

Origin of Infections: Five Independent Pathways

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Corresponding Author:** Alen J Salerian, Modern Psychiatry, Athens, Greece.**Received:** April 07, 2021**Published:** April 30, 2021© All rights are reserved by **Alen J Salerian.*Abstract**

This paper proposes that there maybe five independent pathways for infections to develop; Transformation from organic matter, a non-living protein multiplying in a cell, evolution of microbes, reproduction-contamination and endogenous production.

It has been demonstrated that the Christensenellaceae, a family in the phylum *Firmicutes*, is heritable suggesting that human cells and gut bacterial material are related. It has also been shown that the fetus is exposed to bacteria prior to birth -without any evidence that they are contaminants or acquired from the environment suggesting a possible endogenous origin of bacteria in breast milk, meconium, placenta, umbilical cord blood and amniotic fluid.

Malassezia yeasts are not contagious, not culturable from the environment, cannot colonize human skin by inoculation without occlusion and neonate skin is free of Malassezia but is colonized in the first month of life suggesting that they may be endogenous.

Human stem cells seem to be the most likely candidates to produce microbes: This is because they differentiate to epithelial cells and cancer cells and contain the essentials to transform to microorganisms. Evidence to suggest decomposer microbes and *Pseudomonas aeruginosa* may represent examples of microevolution of microorganisms is presented.

Future experimental studies to demonstrate the transformation of organic matter to microorganisms and also the microevolution of organisms consistent with the Darwinian theory are described.

Keywords: Opportunistic Infections; Contamination; Endogenous Infections; Stem Cells; Chritensenellaceae.

Highlights

- Transformation from organic matter, a non-living protein multiplying in a cell, evolution of microbes, reproduction-contamination and endogenous production may represent pathways of new microorganisms.
- Among many pathways only the germ theory has been experimentally validate.
- Gut microbes are shaped by human genetics and The Christensenellaceae is heritable, bacteria in amniotic fluid, meconium, breast milk and tissue, placenta, umbilical cord are not contaminants and there is no evidence that they are acquired from the environment suggesting that diverse microorganisms may be endogenous.
- Stem cells produce epithelial and cancer cells and are the most likely candidates to produce endogenous microbes.
- Decomposer microbes including *Pseudomonas aeruginosa* may evolve from less complex bacteria consistent with Darwin's theory of evolution.

Since the introduction of the germ theory, it has been accepted that all infections result from foreign invading microbes [1].

Of interest, the history of earth [2,3] and the theory of evolution [4] suggest there may be pathways independent of contamination for microorganisms to develop such as transformation from lifeless organic matter or evolution of microorganisms to more complex microorganisms. It has already been established that viral infections [5] and prion caused diseases [6] result from lifeless proteins multiplying in cells of complex multi-cellular organisms. In essence, our current paradigm of all infections resulting from contamination seems to be less than accurate.

This paper reviews possible diverse origins of infections based upon scientific observations for our better understanding of diverse pathways of infections maybe helpful to combat infectious disorders. Possible diverse origins of infections will be discussed under five headings:

- Transformation from organic matter.
- Organic matter multiplying in a cell of a multicellular organism.
- Reproduction.
- Transformation of human stem cells to unicellular species.
- Evolution of more complex unicellular organisms from less complex organisms.

Unicellular microorganisms from organic matter

The history of life on earth suggests, the first microorganisms were born from lifeless organic matter some 3.6 billion years ago [2,3]. Although there is some controversy over the exact timing and the precise identity of the first living things on earth, in general, the scientific consensus indicates living organisms came from non-living organic matter. It seems reasonable to assume that the very processes that started life 3.6 billion years ago continue to be operational now.

A lifeless protein and a cell of a multicellular organism

Yet not fully understood processes involved in the formation of unicellular organisms from lifeless organic matter may also be observed in the emergence of infectious pathogens such as viruses

[5] and prion associated disorders [6] whereby a lifeless protein-virion or prion-gains the capacity to multiply and reproduce upon entry into a cell of a multicellular organism. Viral infections and prion caused neurodegenerative disorders represent infections that develop by various protein particles becoming pathogens in human and animal cells.

