Molecular analysis of fecal pellets collected by using gel sediment traps in the Indian sector of the Southern Ocean during austral summer

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Sinking particles, an important contributor to biological carbon pump, consist of various types of particles. Export efficiencies and sinking speeds are different among types of sinking particles, for example, phytodetritus and fecal pellets. In the Southern Ocean, the contribution of fecal pellets to carbon flux is expected to be high because of the high abundance of the large zooplankton, such as salps and krills, which excrete fast-sinking large fecal pellets. However, in the Indian sector of the Southern Ocean, the krill-independent ecosystem is expected to be important. It is difficult to identify producer of fecal pellets based on morphological information, and fecal pellets contains large amount of amorphous materials which are difficult to be identified by microscopic analysis. Little is yet known of the sinking process of fecal pellets. In this study, we applied molecular method to individual fecal pellets collected by gel sediment traps for estimating fecal pellet producers and the sinking process of fecal pellets.

Fecal pellet samples were collected from a station (63.5°S, 110°E) during the Southern Ocean cruise of the T/V *Umitaka Maru* of Tokyo University of Marine Science and Technology. The trap system consisted of gel-filled sediment traps deployed at 50, 200 and 500 m depths. Traps were left to drift for 24h (17 January 2019 to 18 January 2019). After recovery, each gel was preserved at <-60°C until analysis. DNA was extracted from individual fecal pellets picked up from gel under a stereo microscope. Sizes of the fecal pellets were varied (<50 μm to 500 μm diameter). To assess the eukaryotic community structure of the fecal pellets, the 18S rRNA gene V9 region was amplified by using primers 1389F and 1510R and the amplicons were sequenced by high throughput sequencer. Bioinformatics analysis of the sequence data were performed using mothur (Schloss et al. 2009).

Eukaryotic community structures of the fecal pellets in 50 m and 200 m mainly consist of Stramenopiles, Metazoa and Dinophyta. This result indicated that the fecal pellets were excreted by particle feeders. Metazoan community structures of the fecal pellets in 50 m and 200 m mainly consist of copepods (>90%) and were homogenized among all types of fecal pellets which were excreted by various species. Thus, it is considered that the fecal pellets were repackaged several times even in 50 m depth which was just under the Chlorophyll *a* maximum (40 m depth) and did not sink directly from 50 m to 200 m. Metazoan community structure also showed that potential producers of large fecal pellets were Malacostraca, which include Euphausiids, and Heterobranchia, which include *Limacina*, but Malacostraca was quite rare. Thus, producer of large fecal pellets is considered to be *Limacina*. Not only salps and krills, but also *Limacina* should be focused as fast-sinking large fecal pellet producer which will affect to the efficiency of the transport of POC in this area.

Reference

Schloss PD, Westcott SL, Ryabin T, Hall JP, Hartmann M, Hollister EB, Lesniewski RA, Oakley BB, Parks DH, Robinson CJ, Sahl JW, Stres B, Thallinger GG, Horn DJV, Weber CF (2009) Introducing MOTHUR: open-source, platform-independent, community-supported software for describing and comparing microbial communities. Appl Environ Microb 75:7537－7541. doi: 10.1128/aem.01541-09