



Profile of quorum sensing signals in a dinoflagellate bloom by metagenomic approach

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Phycosphere environment harbors diverse populations of microorganism, which are thought to play a critical role in algae host and influence mutualistic and competitive interactions. The complicated relationships between the two taxa are regulated by chemical signals, such as quorum sensing (QS). Understanding QS-based signal may shed light on the interaction between algal associated microbial communities in the native environment. Although the characteristic and application of QS have been widely discussed, few researches concerning the role of QS play in the interaction of bacteria and algae were conducted. In this study, we used metagenomic method to examine the profile of AI-1 (AinS, HdtS and LuxI genes) and AI-2 (luxS gene) autoinducers from a deeply sequenced microbial database obtained from a complete dinoflagellate (*Gymnodinium catenatum*) bloom cycle. A total of 3001 AI-1 homologs and 130 putative AI-2 homologs were identified in all. HdtS was the predominant member among the AI groups, the number of which far surpassed the other three. Both AinS, HdtS and LuxS increased their number as the development of the bloom while the abundance of LuxI showed an opposite trend. Phylogenetic analysis based on amino acid sequences suggested that HdtS and LuxI synthase were originated from Alpha-, Beta- and Gammaproteobacteria, and AinS synthase only contributed by Vibrionales. Compared with AI-1, the sequences related to LuxS family (AI-2) demonstrated a much wider taxonomic coverage, which probably originated from Bacteroidetes, Firmicutes and Spirochaetes. These data suggested that QS signals can regulate bacterial biomass and shape microbial communities during the algal-bloom event. This study may help uncover the behavior mechanisms of algae-bacteria interactions, and facilitate improving the understanding of microbial dynamics during the algae bloom from chem-ecological prospect.