Reproduction-contamination

Bacteria reproduce by cell division through binary fission. The germ theory experimentally validated by Louis Pasteur demonstrated that some infections result from bacterial growth [1]. Indeed, the germ theory has been the central paradigm of medicine ever since its introduction in the middle of 19th century.

Possible changes of stem cells to microorganisms

There seems to be some indirect evidence to suggest the possibility that stem cells which are multi potent and capable to differentiate to epithelial cells and cancer may also transform to microorganisms. Although this hypotheses has not been validated by experimental studies, its potential validity is supported by diverse observations that indeed humans and some microorganisms share genetic links. For instance, it has been demonstrated that the Christensenellaceae, a family in the phylum Firmicutes, is heritable suggesting that human genetic material [7] and gut bacterial material are related and human cells may generate some gut microbes. Also, It has been shown that Malassezia yeasts are not contagious [8,9], not culturable from the environment [10], cannot colonize human skin by inoculation without occlusion [11,12] and neonate skin is free of Malassezia [13] but is colonized in the first month of life [14] suggesting that they may be endogenous.

Furthermore, It has also been shown that the fetus is exposed to bacteria prior to birth -without any evidence that they are contaminants or acquired from the environment [15] suggesting a possible endogenous origin of bacteria in placenta [16], amniotic fluid [17] meconium [18] breast milk [19], breast tissue [20] umbilical cord blood [21].

In essence a plethora of observations are consistent with the possibility that the Christensenellaceae, Malassezia yeasts and bacteria in breast milk, meconium, placenta, umbilical cord blood and amniotic fluid are endogenous.

The hypotheses of endogenous infections may suggest that human stem cells are the most likely candidates to produce microbes: This is because human stem cells differentiate to epithelial cells, erythrocytes, lactocytes, cancer cells and have all the essentials to produce bacteria [22,23]. Also, the rate of gut epithelial cell production and cell loss is the same as endogenous bacterial production suggesting that fallen epithelial cells may become bacteria [24]. Understandably, the endogenous infections hypotheses needs future experimental validation.

Microevolution of microbes

Approximately 38 trillion microbes represent the normal flora and are still active when a mammal dies [25]. Decomposer microbes including *Pseudomonas aeruginosa* play an important role in the process of mammalian decomposition [26-28]. In the early stages of decomposition, decomposer bacteria breakdown tissues and produce hydrogen sulfide methane putrescine, cadaverine, which inflate cadaver and eventually trigger the rupture of skin [26-28]. The pre-bloat stage is predominated by *Pseudomonas*, *Streptococcus*, *Staphylococcus*, *Enterobacteriaceae*, *Prevotella*, *Veillonella* and *Actinobacteria*.

Decomposition follows a predicted clock like sequence consistent with a shift from aerobic to anaerobic and ammonium intolerant to ammonium tolerant microbes. suggesting that bacterial communities evolve and gain abilities to survive in rapidly changing environments corresponding with the stages of decomposition [26-28]. Predicted increases in genes related to nitrogen cycling and amino acid degradation including those required for the breakdown of lysine and arginine into cadaverine and putrescine have been noted [26-28]. Later, the decomposer microbial community seems to be capable to survive in ammonium rich environments [26-28].

Hyde., *et al.* suggested that the decomposer bacterial community migrated out of the large intestine, skin or soil [26,27]. Metcalf at al. hypothesized that the microbial decomposers mainly come from the rich microbial biodiversity in soils [28].

Of interest, several observations argue against the hypotheses that soil bacteria are the predominant source of decomposers. For instance, there are some estimated 38 trillion microorganisms that reside in human body are still alive and active at the time of death [25].

