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Short Communication

Infectious Parasitic Protozoa and its Inhibitory Activities

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DESCRIPTION

Endogenous inhibitors regulate the activity of proteases, which is a general tendency in practically all forms of life. The endogenous inhibitors of cysteine proteases of three primary pathogenic parasitic protozoa are reviewed here. The review focuses on *Plasmodium*, *Entamoeba*, and *Leishmania* species. In these pathogens, only chagasin-like inhibitors of cysteine proteases that contain a -barrel immunoglobulin-fold and block the target proteases through a 3-loop inhibitory method have been discovered. Cysteine protease inhibitors are extremely evolvable enzyme that targets a wide range of pathogenic cysteine proteases, with a preference for those implicated in host-parasite interactions [1]. A typical pattern illustrates the fact that cysteine proteases and their inhibitors have little in common in terms of sequence homology.

The inhibitors also are known to assist the parasites with other housekeeping tasks. Thus, generalisations regarding their responsibilities should be avoided. The reader will discover specific info on the cellular location of cysteine protease inhibitors, as well as their composition, function, and related modes of action, in this study [2]. The reader will also discover an in-depth examination of the significance of these inhibitors in parasitic pathogenesis, as well as the general tendencies that relate them to parasitic biology and evolution.

Bivalve mollusks are currently regarded indicator species of human parasite protozoa contamination in aquatic environments. Nonetheless, the potential impacts of such protozoa on their paratenic host immune systems are inadequately characterised [3]. The goal of this study was to see how two protozoa affected hemocyte viability and phagocytosis in two mussels, the zebra mussel (freshwater habitat) and the blue mussel (saltwater habitat). For these goals, the viability and phagocytic markers of mussel hemocytes without biological stress (control hemocytes) and mussel hemocytes subjected to biological stress were examined (*Toxoplasma gondii* and *Cryptosporidium parvum* oocysts).

Entodinium spp. was quite common in silage/grain-fed cattle, although protozoa diversity (as measured by Shannon index) is higher in hay-fed cattle due to increased species evenness. Type B protozoa were much more common in hay-fed cattle, while Type A protozoa were much more common in silage/grain-fed calves [2]. An Analysis of Similarity (ANOSIM) revealed that hay-fed and silage/grain-fed livestock had distinct protozoa communities, and multivariate analysis revealed that pen mates (cattle given the same diet and housed together) had comparable protozoa community types. In summary, we provide a T-RFLP technique for evaluating rumen protozoa populations that complements classic microscopy approaches while also being high-throughput capable.

For the first time, researchers reported interactions between protozoa and hemocytes of mussels from various aquatic habitats [4]. After being exposed to both protozoa, zebra mussel hemocytes decreased their phagocytosis of fluorescent microbeads, but blue oyster hemocytes exclusively responded to *T. gondii* oocysts. These declines in microbead ingestion might be attributed to competing between beads and oocysts, which can be regulated by oocyst size. To comprehend the specific characteristics of both mussels, fresh characterisations of their immunological capabilities, including aggregation, must be created.

CONCLUSION

Protozoa are frequent rumen dwellers, where they contribute to host nourishment and methanogenesis. The absence of effective tools for protozoa population analysis limits our understanding of how changes in protozoa community composition impact these activities. A branched Terminal-Restriction Fragment Length Polymorphism (T-RFLP) test targeting the 18S rRNA gene was created in this work for comparing rumen protozoa populations. T-RFLP analysis provided comparable overall outcome to microscopy analysis when comparing the richness and organisation of protozoa communities between hay-fed *vs.* silage/grain-fed cattle.

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