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Opinion

Listeriosis Patients by *Listeria monocytogenes* Infection: A Resurgent Foodborne Disease in Immune-Compromised Subjects

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Very recently, only 2 days ago, Pitts and D'Orazio [1] reported an interesting outcome on PGE2, a lipid-signaling compound with multiplex tasks in both homeostasis and inflammation. Depending on the cellular context, it may suppress certain immune responses. In their research, they tested whether PGE2 could inhibit bacterial killing by polymorphonuclear neutrophils (PMN) by means of a mouse model of foodborne listeriosis. They found that PGE2 pretreatment dropped-off the aptitude of PMN harvested from the bone marrow of either BALB/cByJ or C57BL/6J mice to kill *Listeria monocytogenes in vitro*. PGE2 treatment supported the migration of PMN toward the chemoattractant leukotriene B4, declined uptake of *Listeria monocytogenes* by PMN, and inhibited the respiratory burst of PMN compared with vehicle-treated cells. When immune cells were isolated from the livers of infected mice and tested directly *ex vivo* for the presence of PGE2, BALB/cByJ cells produced remarkably more than C57BL/6J cells. Thus, these results suggest that robust PGE2 production can suppress PMN effector functions, leading to decreased bacterial killing, which may contribute to the innate susceptibility of BALB/cByJ mice to infection with the facultative intracellular bacterial pathogen *Listeria monocytogenes*. Thus, these important data, have caught my attention given that during my youth, as researcher, I have carried out studies on *Listeria monocytogenes* - see references [2-8] and latterly on bacteriocins as reported in [9] and dairy products like source of beneficial microorganism able to survival on GIT [10-13].

Listeria monocytogenes has been diagnosticated as a human pathogen from about 80 years. The demographic shift and the extensive employment of immunosuppressive pharmaceuticals, to treat malignancy and organize organ transplantation, have make greater in size the immunocompromised community at increased risk of listeriosis. Additionally, consumer lifestyles have evolved, such that less time is available for food preparation and more RTE and takeaway foods are consumed.

In this manner, changes in food production and technology have led to the production of foods with longer shelf-lives that are typical 'Listeria-risk foods', because the bacteria have time to multiply and the food does not undergo a listericidal process, such as cooking, before consumption. Unlike infection with other common foodborne pathogens, listeriosis is associated with a high case-fatality rate of approximately 20 - 30% and *Listeria monocytogenes* continues to cause foodborne diseases with 95% hospitalization [14].

Over 90% of the human listeriosis cases are originated by *Listeria monocytogenes* serotypes 1/2a, 1/2b and 4b strains. Other possibility to antigen-antibody based serotyping, a PCR-based method for serogrouping has been developed and validated. In Laksanalamai and co-authors communication [15], it was reported an in-depth analysis of five 4b variant strains, in wich one environmental isolate from USA and four clinical isolates from Australia. Although these five strains were serotype 4b by classical serotyping method, the serogrouping PCR profiles of these strains display the existence of a 1/2a-3a specific amplicon besides to the standard 4b4d-4e specific amplicons.

These strains were additionally analyzed by Pulsed Field Gel Electrophoresis, binary gene typing, multilocus variable-number-tandem-repeat analysis and a high density pan-genomic Listeria microarray. By means of these sub-typing results, the clinical isolates were grouped into two distinct genomic groups- one of which could be part of an unidentified outbreak. The microarray results when compared with our database of other 4b outbreak isolates indicated that the serotype 4b variant strains show very distinct genotypic profiles than the known reported 4b outbreak strains constituting principal epidemic clones. The asset of serotype 1/2a gene clusters by the 4b variant strains seems to be unconventional in origin, spanning large areas of geographical and temporal space and may designate susceptibility of some 4b strains towards acquiring DNA from related organisms.

Although the majority of listeriosis outbreaks and sporadic cases have been associated both deli meats and dairy products, recent listeriosis outbreaks involving fresh fruits and vegetables, including the cantaloupe associated outbreak in the US, are indicative of the fact that *Listeria monocytogenes* can survive and multiply in foods other than those commonly reported as a vehicle for foodborne listeriosis. Also interesting is the noticeable shift in demography of the individuals contracting listeriosis. During 1980 - 2000, most of the listeriosis cases were pregnancy associated while recent outbreaks show that the majority of the cases were non-pregnancy associated affecting elderly individuals. These considerations emphasize the significance of in-depth genomic characterization and their importance in understanding the emergence of newer pathotypes, linked with newer food groups and the shift in demography. The merit of molecular sub-typing for *Listeria* and other foodborne pathogens during outbreak and traceback researches cannot be overstressed.

In addition to epidemiological investigation, precise determination of the source/s of foodborne outbreaks by comparing molecular sub-typing patterns of clinical, food and environmental isolates produced the scientific basis for fast determination of contaminated food/s thereby reducing the spread and burden of the outbreaks.

Moreover, molecular subtyping is also major for comprehension the pathophysiology of the organisms, source attribution and for knowledge of genomic evolution and emergence of latest traits.

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