



Introduction

Sinking particles connect surface ocean productivity to marine sediments. Particulate organic matter degrades during sinking. Settling velocity is an important factor regulating flux and rate of degradation. However, little is known about how settling rates of particles map to their biological or terrestrial origins and chemical compositions, including their major ballast minerals. To investigate settling rates, we collected sinking particles at the French JGOFS DYFAMED site in the western Mediterranean Sea. In addition to time-series sediment traps, we used a new, conical, free-floating NetTrap, an elutriator, and a sediment trap in settling velocity mode (see Peterson *et al.* poster for details). The elutriator and the settling velocity trap allowed sorting of particles with a wide range of sinking rates. Concentrations and fluxes of mass, organic and inorganic carbon, radionuclides (Po210, Th234 and Th228), and individual organic compounds (17 amino acids, 2 classes of lipids) were measured. Below we present results from a March to mid-May sediment trap deployment at 200 meters.

1. Mass and settling velocity distributions in time-series (TS) and settling-velocity (SV) sediment trap samples

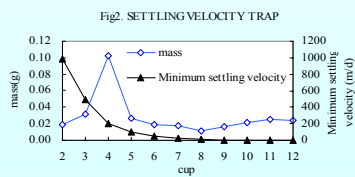
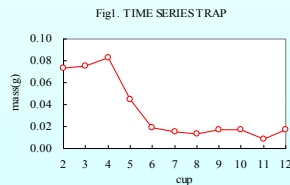


Fig 1. Time-series sample cups 2, 3, 4, and 5 contained 72% of total mass.

Fig 2. Settling velocity sample cups 2, 3, 4, and 5 contained 57% of total mass. Cup 4 alone contained 32% of total mass. Minimum Settling velocity changes by a factor of 2 between adjacent cups.

2. Principal Component Analysis (PCA) and Cluster Analysis

We used statistical techniques to investigate overlap between material in the TS and SV traps. Specifically, we sought to determine whether the most rapidly sinking material sank early in the deployment during the peak flux period. Twenty-six parameters were chosen for PCA. Sixteen independent amino acids were represented as mole percentages of total amino acids. Data for Po, Th, Lipids, IC, OC, and TN were normalized by mass. Each data type was normalized by subtracting the mean of the observations and dividing by its standard deviation. TAA~total amino acids; ASP~aspartic acid; GLU~glutamic acid; SER~serine; GLY~glycine; THR~threonine; BETA~β-alanine; ALA~alanine; GABA~γ-aminobutyric acid; LYS~lysine; Neuts/TFA~ neutral lipids / total fatty acids; OC~organic carbon; IC~inorganic carbon; TN~total nitrogen; Po~Po210; MASS~mass flux.

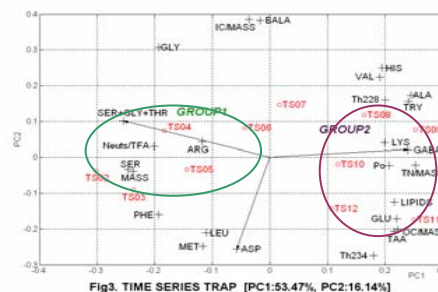


Fig3. TIME SERIES TRAP (PC1:53.47%, PC2:16.14%)

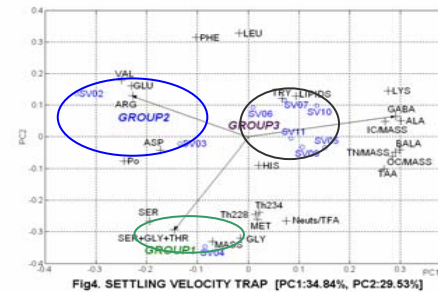


Fig4. SETTLING VELOCITY TRAP (PC1:34.84%, PC2:29.53%)

1) Generally, time-series samples separated into two groups (**Fig 3**). Group 1, which includes cups 2, 3, 4, 5, and 6, had abundant (SER+GLY+THR), Neuts/TFA, and mass, which indicated that the materials in these cups were derived primarily from diatoms. These cups contained most of the mass in the time-series samples. Group 2 includes cups 8, 9, 10, 11, and 12. These cups were enriched in LIPIDS, TAA, GABA, ALA, GLU, LYS, OC, TN, Po, and Th, which indicate the presence of microbially degraded materials.

2) Settling-velocity samples separated into three groups (**Fig 4**). (a) Cup 4 had the highest mass, (SER+GLY+THR), and Neuts/TFA. The mass of cup 4, which represented the 200-500 m/d sinking class, contained 32.3% of the mass of all the samples. Materials of SV cup 4 came mainly from TS cup 2-6, since these samples had similar components, heavily dominated by diatoms. However, SV cup 4 also had higher Po and Th, which possibly came from TS cups 8-12. (b) Cups 2 and 3 are in the second group, which was rich in ASP and GLU, possibly indicating a carbonate organism source.

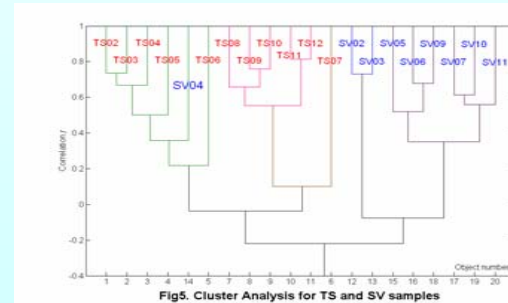


Fig5. Cluster Analysis for TS and SV samples

(c) Settling velocity cups 5, 6, 7, 9, 10, and 11 (data are not available for cups 8 and 12) had very similar components and are in the third group. They were relatively rich in LIPIDS, TAA, LYS, GABA, ALA, BALA, TN, IC, and OC. The materials in these cups had much lower settling velocity, and contained degraded materials.

3) Cluster analysis was used to separate TS and SV cups into 5 groups (shown by color, **Fig 5**). The components of cups within each group are more similar than in cups within different groups. SV cup 4 was in the same group as TS cups 2, 3, 4, and 5. This result is consistent with the PCA results.

Conclusions

- 1) Tracers in SV cup 4 were most consistent with those in TS cups 2, 3, 4, 5, and 6 (see Fig 5). They were all enriched in diatom material. Material in sinking velocity cup 4 was derived mostly from the earliest five cups of the time series.
- 2) Compositions of SV cups 2, 3, 5, 6, 7, 9, 10, and 11 were not consistent with any cup in the TS samples. These SV cups were non-diatoms, but did not constitute a single non-diatom group. Material in SV Cups 2 and 3 sank faster than that in cup 4, and was rich in GLU and ASP, possibly indicating a carbonate organism source. Material in SV cups 5, 6, 7, 9, 10, and 11 sank more slowly than material in cup 4, and was rich in organic components, probably microbially degraded materials. TS cups 8-12 also had abundant organic components that probably came from microbially degraded materials. However, TS cups 8-12 differed from SV cups 5, 6, 7, 9, 10, and 11 in several components, notably BALA, IC, Po, and Th.
- 3) Future work will include using information on settling velocity and chemical compositions to instruct mechanistic modeling.