri. FEBS J, 178(2):519-25.

Nutsch T, Marwan W, Oesterhelt D, Gilles ED 2003. Signal processing and flagellar motor switching during phototaxis of Halobacterium salinarum. Genome research, 13(11):2406-12.

Oesterhelt D, Tittor J 1989. Two pumps, one principle: light-driven ion transport in halobacteria. Trends Biochem Sci, 14(2):57-61.

Oh J, Byrd AL, Deming C, Conlan S, Barnabas B, Blakesley R, Bouffard G, Brooks S, Coleman H, Dekhtyar M, Gregory M 2014. Biogeography and individuality shape function in the human skin metagenome. Nature, 514(7520):59-64.

Pohlschröder M, Giménez MI, Jarrell KF 2005. Protein transport in Archaea: Sec and twin arginine translocation pathways. Curr Opin Microbiol, ;8(6):713-9.

Qin J, Li R, Raes J, Arumugam M, Burgdorf KS, Manichanh C, Nielsen T, Pons N, Levenez F, Yamada T, Mende DR 2010. A human gut microbial gene catalogue established by metagenomic sequencing. Nature, 464(7285):59-65.

Rawal N, Kelkar SM, Altekar W 1988. Alternative routes of carbohydrate metabolism in halophilic archaebacteria. Indian J Biochem Biophys, 25(6):674-86

Relman DA, Falkow S 2000. A molecular perspective of microbial pathogenetic. Principles and practice of infectious diseases. 5th ed. Philadelphia: Churchill living stone.

Rothschild LJ, Mancinelli RL 2001. Life in extreme environments. Nature, 409(6823):1092-101.

Samuel BS, Gordon JI 2006. A humanized gnotobiotic mouse model of host–archaeal–bacterial mutualism. Proc Natl Acad Sci, 103(26):10011-6.

Schlegel K, Müller V 2013. Evolution of Na+ and H+ bioenergetics in methanogenic archaea. Biochem Soc Trans, 41(1).

Seidel R, Scharf B, Gautel M, Kleine K, Oesterhelt D, Engelhard M 1995. The primary structure of sensory rhodopsin II: a member of an additional retinal protein subgroup is coexpressed with its transducer, the halobacterial transducer of rhodopsin II. Proc Natl Acad Sci, 92(7):3036-40.

Severina LO, Pimenov NV, Plakunov VK 1991. Glucose transport into the extremely halophilic archaebacteria. Arch Microbiol, 155(2):131-6.

Sıngh M, Srıvastava PK, Jaıswal VK, Kharwar RN 2017. Biotechnological applications of microbes for the remediation of environmental pollution. Enviro Protec, 1:3.

Sleytr UB, Schuster B, Egelseer EM, Pum D 2017. S-layers: principles and applications. FEMS microbiol rev, 38(5):823-64.

Sment KA, Konisky JO 1989. Chemotaxis in the archaebacterium Methanococcus voltae. J bacteriol, 171(5):2870-2.

Spudich EN, Hasselbacher CA, Spudich JL 1988. Methyl-accepting protein associated with bacterial sensory rhodopsin I. J bacteriol, 170(9):4280-5.

Storch KF, Rudolph J, Oesterhelt D 1999. Car: a cytoplasmic sensor responsible for arginine chemotaxis in the archaeon Halobacterium salinarum. EMBO, 18(5):1146-58.

Streif S, Oesterhelt D, Marwan W 2010. A predictive computational model of the kinetic mechanism of stimulus-induced transducer methylation and feedback regulation through CheY in archaeal phototaxis and chemotaxis. BMC systems biology, 4(1):27.

Summons RE, Powell TG, Boreham CJ 1988. Petroleum geology and geochemistry of the Middle Proterozoic McArthur Basin, Northern Australia: III. Composition of extractable hydrocarbons. Geochim Cosmochim Acta, 52(7):1747-63.

Thauer RK, Kaster AK, Seedorf H, Buckel W, Hedderich R 2008. Methanogenic archaea: ecologically relevant differences in energy conservation. Nat Rev Microbiol, 6(8):579-91.

Tomlinson GA, Hochstein LI 1972. Isolation of carbohydrate-metabolizing, extremely halophilic bacteria. Can J Microbiol, 18(5):698-701.

Tomlinson GA, Hochstein LI 1972. Studies on acid production during carbohydrate metabolism by extremely halophilic bacteria. Canb J Microbiol, 18(12):1973-6.

Turnbaugh PJ, Ley RE, Mahowald MA, Magrini V, Mardis ER, Gordon JI 2006. An obesity-associated gut microbiome with increased capacity for energy harvest. Nature, 444(7122):1027.

Walters WA, Caporaso JG, Lauber CL, Berg-Lyons D, Fierer N, Knight R 2011. PrimerProspector: de novo design and taxonomic analysis of barcoded polymerase chain reaction primers. Bioinformatics, 27(8):1159-61.

Woese CR, Kandler O, Wheelis ML 1990. Towards a natural system of organisms: proposal for the domains Archaea, Bacteria, and Eucarya. Proc Natl Acad Sci, 87(12):4576-9.

Yao VJ, Spudich JL 1992. Primary structure of an archaebacterial transducer, a methyl-accepting protein associated with sensory rhodopsin I. Proc Natl Acad Sci, 89(24):11915-9.

Zaremba-Niedzwiedzka K, Caceres EF, Saw JH, Bäckström D, Juzokaite L, Vancaester E, Seitz KW, Anantharaman K, Starnawski P, Kjeldsen KU, Stott MB 2017. Asgard archaea illuminate the origin of eukaryotic cellular complexity. Nature 541(7637):353-8.