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Resumo	<p>Background: The hard tick <i>Hyalomma dromedarii</i> is one of the most injurious ectoparasites affecting camels and apparently best adapted to deserts. As long-term blood feeders, ticks are threatened by host defense system compounds that can cause them to be rejected and, ultimately, to die. However, their saliva contains a cocktail of bioactive molecules that enables them to succeed in taking their blood meal. A recent sialotranscriptomic study uncovered the complexity of the salivary composition of the tick <i>H. dromedarii</i> and provided a database for a proteomic analysis. We carried out a proteomic-informed by transcriptomic (PIT) to identify proteins in salivary glands of both genders of this tick species.</p> <p>Results: We reported the array of 1111 proteins identified in the salivary glands of <i>H. dromedarii</i> ticks. Only 24% of the proteins were shared by both genders, and concur with the previously described sialotranscriptome complexity. The comparative analysis of the salivary glands of both genders did not reveal any great differences in the number or class of proteins expressed their enzymatic composition or functional classification. Indeed, few proteins in the entire proteome matched those predicted from the transcriptome while others corresponded to other proteins of other tick species.</p> <p>Conclusion: This investigation represents the first proteomic study of <i>H. dromedarii</i> salivary glands. Our results shed light on the differences between the composition of <i>H. dromedarii</i> male and female salivary glands, thus enabling us to better understand the gender-specific strategy to feed successfully.</p>
Fomento	