

Effects of different microplastic polymers on the terrestrial woodlouse *Porcellio scaber* and the associated gut microbiome



[334529]



MIKROPLASTIK



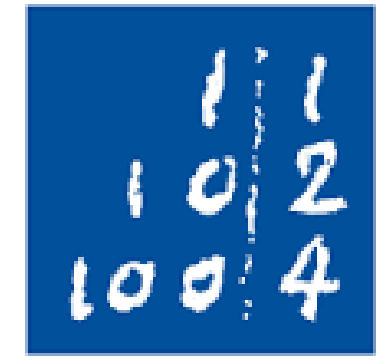
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Introduction

- P. scaber* is a widespread, important decomposer associated with nutrient cycling in soil
- Microplastic (MP) is an ubiquitous pollutant in terrestrial and many other ecosystems
- MP might enter food webs via unintentional ingestion and affects gut microbiomes (important for digestion)
- Assessment of MP effects on *P. scaber* warranted

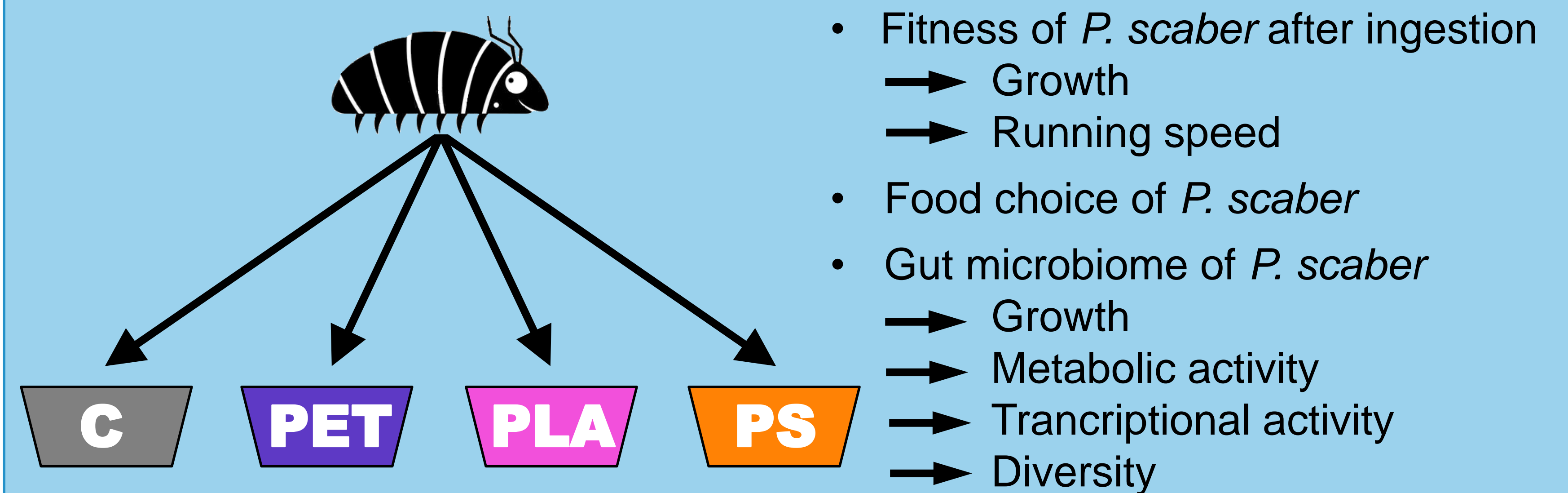
Hypothesis

Biodegradable (PLA) and non-biodegradable (PET and PS) MP have contrasting effects on *P. scaber* and its gut microbiome

Aim of the study

To assess the effects of common MP polymers (PET, PLA and PS) on the fitness of the soil-dwelling woodlouse *P. scaber* and the associated gut microbiome

