Structural Analysis of *Echinococcus granulosus* Antigen B Oligomers and High-Molecular-Weight Aggregates

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Echinococcus granulosus is the causative agent of cystic hydatid disease, a worldwide zoonosis. Antigen B (AgB) is a major antigenic protein expressed by the *E. granulosus* pathogenic larval stage (hydatid cyst), which plays important roles in parasite evasion strategies and presents high diagnostic value for human infections. AgB is an 120-160 kDa oligomeric protein composed by related 8 kDa subunits (AgB8/1-AgB8/5) with high aggregative behavior. The aim of this work is the structural characterization of AgB oligomers and high-molecular-weight aggregates using recombinant subunits (rAgB8s) as models. The aggregation of rAgB8s was monitored by dynamic light scattering and atomic force microscopy (AFM), revealing an AgB8/3>AgB8/2>AgB8/1 aggregative tendency, and the formation of high-molecular-weight aggregates (with hydrodynamic radius >2 µm). AFM also showed that AgB8/3 homo-aggregates are morphologically more similar to the parasite-produced AgB. Pressure-induced dissociation analyses of AgB recombinant oligomers demonstrated a higher stability of AgB8/3 homo-oligomers. These results point to a role of AgB8/3 as a structurating subunit of AgB oligomers. Mass spectrometry analyses of AgB samples purified from different hydatid cysts detected AgB8/1, AgB8/3 and AgB8/4 subunits, and peptides corresponding to antigen 5 (Ag5), another major antigenic component of *E. granulosus* larvae. Next, co-expression of different rAgB8s in *Escherichia coli* and cross-linking analyses will be carried out to test AgB hetero-oligomerization and to confirm AgB-Ag5 interactions, respectively. We expect that our results provide relevant information for the improvement of AgB-based strategies of diagnostic, treatment and prevention of cystic hydatid disease.

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