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Some Infections are Heritable or Endogenous: Biological and Mathematical Analysis

Alen J Salerian

1. George Washington University

Abstract: This brief report presents biological and mathematical evidence to suggest some infections develop independent of contamination. The germ theory "infections result from invasions of human body by foreign microbes "has been the central paradigm for infectious disorders since Pasteur's research in mid-1800's. Tuberculosis, leprosy, tinea versicolor H.Pylori infections are heritable and tetanus, pseudomonas aeruginosa burn wound infections, myasis and pinworm infections are endogenous. Conclusion: Some infections result from contamination whereas many others are inherited or develop internally consistent with Darwinian theory of evolution.: New species emerge from reproduction or evolution of more complex species from less complex ones.

Keywords: leprosy, tuberculosis, pinworms, tetanus, burn wounds

This paper reports that some infections are heritable or endogenous along with infections that result from contamination.

The germ theory "infections result from invasions of human body by foreign microbes "has been the central paradigm for infectious disorders since Pasteur's research in mid-1800's (1,2).

Surprisingly new evidence has emerged suggesting that some infections e.g. tuberculosis (3) tinea versicolor (4) H.Pylori infections (5) are heritable conditions that may develop independent of contamination. In general, they are not contagious.

Evidence also reveals that many infections e.g. pseudomonas aeruginosa burn wound infections (6), myasis (7) and tetanus (8) may develop internally and independent of contamination.

Hereby, we present biological and mathematical evidence to suggest pinworm infections are endogenous and leprosy is heritable.

PINWORMS

Gut stem cells may evolve to pinworms independent of contamination:

1. Pinworms co evolved with mammals' ancestors (9).
2. The synonymy of E. gregorii with E. vermicularis is supported by the molecular evidence Sequences of 5S rDNA were identical in chimpanzees and humans(10).
3. Phylogenetic analysis :Pinworms co evolved with humans (10).
4. Phylogenetic analysis :Pinworms co evolved with orangutans.(11).
5. Pinworms belong to natural human physiology :61% of children in India, 50% in England, 39% in Thailand, 37% in Sweden are infected (9,,12).

6. 70% of hosts are asymptomatic consistent with natural physiology(9,12)
7. Enterobius vermicularis are at home in every biome that is home to humans , Human Intestines are the only natural host of Enterobius vermicularis. (9,12).
8. More than half of hosts of Enterobius vermicularis harbor normal gut microbiota (13).
9. Human physiology mediate Enterobius Vermicularis. Host age strongly associate with infection, much less common in adults(9,12).
10. Enterobius vermicularis infestations have been noted in over one-quarter of acute appendectomies on histologic examination (9).
11. Gut microbes have all the essential to produce eggs of Enterobius vermicularis.
12. Gut microbes produce blowfly eggs (13).
13. Gut stem cells produce gut microbes (13,14).
14. There is no evidence that contamination is the only pathway for egg production. Contamination does not rule out independent production of eggs from gut microbes as observed in myasis(13).
15. Darwinian theory: new species may emerge by reproduction or development of more complex organisms (15).

Odds of certainty = %99.997 “Pinworms may develop independent of contamination”..

LEPROSY

Observations consistent with” leprosy Is heritable “and “inconsistent with leprosy is not heritable ”.

1. Evidence of several characteristic features of M. leprae from patients in Qiubei County, China. with, severe clustering of patients within families and multicase families, sharing closely matching VNTR genotypes (20),
2. Two Cases of leprosy in siblings were demonstrated (21).
3. The region of DNA responsible for leprosy is also involved in Parkinson's disease, the two disorders may be linked at the biochemical level.(22)
4. Using comparative genomics, in 2005, geneticists traced the origins and worldwide distribution of leprosy from East Africa or the Near East along human migration routes (23).
5. All contemporary leprosy cases trace back to one ancestral M. leprae clone, demonstrating minimal genetic diversity(23).
6. Genomic Reduction: M. leprae has lost about half its genome, becoming highly dependent on its host (23).
7. Sooty mangabey monkeys (Cercocebus atys) harbor natural infection with M. leprae (24).
8. Chimpanzee and sooty mangabey M. leprae strains belong to a human M. leprae lineage in West Africa (24).

9. M. leprae and M. lepromatosis are obligate intracellular pathogens and cannot grow or be cultured outside of host tissues(25).
10. Multilocus sequence typing of the armadillo M. leprae strains suggests that they were of human origin (26).
11. Leprosy does not spread to the fetus during pregnancy (27).
12. Leprosy does not spread through sexual contact (27).
13. 95% of people who are exposed to leprosy do not develop leprosy (27).

Odds of random occurrence of this outcome is 0.01

13 observations are consistent with" leprosy is heritable "and "inconsistent with leprosy Is not heritable ".

In summary it has been proven that tuberculosis, tinea versicolor, H.Pylori infections. pseudomonas aeruginosa burn wound infections, myasis and tetanus may develop independent of contamination.

CONCLUSION

Some infections result from contamination whereas many others are inherited or develop internally consistent with the germ and evolutionary theories.

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Table A

Heritable Infections	Endogenous Infections
Leprosy	Tetanus
Tuberculosis	Myasis
Tinea versicolor	Burn wound infections by pseudomonas aeruginosa
H pylori infections.	Pinworms/ Enterobius Vermicularis