Methods

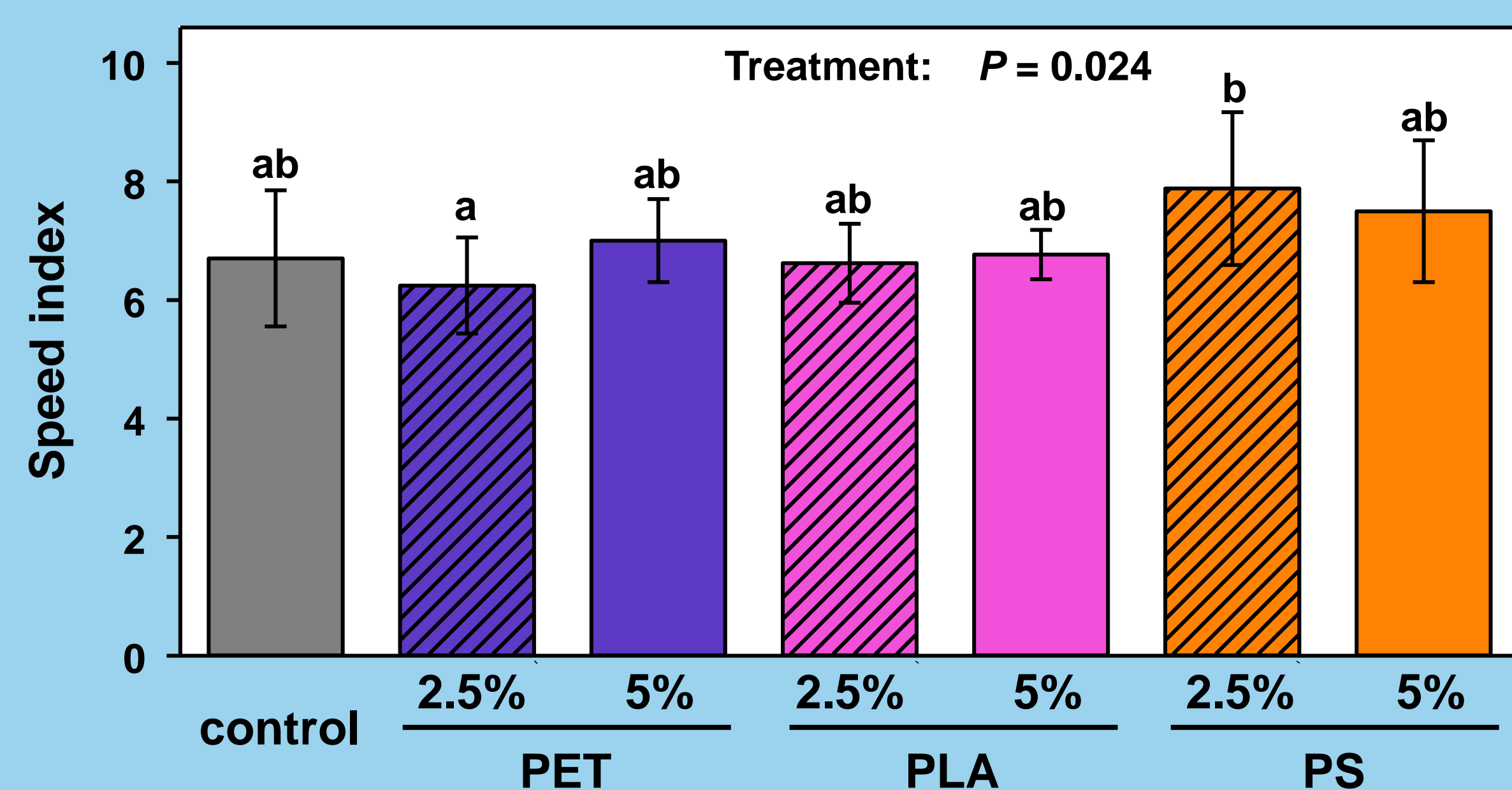
