Supplementary Figure and Table Legends for Saleem et al: *Trophic complexity in aqueous systems: Bacterial species richness and protistan predation regulate DOC and DTN removal*

Supplementary Figure S1

The C:N ratio of microcosms with different bacterial monocultures after 48h of incubation. Every point represents an average of three replicates. The statistical differences were determined by ANOVA followed by a Tukey's test. Both carbon and nitrogen contents are represented as mg/l.

Supplementary Figure S2

(a) Relative carbon (DOC) removal and (b) relative nitrogen (DTN) removal by single bacterial monocultures (B1 to B5) after exposure to different predation treatments. The letters indicate statistically significant differences among treatments. The significance was determined using ANOVA test followed by Tukey's Test.

Supplementary Figure S3

Differences in relative removal of DOC and DTN across all predation treatments. Every point represents the average removal of these nutrients across all bacterial diversity levels. The significance was determined using ANOVA test followed by Tukey's Test.

Supplementary Figure S4

Statistical difference of D_{max} values from zero in all experiments. Every point represents the average D_{max} values of all mixture combinations (n=26, in triplicate = 78) across all predation treatments. We used Wilcoxon signed rank test with continuity correction to compare the D_{max} values of all experiments. The * above or below the zero line depicts the positive or negative significant difference of D_{max} from zero.

Supplementary Figure S5

Relative removal (a, b) and transgressive (D_{max}) removal (c, d) of DOC and DTN in bacterial

mixtures either containing the species B3 or without the species B3 (W-B3). Each point

corresponds to the average of all replicates of each bacterial species combination in these

specific mixtures across the bacterial species richness level. The bar represents standard error.

The significance was determined using Student's t-test. Abbreviations: no-pr = predation free

control; Ac = predation by *Acanthamoeba* sp.; Pot = predation by *Poterioochromonas* sp.; Tet

= predation by *Tetrahymena* sp.; mul = predation by multiple predators

Supplementary Figure S6

Relationship between predator production and relative DTN removal in microcosms exposed

to multiple predators. Each point represents one individual replicate of both parameters

plotted against each other. The significance was determined using linear regression followed

by ANOVA.

Supplementary Figure S7

Bacterial combinations which resulted in negative relative DTN removal values in the

presence to multiple predators indicating a predator-driven release of bacterial N. Relative

amounts are based on the comparison of DTN concentrations in multiple-predation treatments

and blank (microbe free microcosms) controls. The significance was determined using

ANOVA test followed by Tukey's Test.

Supplementary Figure S8

The C:N ratio of microcosms in the medium before incubation, and in all predation treatments

after 48h of incubation. Every point represents an average of all replicates of each

experiment. The statistical differences were determined by ANOVA followed by a Tukey's test. Both carbon and nitrogen contents are represented as mg/l.
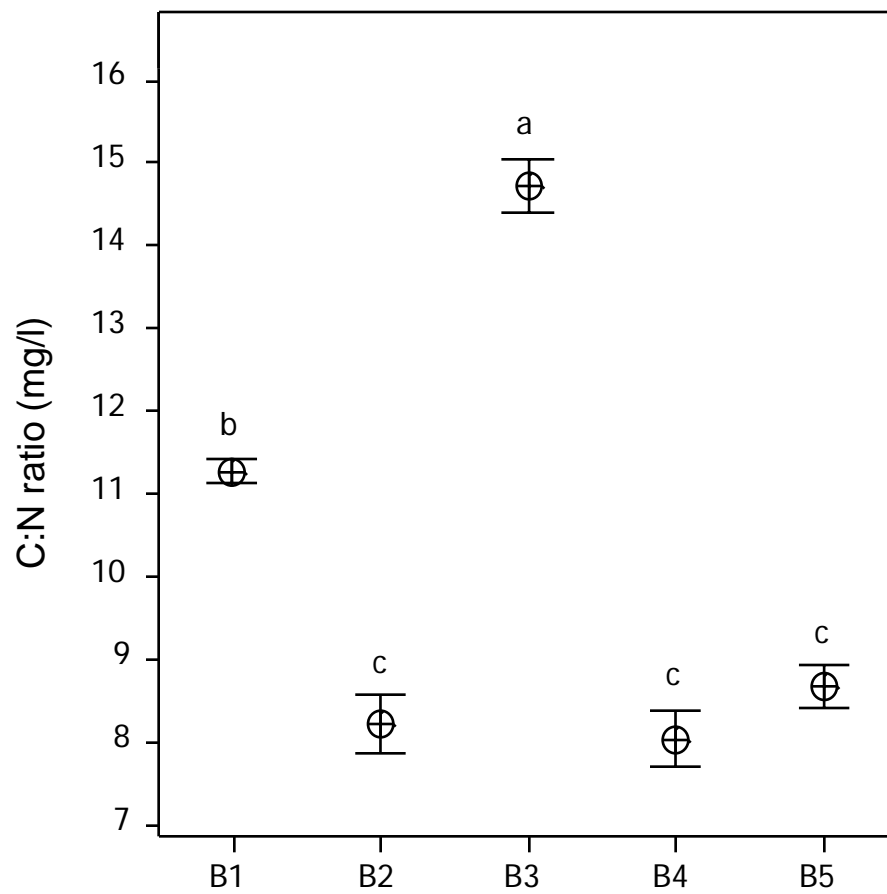
Supplementary Figure S9