Decomposition has been observed in pig carcasses in tightly wrapped plastic bags in water [29]. It has also been demonstrated

that in sterile soil decomposition occurred [30]. In summary, host specific intrinsic biological processes -independent of the environment -shape the bacterial communities involved in mammalian decomposition. This observation suggests that the most likely candidate of origin of decomposer microbes including *Pseudomonas* are the endogenous bacteria of the host body and not contaminants from the soil. Worthy of emphasis is the observation that during mammalian decomposition bacterial communities continue to change and evolve in a predicted schedule without any evidence that those changes correspond to input from microorganisms that are getting acquired from the environment. This observation also suggests that environmental conditions shared by a dead host may promote evolution of decomposing microbes including *Pseudomonas* from host microbes. *Pseudomonas* has larger genome size and greater cellular and functional complexity-more evolved- than common bacteria [31].

The possible evolution of complex unicellular organisms such as *pseudomonas aeruginosa* from less complex unicellular organisms such as human bacterial flora lacks experimental validation however is supported by indirect scientific observations on burn wound infections and studies of decomposer species.

During mammalian decomposition host gut bacteria-and not contaminants from the environment- seem to be the predominant source of decomposers suggesting that decomposer bacteria may be endogenous and represent evolution of host bacteria. In essence, decomposer bacteria including *Pseudomonas* may result from contamination or may evolve from host gut bacteria consistent with what Charles Darwin once observed - all species have two possible pathways of origins, reproduction or evolution from a less complex organism.

Discussion

Scientific data suggest there may indeed multiple pathways of origin for infections to develop independent of contamination. It is true that among many possible pathways of infections only the germ theory has been experimentally validated.

However compelling the supporting evidence, neither the birth of first microorganisms from organic matter nor the evolution of species has been experimentally demonstrated.

Bacteria in the fetus that are not contaminants, the observation that some gut bacteria and *Malassezia* species are heritable strongly support an endogenous origin of some infections.

If indeed some infections are endogenous and do not result from contamination, human stem cells are the most likely candidates to produce microbes: This is because human stem cells differentiate to epithelial cells, erythrocytes, lactocytes, cancer cells and have all the essentials to produce bacteria. Also, the rate of gut epithelial cell production and cell loss is the same as endogenous bacterial production suggesting that fallen epithelial cells may become bacteria

Also of significance, the emergence of more complex microorganisms during mammalian decomposition without any evidence of their foreign origin maybe viewed as evidence of microevolution of normal gut bacteria.

It seems possible to conduct novel studies to demonstrate the transformation of organic matter to microorganisms and also the microevolution of organisms. It can easily be demonstrated that sterilized organic matter [milk and eggs] would generate microorganisms in sterile conditions in ambient temperatures. For the record, this author conducted a home experiment in which microwave sterilized eggs in sterile conditions and in temperatures between 20 and 30 Celcius showed visually observable evidence of spoilage. It seems equally feasible to demonstrate microevolution of common bacteria to more complex bacteria in conditions similar to mammalian decomposition.

Further experimental validation of the central paradigm of this paper-possible multiple pathways of infections-may help us better combat infectious disorders.