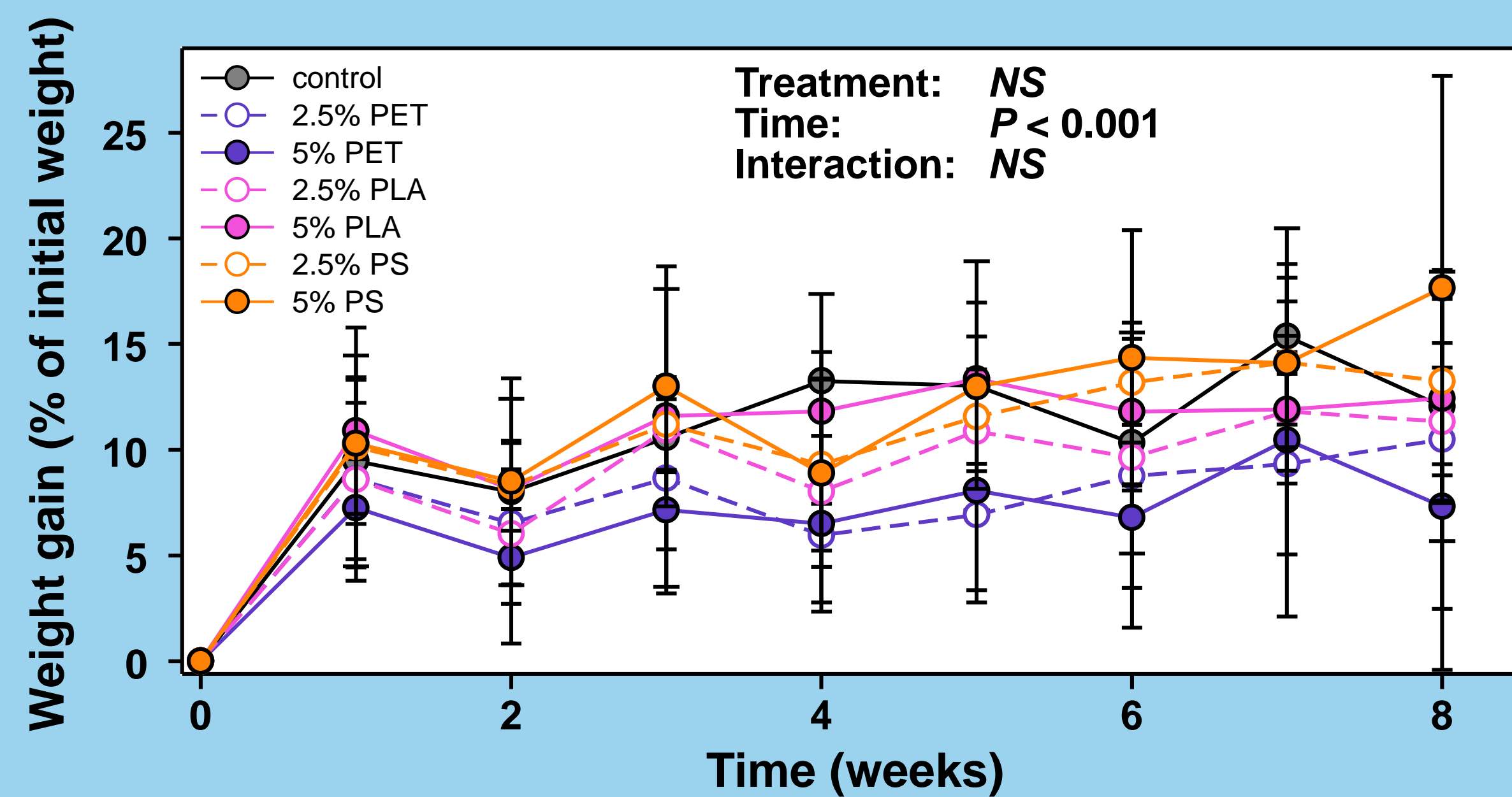


