“Characterizing pleomorphic round-bodied forms of *Borrelia burgdorferi*, the etiological agent of Lyme Disease”

*Borrelia burgdorferi* (Bb) is the pathogenic spirochete responsible for Lyme disease (LD) and is primarily transmitted to humans through the tick vector, *Ixodes scapularis*. As the rate of LD cases is dramatically rising in Canada and the United States, efforts to effectively treat and diagnose LD has become a great concern. Presently, about 10-20% of patients who receive treatment will experience recurring symptoms in what has been dubbed post-treatment Lyme disease syndrome (PTLDS). The exact cause of this condition has yet to be described. Some studies implicate cystic “round-bodied” forms of Bb that exhibit greater resistance towards β-lactam antibiotics as the culprit. This hypothesis, however, has not been robustly tested. Presently, the literature lacks consistent standards for evaluating atypical morphologies of Bb, due to the wide range of methods employed in their induction *in vitro*. While proteomic approaches have generated incredible insight into elucidating mechanisms of resistance and persistence in several pathogenic bacteria, its application to morphological variants of Bb remains limited. This proposal intends to bridge these disparities by (1) employing high-resolution scanning electron, transmission electron, and fluorescence microscopy to identify morphological traits and protein markers in round-bodies, and (2) identifying shifts in protein abundance between these forms. This research will help to identify the similarities and differences found between distinctively generated Bb round-bodies with the intent of improving the diagnostics and treatment of PTLDS.