Bibliography

- Pasteur L. "And the extension of the germ theory to the aetiology of certain common diseases". *Comptes rendus del'Academie des Sciences*. xc. Ernst, (Ttrans) (1880): 1033-1044.
- Schopf JW. "Fossil evidence of Arcaean Life". *Philosophical Transactions of the Royal Society Biological Sciences* 361.1470 (2006).
- Cavalier-Smith T. "Cell evolution and Earth history: Stasis and revolution". *Philosophical Transactions of the Royal Society Biological Sciences* 1470 (2006): 969-1006.
- Darwin C. "On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life" (1859).
- Breitbatr M and Rohwer F. "Here a virus, there a virus, everywhere the same virus?". *Trends in Microbiology* 13.6 (2005): 278-284.
- Brown P, *et al.* "Bovine spongiform encephalopathy and variant Creutzfeldt- Jacob disease: background evolution and current concerns". *Emerging Infectious Diseases* 7.1 (2001): 6-16.
- Waters JL, *et al.* "The human gut bacteria Christensenellaceae are widespread, heritable, and associated with health". *BMC Biology* 17 (2019): 83.
- He SM, *et al.* "The genetic epidemiology of tinea versicolor in China". *Mycosis* 51 (20007).
- Salerian AJ. "Twins With Endogenous Tinea Versicolor". *International Journal of Case Reports* 4 (2019): 81.
- Velegraki A, *et al.* "Malassezia Infections in Humans and Animals: Pathophysiology, Detection, and Treatment". *PLoS Pathogen* 11.1 (2015): e1004523.
- Faergemann J and Fredricksson T. "Experimental infections in rabbits and humans with Pityrospum orbiculare and Povale". *Journal of Investigative Dermatology* 77.3 (1981): 314-318.
- Faergemann J, *et al.* "Skin occlusion : effect on Pityrospum orbiculare,skinP-CO2,ph, trans epidermal water loss, and water content". *Archives of Dermatological Research* 275.6 (1983): 383-387.
- Bell L, *et al.* "Malassezia furfur Skin Colonization in Infancy". *Infection Control and Hospital Epidemiology* 9.4 (1988): 151-153.
- Powell D, *et al.* "Malassezia furfur colonization of infants hospitalized in intensive care units". *The Journal of Pediatrics* 111.2 (1987): 217-220.
- Stinson L F, *et al.* "The Not-so-Sterile Womb: Evidence That the Human Fetus Is Exposed to Bacteria Prior to Birth". *Frontiers in Microbiology* 10 (2019): 1124.
- Digiullo DB. "Diversity of microbes in amniotic fluid". *Seminars in Fetal and Neonatal Medicine* 17.1 (2012): 2-11.
- Collado MC, *et al.* "Human gut colonization maybe initiated in utero by distinct microbial communities in the placenta and amniotic fluid". *Scientific Reports* 6 (2016): 23129.
- Jimenez E, *et al.* "Is meconium from healthy mothers sterile?". *Research in Microbiology* 159.3 (2008): 187-189.
- Martin R, *et al.* "Human milk is a source of lactic acid bacteria for the infant gut". *The Journal of Pediatrics* 143.6 (2003): 754-758.

20. Urbaniak C., *et al.* "Microbiota in human breast tissue". *Applied and Environmental Microbiology* 80 (2014): 3007-3014.
21. Jiménez E., *et al.* "Isolation of Commensal Bacteria from Umbilical Cord Blood of Healthy Neonates Born by Cesarean Section". *Current Microbiology* 51 (2005): 270-274.
22. Van der Flier LG., *et al.* "Stemcells, Self Renewal, and Differentiation in the intestinal Epithelium". *Annual Review of Physiology* 71.1 (2009): 24-260.
23. Reya T., *et al.* "Stem cells, cancer, and cancer stem cells". *Nature* 414 (2001): 105-111.
24. LOPEZ-GARCIA C., *et al.* "Intestinal Stem Cell Replacement Follows a Pattern of Neutral Drift". *Science* 327 (2010): 822-825.
25. Sender R., *et al.* "Revised Estimates for the Number of Human and Bacteria Cells in the Body". *PLoS Biology* 14.8 (2016): e1002533.
26. Hyde ER., *et al.* "The Living Dead: Bacterial Community Structure of a Cadaver at the Onset and End of the Bloat Stage of Decomposition". *PLoS One* 10 (2013): e77733.
27. Hyde ER., *et al.* "Initial insights into bacterial succession during human decomposition". *International Journal of Legal Medicine* 129 (2015): 661-671.
28. Metcalf JL., *et al.* "Microbial community assembly and metabolic function during mammalian corpse decomposition". *Science* 351.6269 (2016): 158-162.
29. Pakosh C M and Rogers T L. "Soft tissue decomposition of submerged dismembered pig limbs enclosed in plastic bags". *Journal of Forensic Sciences* 54.6 (2009).
30. Lauber CL., *et al.* "Vertebrate Decomposition Is Accelerated by Soil Microbes". *Applied and Environmental Microbiology* 80.16 (2014): 4920-4929.
31. Stover CK., *et al.* "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen". *Nature* 406 (2000): 959-964.

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