Differences in the average relative removal of DOC and DTN by bacterial monoculture across all predation treatments. Every point represents the average removal of all monocultures in each experiment. The significance was determined using ANOVA test followed by Tukey's Test.
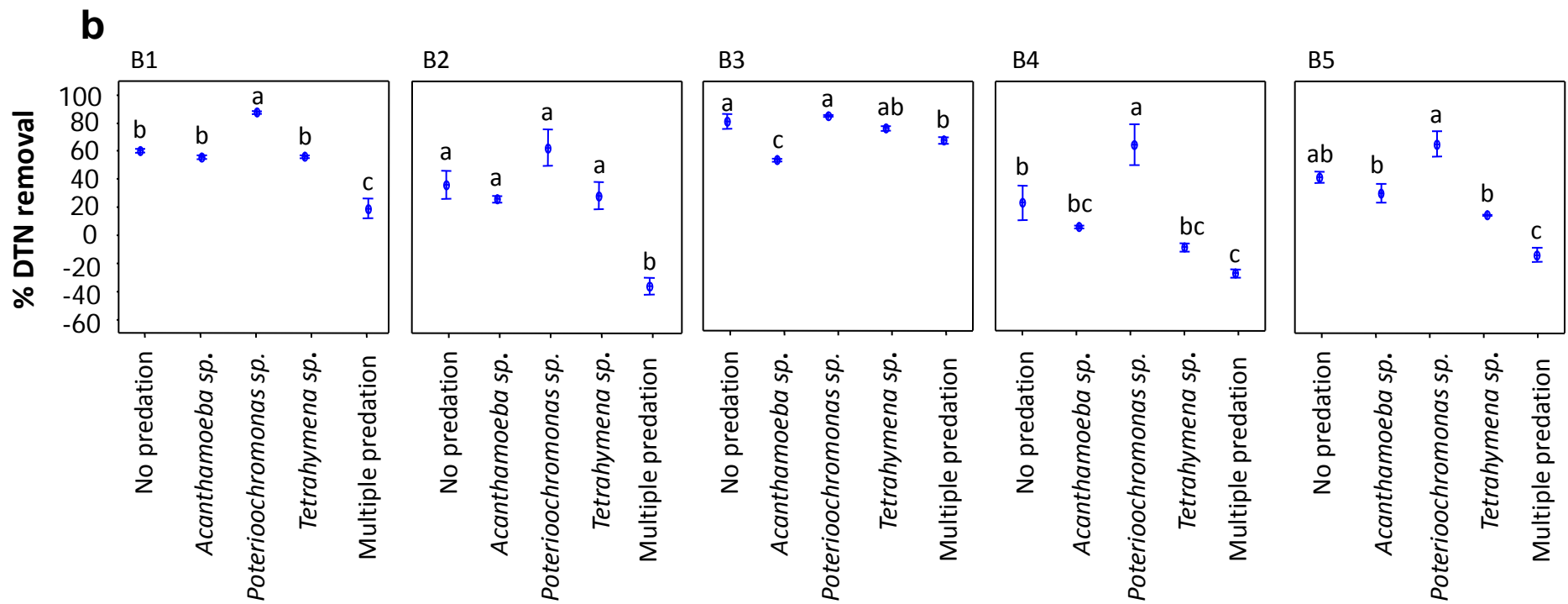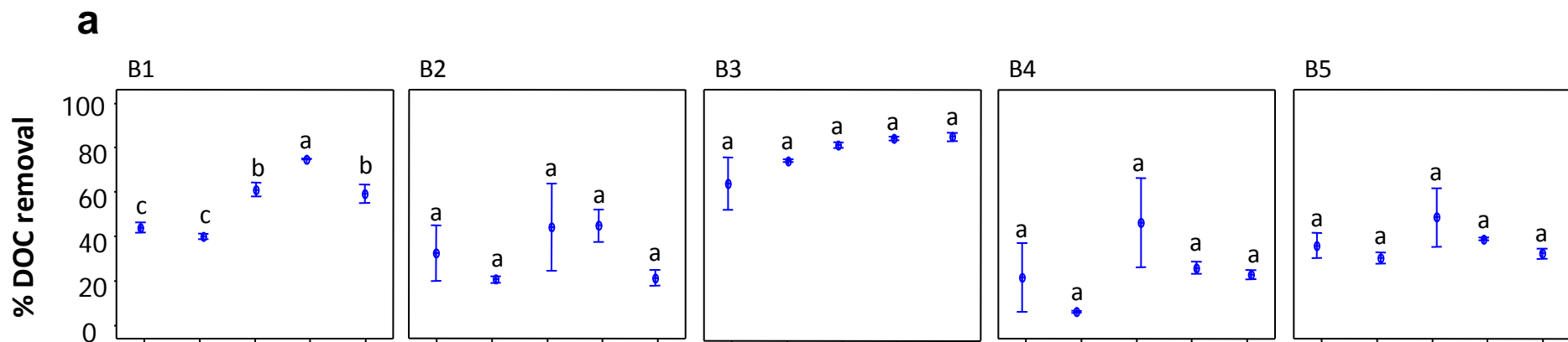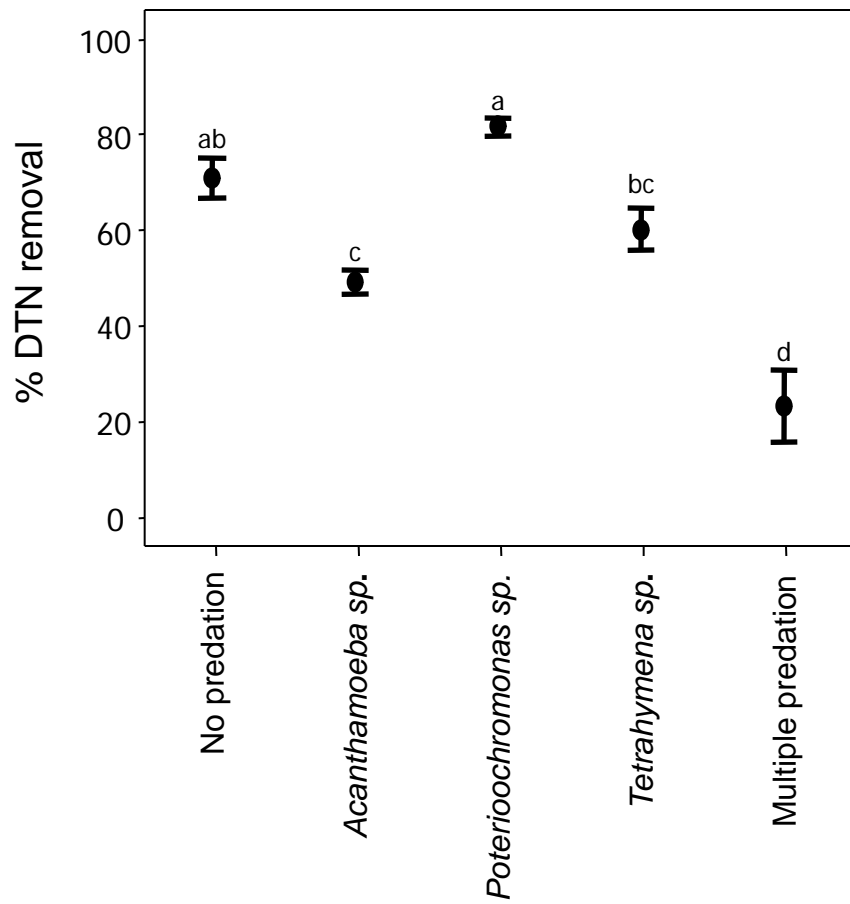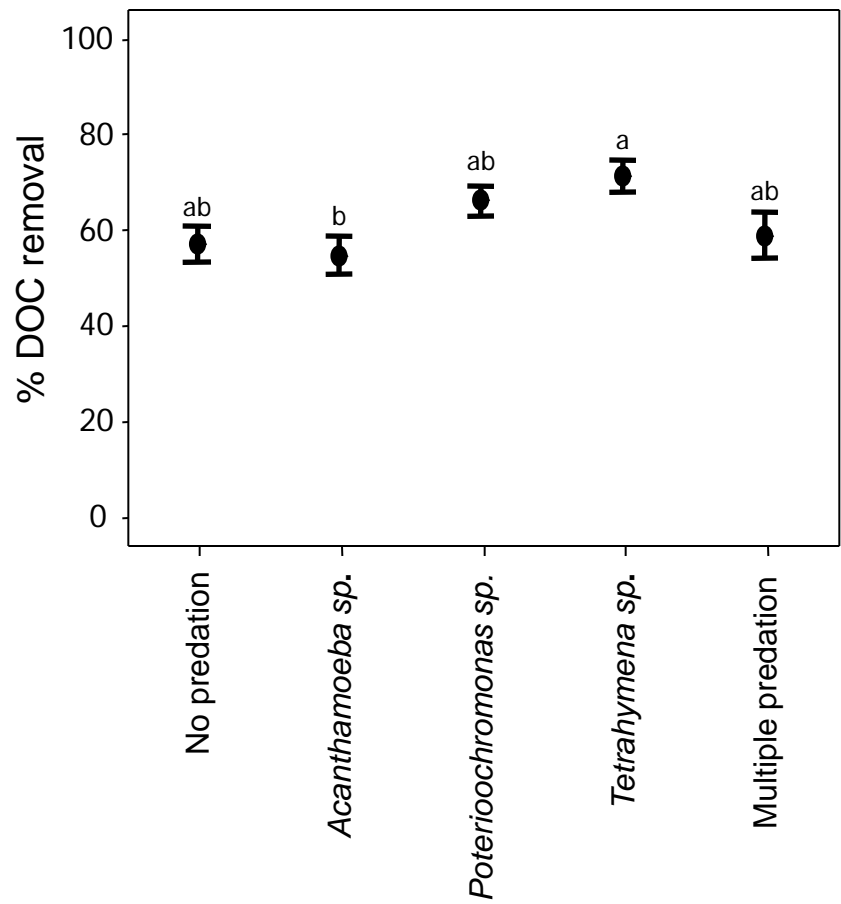
Supplementary Figure S10