Summary and conclusions

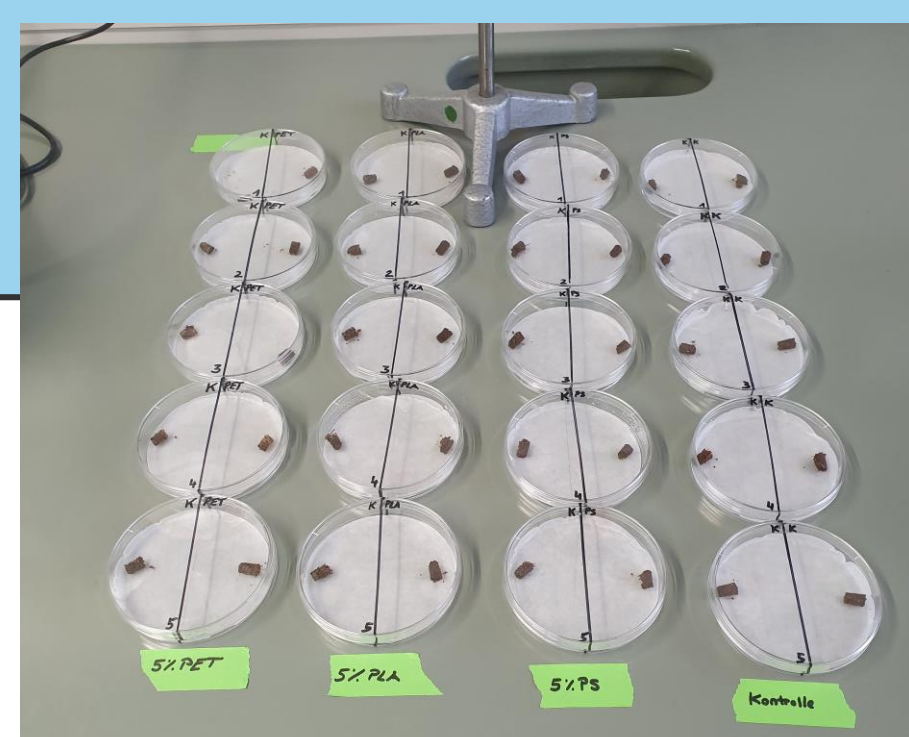
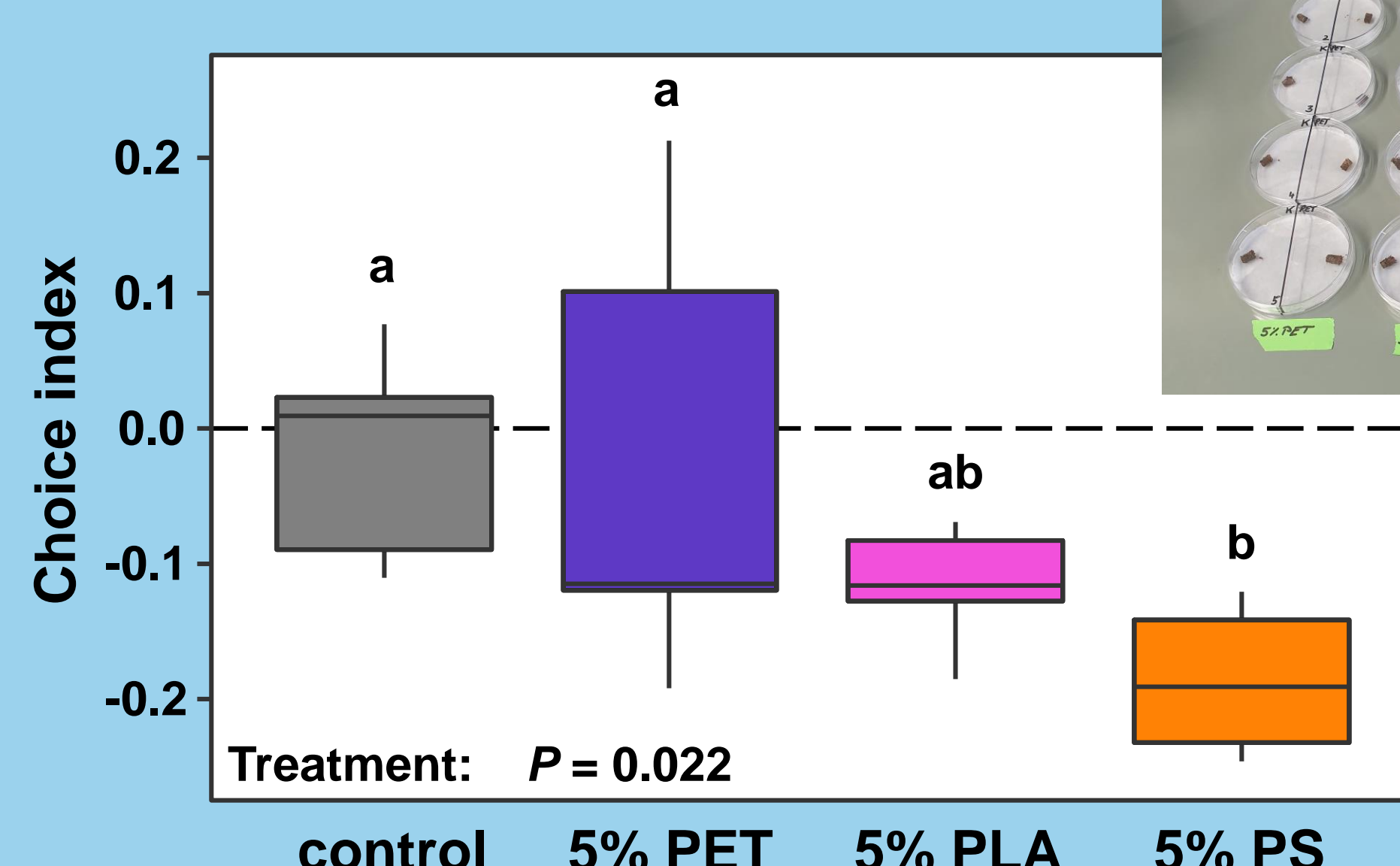
- P. scaber* is widely unaffected by MP reflecting resilience of adult woodlice
- Food containing PS is less preferable
- Woodlice are a source of hydrogen in oxic environments
- Positive effect of PLA on the activity of the gut microbiome likely due to hydrolysis and fermentation of lactic acid
- PET and PS ingestion leads to negative effects on fermentation

