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Characterizing the role of Glycine max NHL gene family members in plant-nematode interactions

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Soybean cyst nematode (SCN; Heterodera glycines) is a microscopic parasitic roundworm of soybean that causes nearly $1 billion dollars in annual yield loss in the United States. SCN damages the plant by attaching itself to the soybean root system, where it forms a complex feeding site and drains vital nutrients from the plant. Naturally resistant soybean lines have been used as the primary strategy to manage SCN, because they have evolved a natural mechanism for resisting SCN infection. However, soybean resistance against SCN is derived from a small genetic base and repeated annual plantings of these same resistant lines has selected for populations of SCN that can reproduce on the resistant lines. Therefore, understanding the molecular mechanisms of how some soybean plants have the ability to naturally resist infection by SCN is critical for designing new strategies to improve crop plant resistance to SCN. My project focuses on soybean NDR1/HIN1-like (NHL) genes found to be expressed at higher levels specifically within SCN-induced feeding cells of resistant soybean as compared to susceptible soybean. To gain insight into the potential role of these genes in soybeans ability to resist SCN, full-length gene and cDNA sequences have been isolated using techniques known as genome walking and RACE PCR. RNAi and overexpression constructs have been generated to directly test the function of these genes in SCN resistance. To gain insight into the nematode-responsive regulation of each gene, the endogenous promoter sequences have been isolated and fused to the _-glucuronidase reporter gene for expression studies. This project will give insight into the mechanisms the soybean plant uses to defend itself against SCN infection and hopefully reveal crucial results which aid in the goal of developing SCN resistant soybean.