

Interaction between Bdellovibrio Bacterivorous and it Hosts

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Abstract:- *Bdellovibrio bacteriovorus* is a Gram-negative, predatory bacterium that has become one of the most significant species of the genus, so it has been taken as a reference, for a group of microorganisms like this, BALOs by its acronym in english "*Bdellovibrio* and like organisms". There are reports of the ability of this bacteria to prey on other Gram-negative bacteria. There is evidence within the life cycle that *Bdellovibrio bacteriovorus* requires the periplasmic space of Gram-negative bacteria for its survival and reproduction. However, in recent years it has been shown that they also have activity against some bacteria of the Gram-positive group, and/or in the reduction of their colonies.

In different reports there is an interest to look for the range of prey, that is, the specificity or preference of the strains of *Bdellovibrio* spp. by one or several prisoners. McNeely *et al.* (2017), shows that *Bdellovibrio bacteriovorus* DM11 can prey on *Agrobacterium tumefaciens*, but *Bdellovibrio bacteriovorus* DM8 does not. There are some strains that can attack different prey and can have a wide range of prey, and some others seem to be very specific. The process of depredation has not been fully understood, so more in-depth studies are needed to understand these interactions.

Keywords:- Interactions, *Bdellovibrio Bacteriovorus*, Prey.

I. INTRODUCTION

There are several classifications of bacteria, one of these has to do with the interaction between them, of which they can be: positive, where both organisms are benefited; or negative, where one of the two is affected by the interaction, predation is a form of negative interaction, in which a microorganism joins and attacks its prey in order to obtain the necessary nutrients for its development and reproduction. *Bdellovibrio bacteriovorus* is a Gram-negative bacterium, highly motile due to its flagellum. It is a microorganism of relatively small size, from 0.2 to 0.5 µm wide by 0.5 to 2.5 µm long, typically depredates Gram-negative bacteria. Coding genes have been reported in pili which are thought to help in the process of attack and hydrolysis of cellular components, which could open a window of opportunity in the face of recent discoveries of predation to Gram-positive bacteria. However, little is known about predation on this

type of bacteria, it is known that *B. bacteriovorus* needs the periplasmic space that Gram-negative bacteria provide to grow and reproduce.

Also, *Bdellovibrio* sp. can have different affinities for certain hosts depending on the strain, this is known as the range of prey, which can be specific to a specific bacterium, or have a broad spectrum of attack. To understand the interactions between *Bdellovibrio* spp. and its prey, it is necessary to completely understand the process of predation (Rendulic *et al.*, 2004; McNeely *et al.*, 2017; Palacios-López *et al.*, 2011).

II. RESULTS

➤ Interaction between microorganisms

The habitat of microorganisms is mediated, among other things, by the interaction between them. Some classifications are positive or beneficial; as symbiosis, mutualism and commensalism, where both microorganisms are favored in such a way that both can live, and even enhance their activity; On the other hand, there is negative interaction, where one microorganism benefits from another, such as parasitism, antagonism or predation, among others (Palacios-López *et al.*, 2011).

➤ Interaction *Bdellovibrio bacteriovorus* - host

Bdellovibrio spp. it maintains a negative interaction, properly predatory since it detects, attacks and kills its prey in order to obtain nutrients and reproduce. There is another classification that goes from epibiotic or external predation to prey, endobiotic or direct invasion, and group predation (Martin, 2002; Pérez *et al.*, 2016; Velicer and Mendes-Soares, 2009).

Bdellovibrio bacteriovorus is usually a prey-dependent bacterium of Gram-negative bacteria, so it has been classified among the bacteria of endobiotic predation, since *B. bacteriovorus* penetrates its host and invades the periplasm in order to obtain nutrients until it lyses the host cell to start its life cycle again and in this way use them for its growth and reproduction (Sockett, 2009), as well as in Figure 1 (Lerner *et al.*, 2012).

