Allorecognition in Hydractinia symbiolongicarpus: Determining the Loci of Genes Controlling Allorecognition in Addition to Alr1 and Alr2 Using Machine Learning

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Allorecognition, the process of recognizing tissue of self or close kin through genetic similarity, plays an important role in organ and graft transplant success because it can trigger rejection responses. While the similarity between invertebrate and human allorecognition is not yet completely clear, Hydractinia symbiolongicarpus, a colonial marine invertebrate capable of allorecognition, could become a model organism for studying human transplantation, as it is cheap and easy to maintain and study ethically. It was previously believed that Hydractinia allorecognition was controlled by two genes, alr1 and alr2, and the number of matching alleles at these genes determined whether the tissue of two organisms would fuse, reject, or transitory fuse (when colonies would start fusing, then separate). However, this rule only works for inbred colonies, and not wild-type. It was hypothesized that additional genes could contribute to determining Hydractinia's allorecognition response. After sequencing the genome of wild-type Hydractinia, eight new genes sequentially similar to alr1 were found, potentially playing a part in allorecognition. To test these new alr-like genes' contribution to allorecognition, fusion tests were conducted between animals with genetic identity at various distinct molecular markers. Through the use of multiple machine learning analysis methods, the loci of genetic identity and fusion test phenotype were compared to determine the effect of various regions of the Hydractinia chromosome on allorecognition. Two distinct regions on the chromosome were found to influence allorecognition, containing several alr-like genes, demonstrating that at least two of those genes likely participate in producing an allorecognition response.

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