Differences in the average relative removal of DOC and DTN by bacterial mixtures (i.e., with 2-5 species) across all predation treatments. Every point represents the average removal of all mixtures in each experiment. The significance was determined using ANOVA test followed by Tukey's Test.

Supplementary Table S1.

Spearman rank order correlation between bacterial and protist biodiversity mechanisms (i.e., complementarity and selection effects) and nutrient removal.
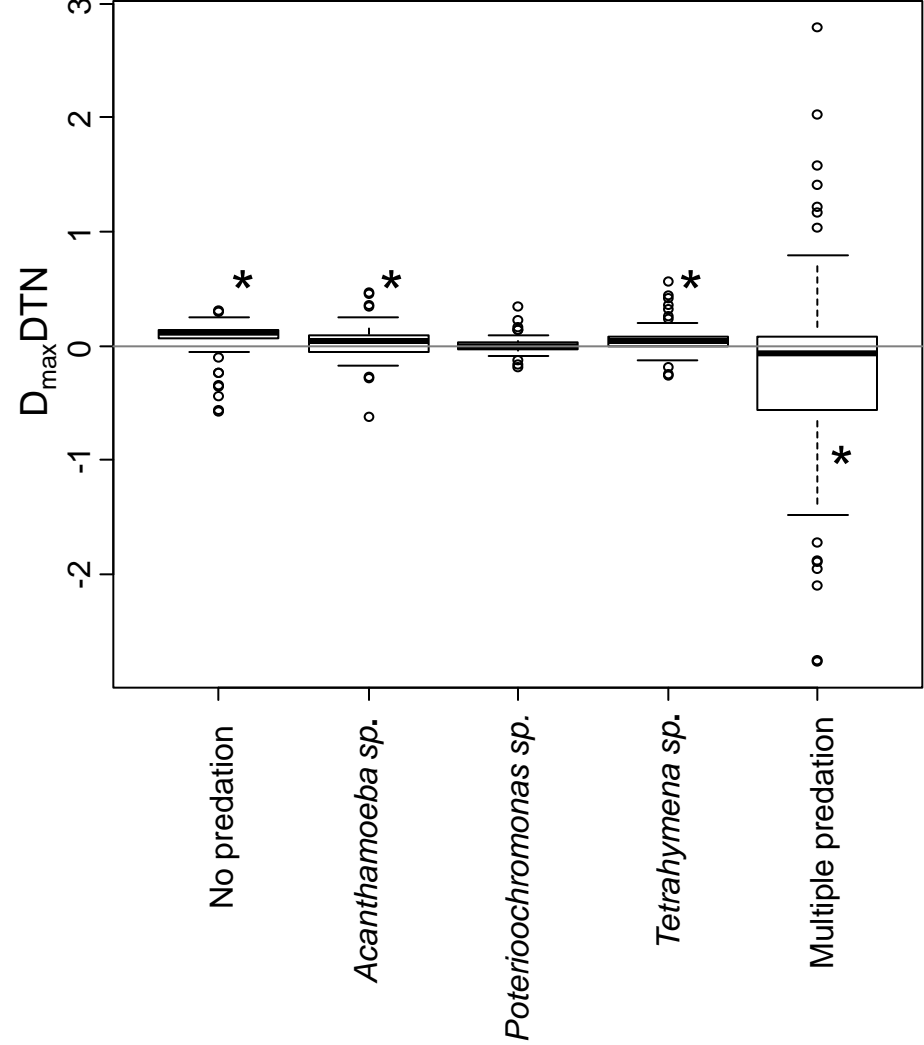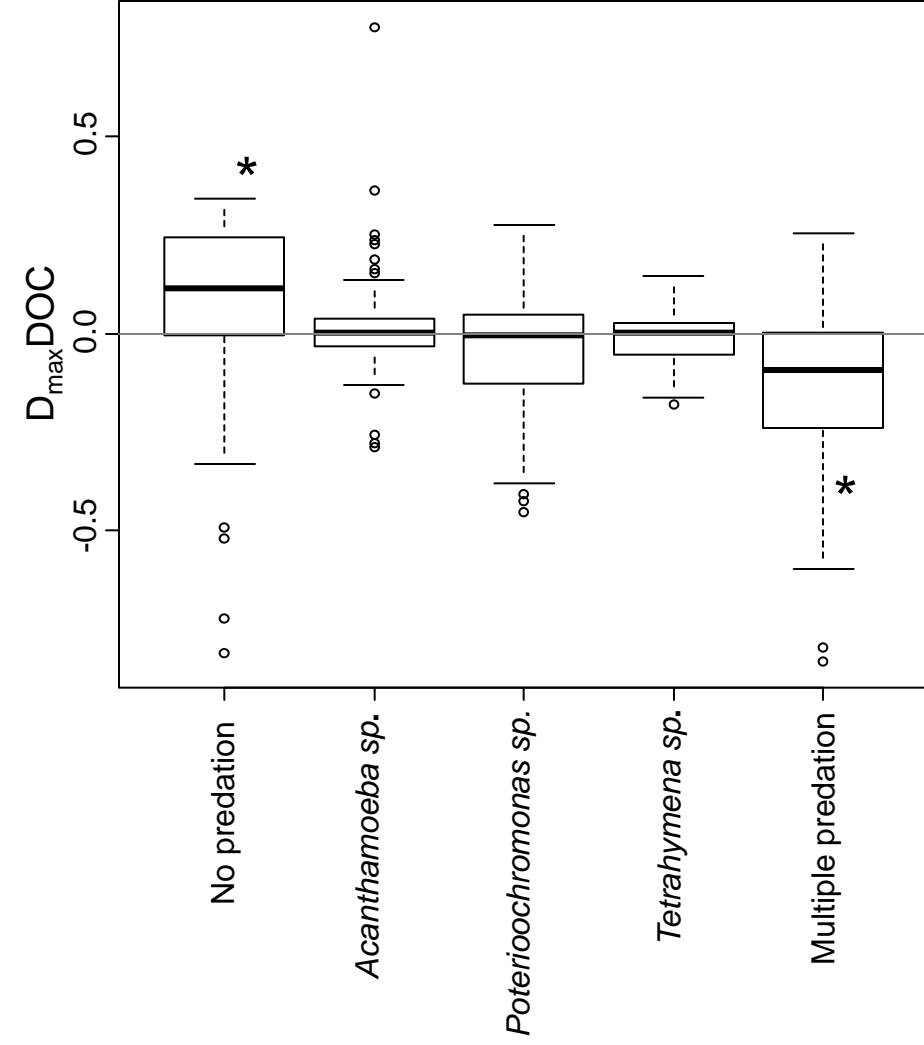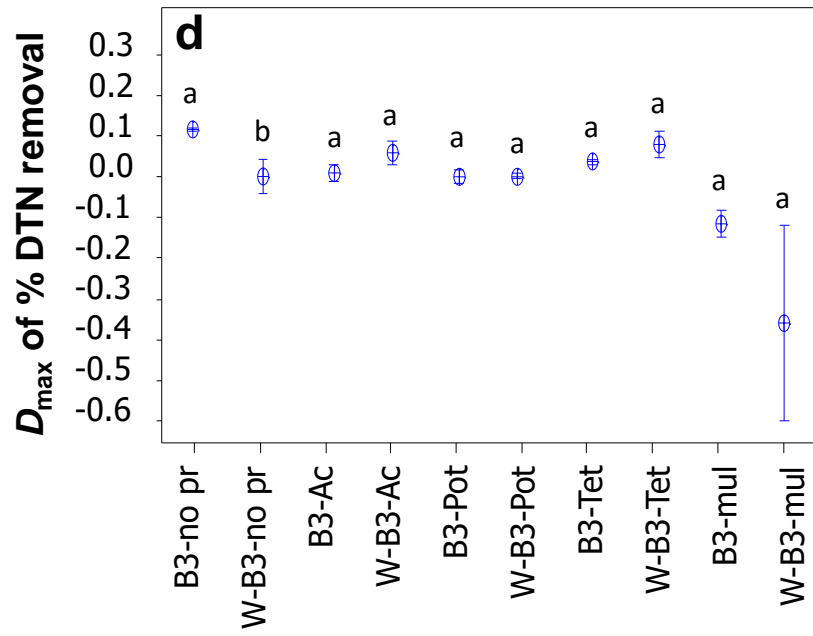
Supplementary Figure S1