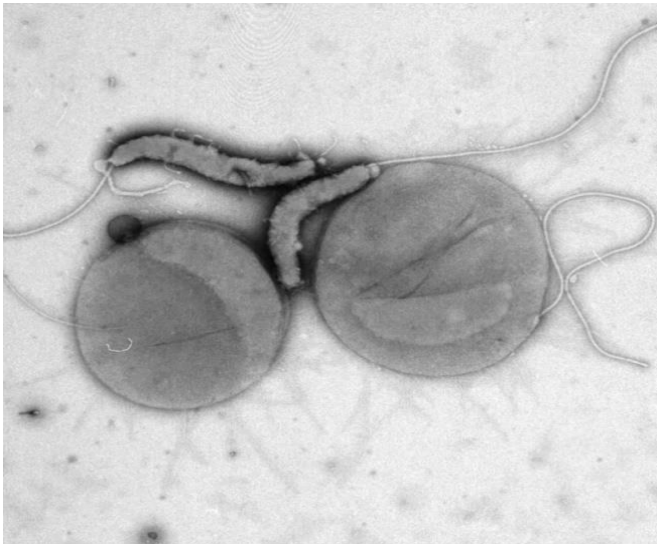


Fig 1:- Peptidoglycan-endopeptidase enzymes of PBP4 carry out the coating of the host bacteria, which avoids a predatory double invasion. The image shows two predators stalking two hosts colonized in the bdelloplasto phase (Lerner *et al.*, 2012).

➤ *Bdellovibrio bacteriovorus*

B. bacteriovorus is a Gram-negative, highly motile bacterium of tiny dimensions ranging from 0.5 to 2.5 μm long, 0.2 to 0.5 μm wide, is a uniflagellated, ubiquitous and non-pathogenic bacterium. Discovered for the first time in 1962 by Stolp and Petzold, described as a parasitic-obligate bacterium with lytic activity to *Pseudomonas*. Stolp and Starr, in 1963, they gave it the name describing it as an ectoparasite bacterium with bacteriolytic activity (Figure 2) (Stolp and Petzold, 1962; Stolp and Starr, 1963; Rendulic *et al.*, 2004).



Fig 2:- Electron micrograph of *Bdellovibrio bacteriovorus* in free phase (Image taken from Stolp and Starr, 1963).

Typically, predator of other Gram-negative bacteria, in addition, its interaction with Gram-positive bacteria has been demonstrated when in a study a strain of the bacteria against *Staphylococcus* sp. (Iebba *et al.*, 2014; Pantanella *et al.*, 2018).

The genome of *Bdellovibrio bacteriovorus* SSB218315 was recently reported, where it was found to have 3,769,531 pb, with 50.5% GC content, 41 total RNA, 34 tRNA, 3620 genes, 3579 total coding sequences (for its acronym in english "CDS") and 69 genomic islands (Oyedara *et al.*, 2018).

➤ *Life cycle of Bdellovibrio bacteriovorus*

The life cycle described so far for this bacterium consists of two phases, one of free life and the other of attack to the host, which are divided into eight stages: 1) *B. bacteriovorus* swims with its free-form flagellum in the middle, 2) later when the bacterium finds its prey, collides, joins it and remains in a stage of "recognition" which lasts a few seconds, 3) *B. bacteriovorus*, performs mechanical movements on its own axis to make an opening in the outer membrane of the prey, once inside the predator closes again by some enzymes secreted by it, in this stage *B. bacteriovorus* detaches from its flagellum, 4) begins the DNA replication and the synthesis of biopolymerases, 5) *B. bacteriovorus* forms a structure called bdelloplasto which is responsible for maintaining an appropriate medium for its growth and reproduction, 6) the filaments of the predator have grown several times their size and begin to form a wall, 7) *B. bacteriovorus* becomes a flagellated cell and lists again, at this point, 8) the predator produces hydrolytic enzymes with the purpose of dissolving the peptidoglycan layer and the outer membrane of the prey cell to release the progeny (Figure 3) (Rendulic *et al.*, 2004; Hampton, 2004).

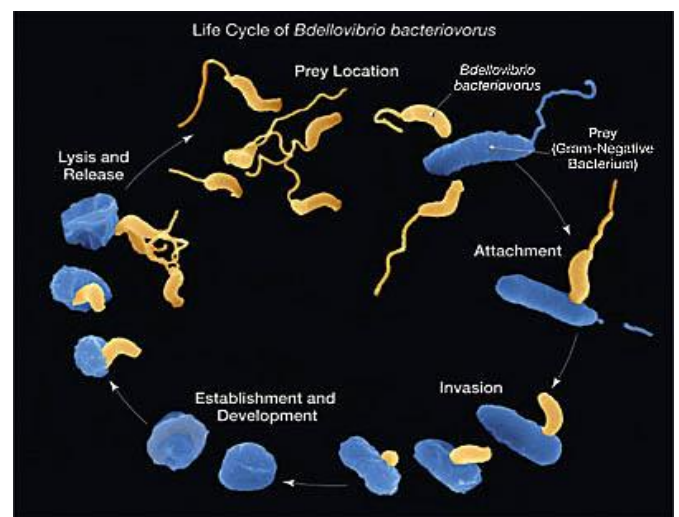


Fig 3:- Image taken from Hampton, 2004, where the life cycle of the predatory bacterium *Bdellovibrio bacteriovorus* (yellow) and prey (blue) is illustrated. (Hampton, 2004).

