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The purpose of my time spent at the Pfizer Laboratory was to conduct my undergraduate thesis research into the identity of the rhizophore, a root-bearing organ found in certain members of the *Selaginella* genus. Because *Selaginella*, belonging to the lycophyte division of plants, represents one of the oldest extant groups of vascular plants there is considerable interest within the scientific community in developing a model system for comparative studies involving this taxon. As such, the purpose of my project was two-fold: to use current, transcriptomic approaches to conduct comparative analyses of gene expression in the meristematic regions in the roots, shoots, and rhizophores of *Selaginella apoda*; and to construct these expression datasets for the purpose of improving *S. apoda*'s tractability as a model organism. Thus, my work consisted primarily of: establishing a means of cultivating *S. apoda* under laboratory conditions; characterizing the developmental timeline of the rhizophore through anatomical and morphological evaluation; and refining the procedure for transcriptome library preparation to account for the presence of secondary metabolites and small amounts of tissue. Because of the inherent difficulty of collecting root tissue from *S. apoda* – the primary, "embryonic" roots are transient and degrade shortly after the first rhizophores contact the soil and develop into roots – my work was delayed by several months while I was in the process of accumulating sufficient tissue to begin the process of optimizing the RNA extraction procedure. Because my thesis research continued into the academic year, I was able to continue working with Barbara Ambrose and eventually developed a protocol for generating high-quality, high-concentration cDNA libraries from small (<0.1 g) amounts of starting plant tissue. This protocol involves both the use of commercial kits and self-prepared reagents, and is presented in condensed form below.