Results

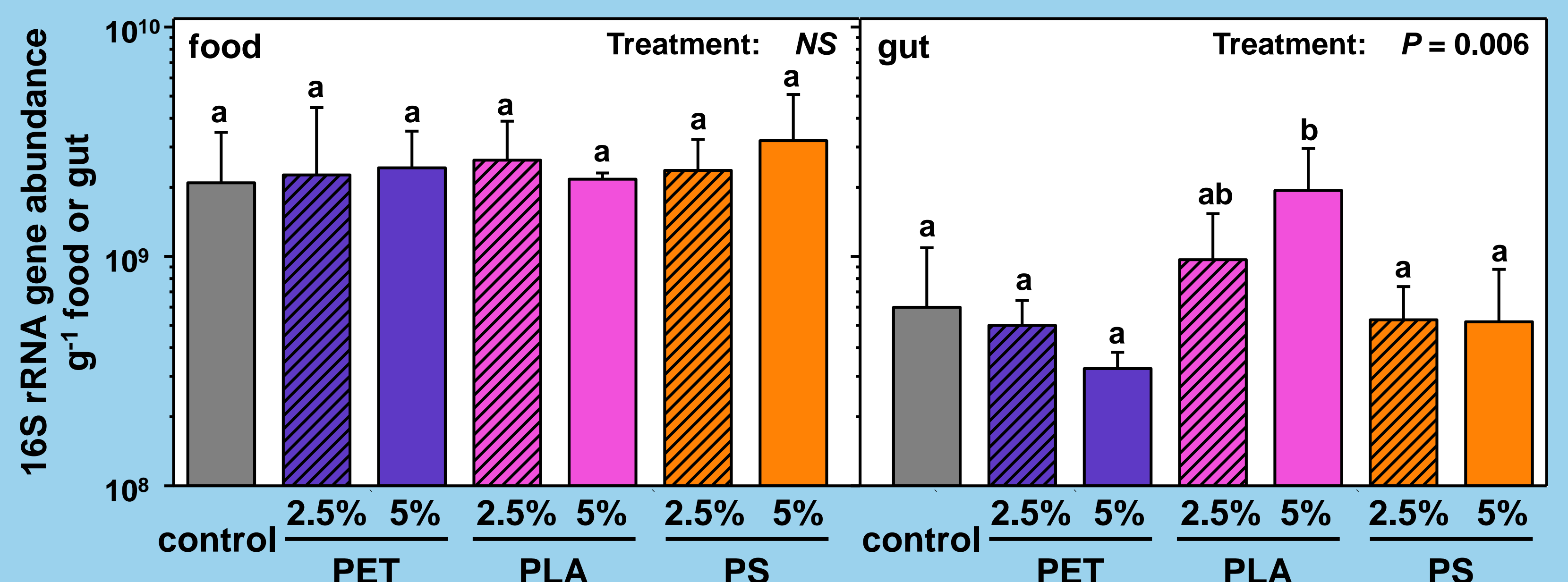
Resilience of adult woodlice



Avoidance of PS

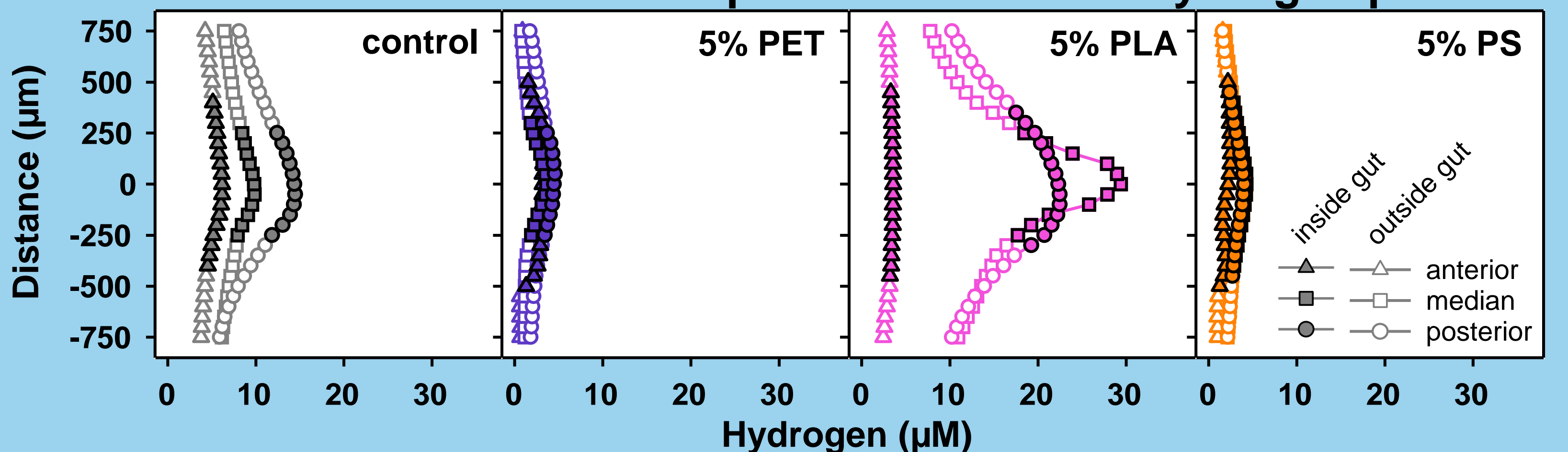


Microbial growth in the gut

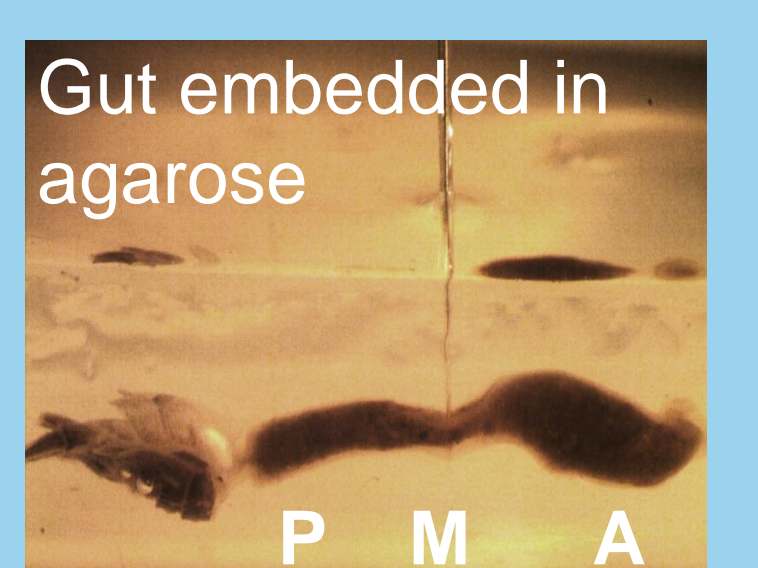


Microbial activity in the gut

Microsensor measurements - Representative radial hydrogen profiles



position	max. hydrogen concentration (µM)			
	Control	5% PET	5% PLA	5% PS
anterior	4.6 (1.6) ^{ab}	3.4 (1.0) ^{ab}	6.7 (3.4) ^{ab}	4.0 (1.0) ^{ab}
median	7.9 (1.8) ^{bc}	2.6 (0.9) ^a	30.5 (3.7) ^d	5.0 (0.7) ^{ab}
posterior	17.2 (3.8) ^{cd}	5.1 (2.3) ^{ab}	24.0 (11.6) ^d	4.3 (2.7) ^{ab}



Further microsensor measurements: oxygen and pH
 Anoxia and acidic pH (~5.6) determined for all guts

Coming soon...

- Quantification of short chain fatty acids in the gut
- Analysis of microbial community composition and transcriptionally active taxa in the gut