a

B1 B2 B3 B4 B5

% DOC removal

b

B1 B2 B3 B4 B5

% DTN removal

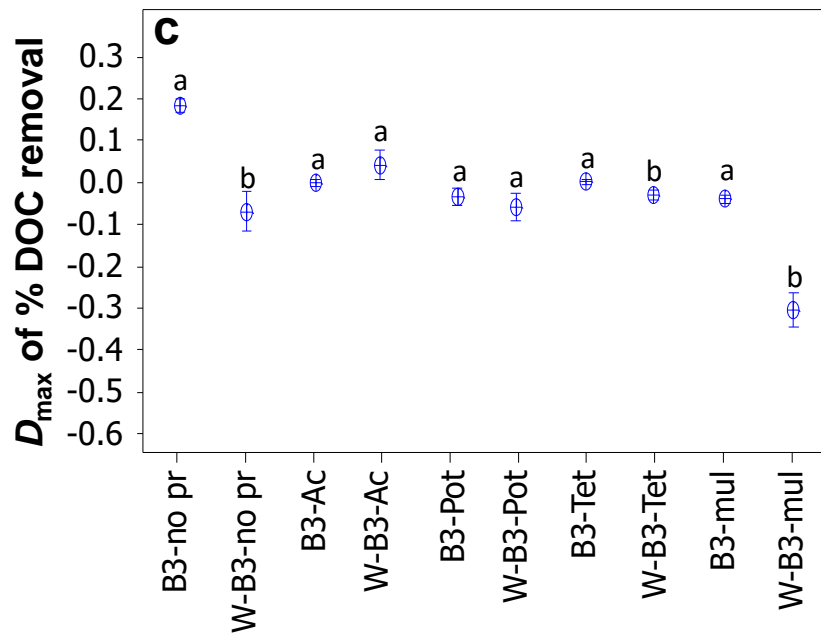No predation
Acanthamoeba sp.
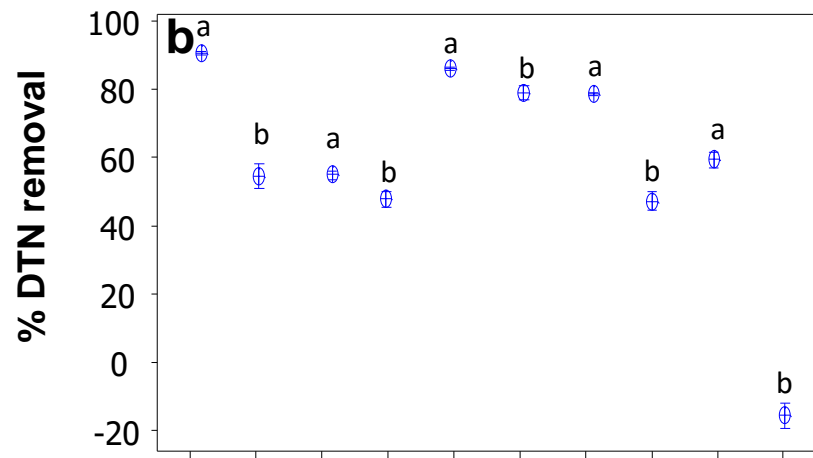*Poterioochromonas sp.*
Tetrahymena sp.
Multiple predation

