A MINIMAL MICROBIOTA IN TICK GUT

Melina Garcia Guizzo¹, Rodrigo Dutra Nunes¹, Renata Schama², Felipe Dias¹, Rodolpho Albano³, Ricardo Pilz Vieira¹, Milane de Souza Leite⁴, Orlando Martins¹, Itabajara da Silva Vaz Júnior⁵,⁶,⁷, Pedro L. Oliveira¹,⁷

¹Instituto de Bioquímica Médica, UFRJ, Rio de Janeiro, RJ, Brazil; ²Laboratório de Biologia Computacional e Sistemas, IOC - Fiocruz, Rio de Janeiro, RJ, Brazil; ³Instituto de Biologia Roberto Alcantara Gomes, UERJ, Rio de Janeiro, RJ, Brazil; ⁴Departamento de Química, Universidade Federal Rural do Rio de Janeiro, Seropédica, RJ, Brazil; ⁵Centro de Biotecnologia, UFRGS, Porto Alegre, RS, Brazil; ⁶Faculdade de Veterinária, UFRGS, Porto Alegre, RS, Brazil; ⁷Instituto Nacional de Ciência e Tecnologia em Entomologia Molecular (INCT-EM), Brazil

INTRODUCTION: The advent of metagenomic analyses enable culture-independent identification of microorganisms in different biological systems. In many organisms the microbiome in gut outnumber the cells of body, affecting the host biology. Although several reports on gut microbiota in ticks are available, the size of total bacteria populations has not been determined. In addition, the origin of bacteria, which colonizes tick gut, remains unknown. The cattle tick *Rhipicephalus microplus* performs the development and reproduction in a single host. The bovine blood is presumable sterile, so it is plausible that the gut bacteria come from host skin.

OBJECTIVES: This work aims to quantify the total bacteria in gut of different species of ticks and to investigate if skin bovine microbiota is the source of the gut microbiota of *R. microplus*. 


MATERIALS AND METHODS: The absolute quantification of 16SrRNA copy number was performed in gut of fully engorged females from different species of ticks and in *Aedes aegypti* blood fed using quantitative PCR. The microbiota from bovine skin, gut of partially and fully engorged females from *R. microplus* was identified through a metagenomic analyses from the 16SrRNA amplicom using Illumina technology.

DISCUSSION AND RESULTS: In different species of ticks of both families Argasidae and Ixodidae, the microbiota in gut after blood feeding is extremely small (<10^3 bacteria per gut) when compared with other hematophagous arthropod, such as *A. aegypti*. In contrast, the *R. microplus* has high levels of a bacterium from the genus *Coxiella* in ovary. To our knowledge, this is major departure from most reports on microbiota of metazoans, where the largest microbial communities are always found in the digestive system. The bacteria species found in tick gut are also found in the bovine skin, showing an influence of host in microbiome of *R. microplus*.

CONCLUSIONS: So, the tick gut microbiota, which in *R. microplus* has the origin on host skin, although very diverse in genera, is minimal in size.

KEY WORDS: Tick, microbiota, gut.

ACKNOWLEDGEMENTS: CNPq, FAPERJ, FAPERGS and INCT-Molecular Entomology.