➤ *Bdellovibrio bacteriovorus* and Gram-positive bacteria

It has been detected that in the decrease of biofilms being these Gram-positive bacteria, this could be since in case of lack of nutrients in the environment or of Gram-negative bacteria, *B. bacteriovorus* depredates the Gram-positive species, attacking and affecting the cellular wall of the host in an epibiotic phase. The most studied hosts have been *Staphylococcus aureus*, a bacterium of clinical importance, since it is present in the pathogenesis of intestinal diseases, in ulcers such as diabetic foot, among others. That is why this bacterium would represent an adjuvant in infectious treatments as a living agent, mainly against drug-resistant bacteria (Iebba *et al.*, 2014; Pantanella *et al.*, 2018; Chu and Zhu, 2010; Im *et al.*, 2017).

➤ Range of prey

The range of prey is the total of species that can be attacked by certain strains of *Bdellovibrio* spp. In one study, several strains of *Bdellovibrio* were isolated from agricultural soil and rhizosphere of plants grown in soil, where thirteen soil species and seven rhizosphere bean species using *Pseudomonas corrugata*, seven soil species and two rhizosphere species using *Erwinia* stand out. *Carotovora* sp. and *Agrobacterium tumefaciens*, and a tomato rhizosphere strain using *A. tumefaciens* as prey. In this way, we can understand that not all strains of the predator attack by the simple fact of having bacteria in the middle but depends on the medium in which it is found, which is what it can possibly infer in the selectivity of the host (Jurkevitch *et al.*, 2000).

➤ Possible responsible region

The study of genomics has made it possible to assume part of the process involved in the interaction with its host part of the complex involved in the regulator of the extrusion of pili type IV which is made up of eight genes bd0110-bd0114, bd0118, bd0119 and bd1290, which in turn is regulated by two proteins bd0108 and bd0109 (Capeness *et al.*, 2013; Rendulic, 2004; Prehna *et al.*, 2014).

III. DISCUSSION

Bdellovibrio bacteriovorus is a potential bacterium as a biological control agent, some authors call it a possible live antibiotic, which would not only be attacking highly pathogenic Gram-negative bacteria, but also Gram-positive bacteria (Sockett, 2009; Baker *et al.*, 2017; Pantanella *et al.*, 2018). There have been studies in which they mention a synergy and greater effectiveness in the treatment of infections with antibiotics (Im *et al.*, 2017).

It is mentioned that it is a bacterium of clinical and veterinary interest and its possible use as a live antibiotic because it is not a pathogenic bacterium. The study models were murine, crustacean and vertebrate (Willis *et al.*, 2016, Shatzkes *et al.*, 2017, Cao *et al.*, 2015). Some reports demonstrate the non-pathogenicity to humans of certain

strains, since it has been possible to isolate *Bdellovibrio bacteriovorus* from colon biopsies, demonstrating that depending on the place of the sample is the density of bacteria found (Iebba *et al.*, 2013, Iebba *et al.*, 2014).

This review serves as a precedent for the possible use of this interesting bacterium, which even depredates not only one specific bacterium at a time but can also decrease the biomass of a bacterial group. Therefore, in a *Bdellovibrio* sp. Infection, it could be an option to help improve the patient (McNeely *et al.*, 2017).

IV. CONCLUSIONS

Based on the review of *Bdellovibrio bacteriovorus*, it seems that we are on the right track for an antimicrobial alternative, which could help in the improvement of patients with infectious diseases caused by bacteria resistant to synthetic antibiotics.

At this point, in addition to understanding the host-predator interaction, it is of interest to know how confers the range of prey to certain strains, that is, why a *Bdellovibrio bacteriovorus* DM11 can prey on *Agrobacterium tumefaciens*, but a *Bdellovibrio bacteriovorus* DM8 does not. A strain may have a wide range of prey, some others seem to be very specific. Part of the selectivity of the predator may be due to the environment in which it is found, the range of prey may vary between strains.

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