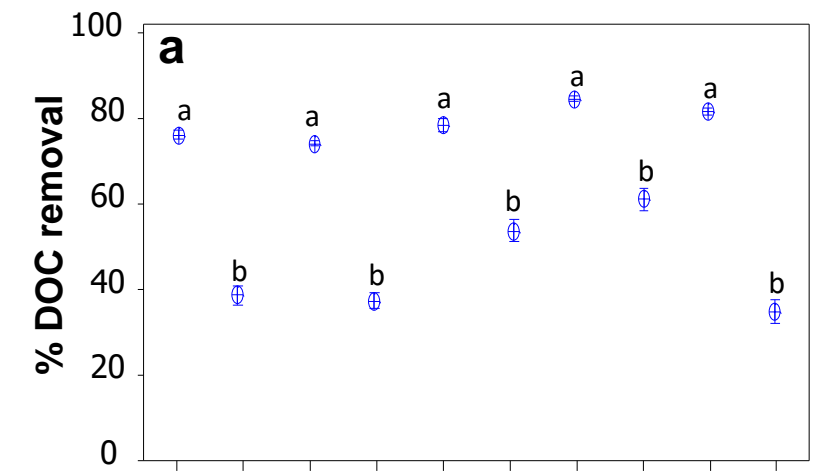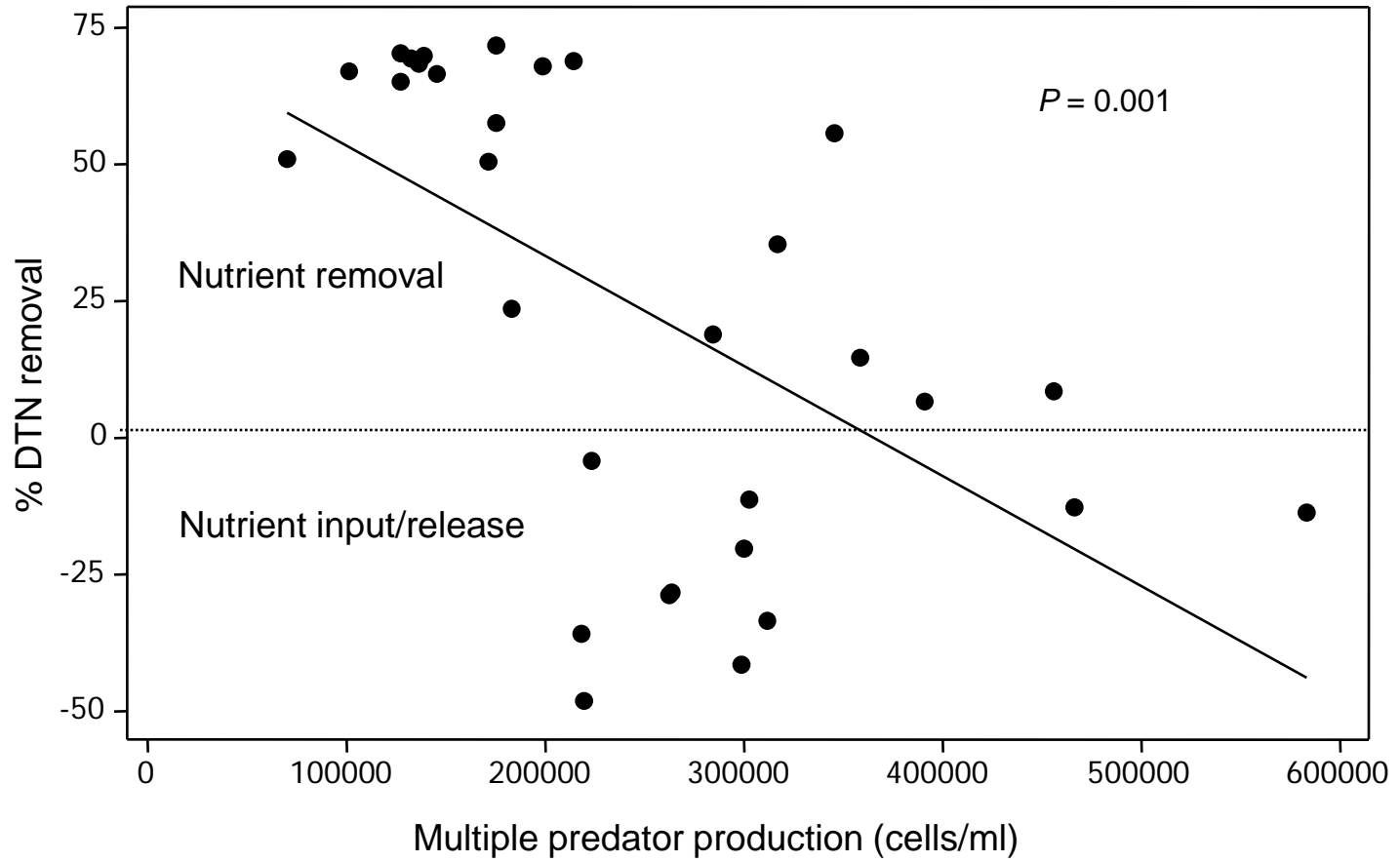