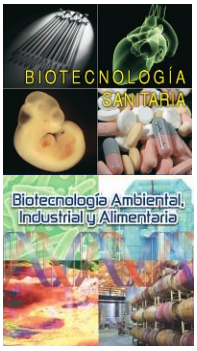
Poster



Immune response of hMSC preconditioned with Bartonella bacilliformis-derived immunogenic peptides

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ABSTRACT

Bartonellae are Gram-negative facultative intracellular bacteria first described in 1909. Since the last reclassification in 1993, the number of Bartonellae species has increased to 45, with new species continuing to be identified in recent years [1]. Among all species, Bartonella bacilliformis affects humans, causing the disease known as bartonellosis, hich is a neglected disease that only occurs in the inter-Andean valleys of Colombia, Ecuador and Peru

In this project, we will study four synthetic peptides designed in silico from the immunogenic protein data of this bacterium. To do so, we will use mesenchymal stem cells (MSC), to which we will add different concentrations of these four peptides and study which one elicits a more pronounced immune response. This will be verified through various studies. On one hand, we will analyze the secretome of the cells to determine the presence of both Interleukin-6 and the IDO enzyme, two compounds crucial in regulating the immune system. On the other hand, we will examine the expression of various genes related to the regulation of the immune system, such as those synthesizing beta-defensins 1, 2, and 3, hepcidin, and LL-37. The expression of GAPDH, a gene commonly used as a reference gene, will also be studied and used to compare the expression levels of the other mentioned genes. Finally, the expression of certain proteins involved in the immune system will be analyzed, but unlike the previous case, this time it will be at the protein presence level rather than gene expression.

In conclusion, this study will allow us to determine if any of the initial four proteins could trigger a sufficiently significant immune response to be considered as a potential antigen.

REFERENCES

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