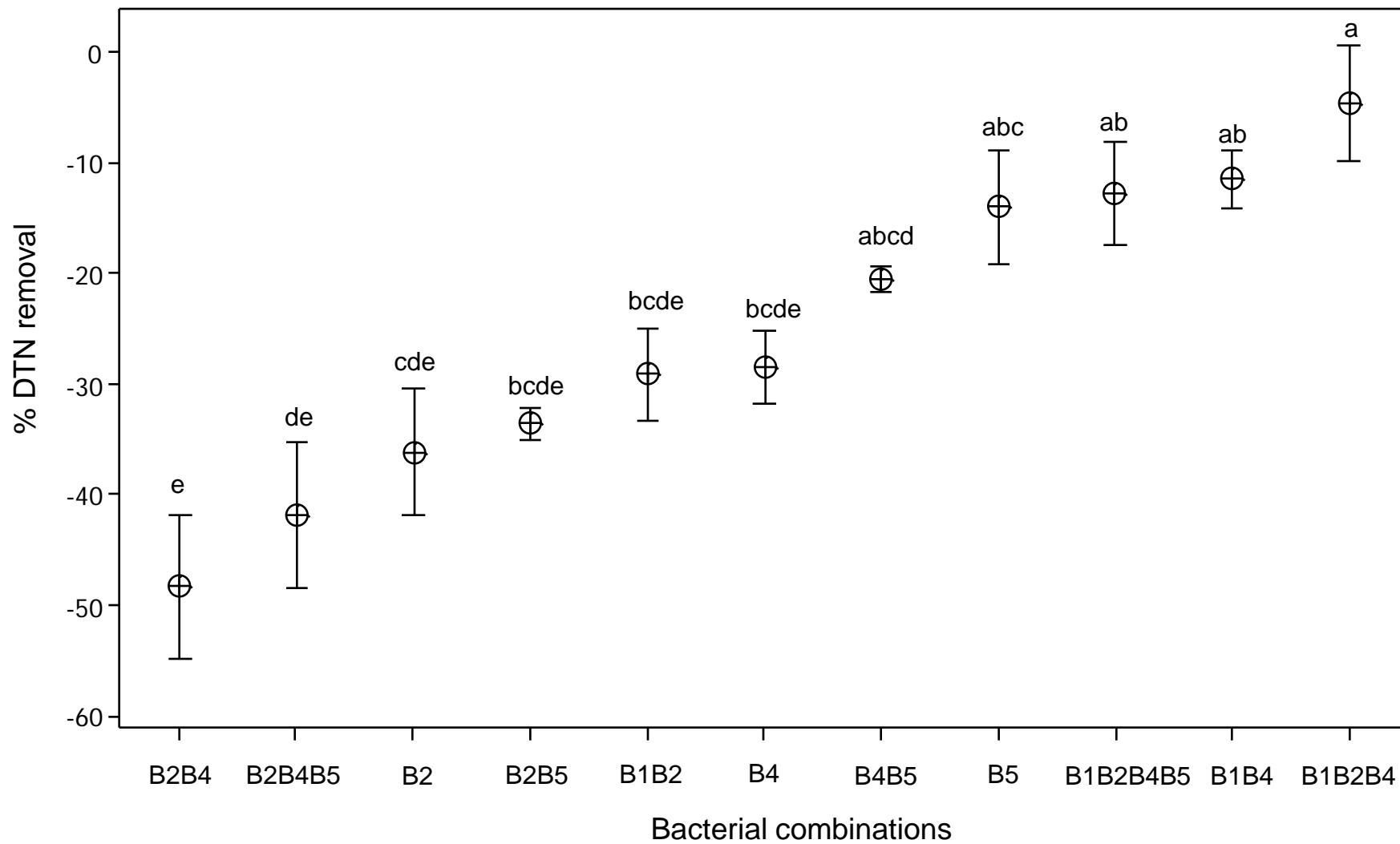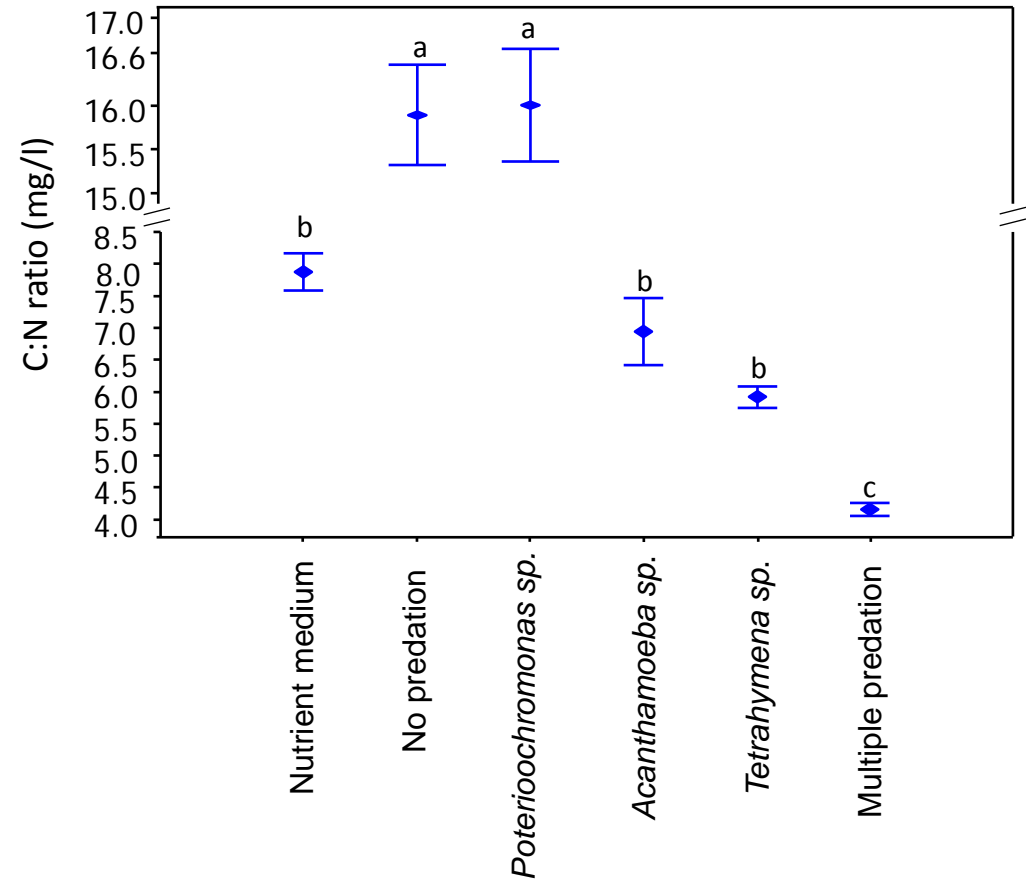Supplementary Figure 2

Supplementary Figure S3

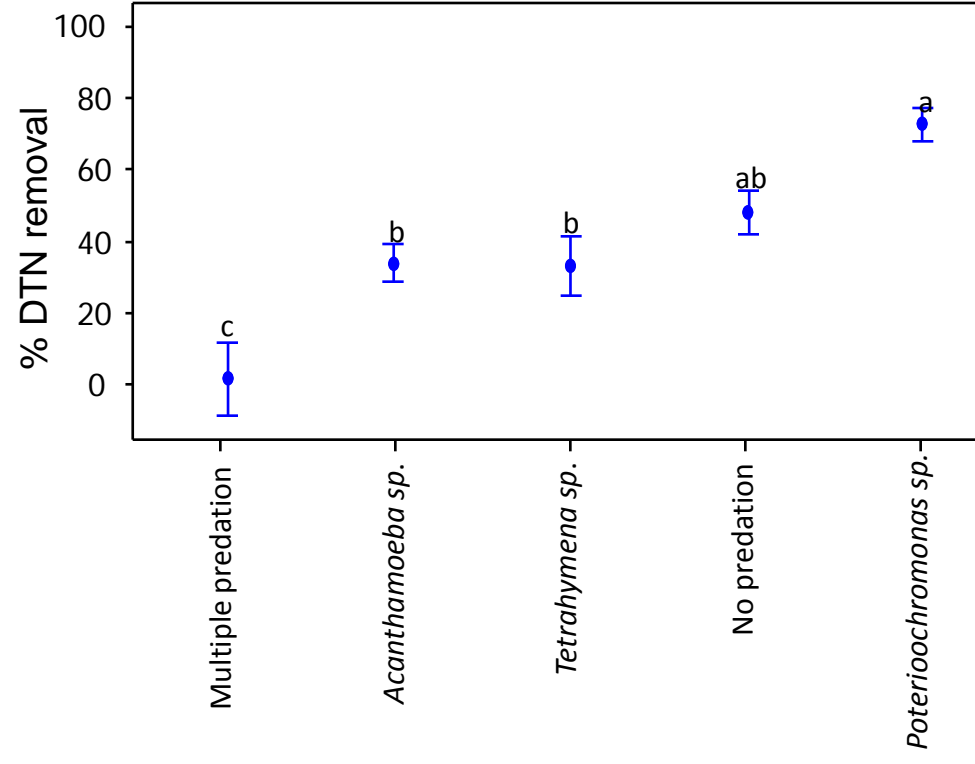Supplementary Figure S4
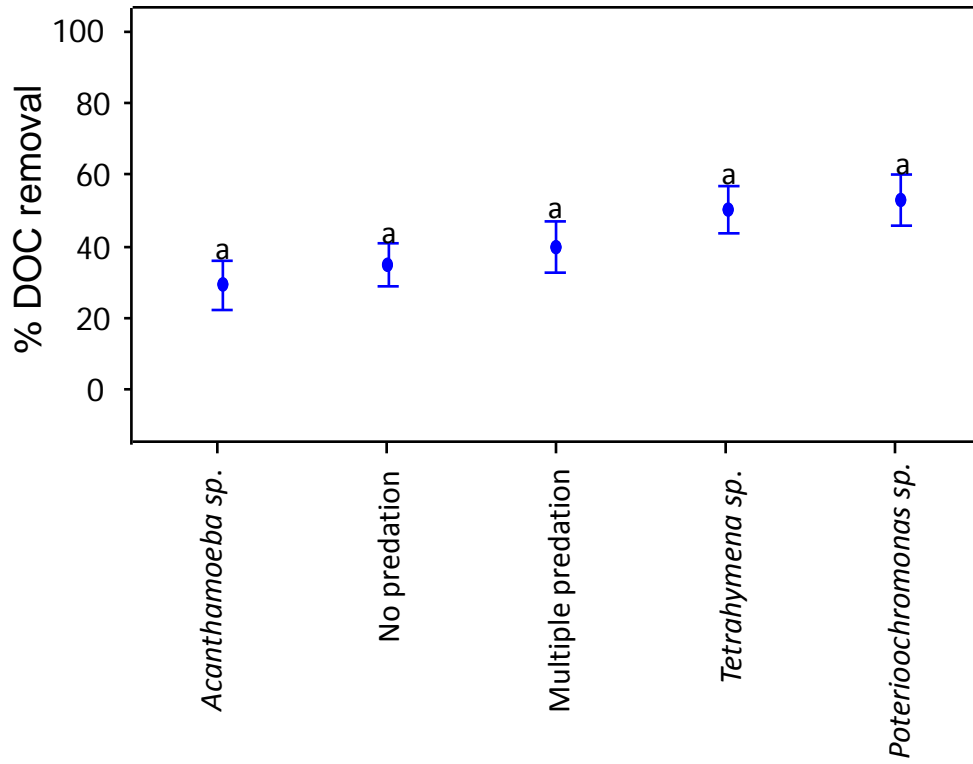
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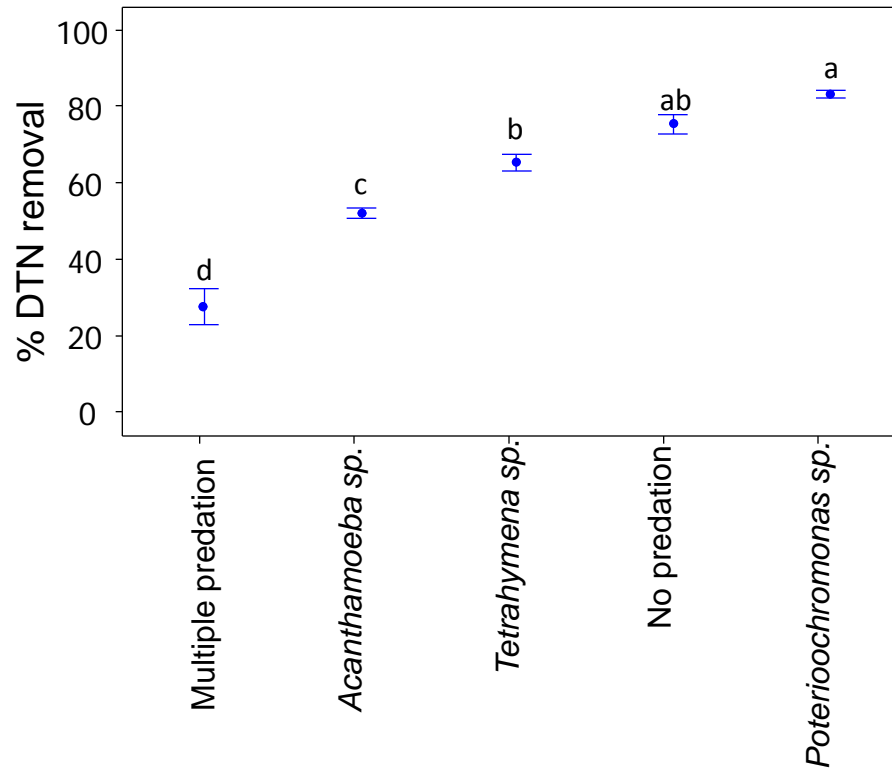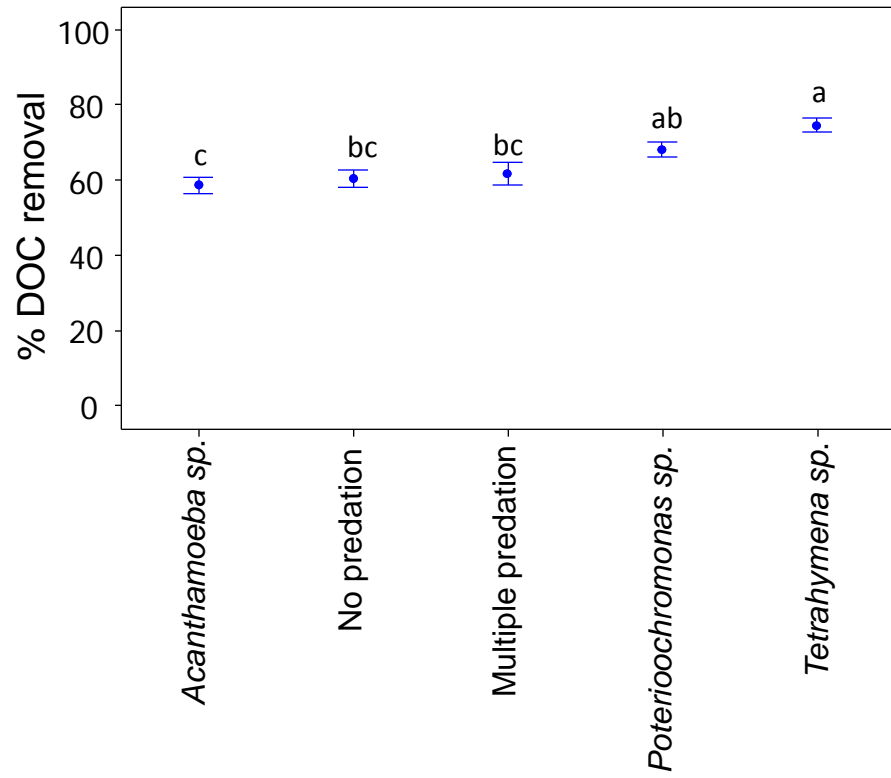
Supplementary Figure S6

Supplementary Figure S7

Supplementary Figure S8

Supplementary Figure S9

Supplementary Figure S10

Table S1. Spearman rank order correlation between bacterial and protist biodiversity mechanisms (i.e., complementarity and selection effects) and nutrient removal.

Partitioned bacterial prey diversity effects on carbon and nitrogen removal

	Complementarity effect		Selection effect		Complementarity effect		Selection effect	
	Carbon removal				**Nitrogen removal**			
	r	p	r	p	r	p	r	p
Control (predation free)	0.226	0.264	-0.231	0.252	0.256	0.204	-0.275	0.171
Poterioochromonas sp.	0.385	0.052	-0.199	0.327	0.314	0.117	-0.229	0.256
Acanthamoeba sp.	-0.566	0.0027	0.385	0.0516	-0.157	0.44	0.177	0.382
Tetrahymena sp.	0.044	0.828	0.0496	0.807	0.0619	0.761	-0.094	0.644
Multiple predation	0.37	0.0626	-0.259	0.198	0.375	0.0586	-0.303	0.13

Partitioned protistan predator diversity effects on carbon and nitrogen removal

Multiple predation	-0.475	0.0072	-0.319	0.0794	-0.477	0.007	-0.319	0.0794