

**Fig. S1. Rarefaction plot of the OTUs (species richness) versus the number of sequences, subsampling from 500 to 20,000 reads in increments of 500 reads.** Sample: culture containing amoebae. Medium: culture without amoebae (“negative control”).

**Detailed protocol of NGS:**

Samples were amplified for sequencing at RTL Genomics in a two-step process. The forward primer was constructed with the Illumina i5 sequencing primer (5’- TCG TCG GCA GCG TCA GAT GTG TAT AAG AGA CAG -3’) and the 28f primer. The reverse primer was constructed with the Illumina i7 sequencing primer (5’ – GTC TCG TGG GCT CGG AGA TGT GTA TAA GAG ACA G – 3’) and the 388r primer. Amplifications were performed in 25 µl reactions with Qiagen HotStar Taq master mix (Qiagen Inc, Valencia, California), 1 µl of each 5µM primer, and 1µl of template. Reactions were performed on ABI Veriti thermocyclers (Applied Biosystems, Carlsbad, California) under the following thermal profile: 95°C for 5 min, then 25 cycles of 94°C for 30 s, 54°C for 40 s, 72°C for 1 min, followed by one cycle of 72°C for 10 min and 4°C hold. Products from the first stage amplification were added to a second PCR based on qualitatively determined concentrations. Primers for the second PCR were designed based on the Illumina Nextera PCR primers as follows: forward - AATGATACGGCGACCACCGAGATCTACAC[i5index]TCGTCGGCAGCGTC and reverse - CAAGCAGAAGACGGCATACGAGAT[i7index]GTCTCGTGGGCTCGG. The second stage amplification was run as for the first stage except that 10 cycles were used instead of 25. Amplification products were visualized with eGels (Life Technologies, Grand Island, New York). Products were then pooled in equimolar amounts and each pool was size selected in two rounds using SPRIselect (BeckmanCoulter, Indianapolis, Indiana) at a 0.7 ratio for both rounds. Size selected pools were then quantified using the Quibit 2.0 Fluorometer (Life Technologies) and loaded on an Illumina MiSeq (Illumina, Inc. San Diego, California) 2 x 300 flow cell at 10pM and sequenced. Generated sequences were processed by the RTL Genomics data analysis pipeline consisting of two major stages, 1) the denoising and chimera detection stage for quality checking to remove failed sequence reads, sequences with low quality tags, and sequences that were less than half the expected amplicon length; and 2) the microbial diversity stage. The process of denoising is used to correct errors in reads and usually observed error rates generated by Illumina MiSeq are less than 0.4%. Briefly, paired sequences were merged using the PEAR Illumina paired-end read merger and then reads were run through a RTL internal trimming algorithm.

**Detailed protocol for the models in Results 3.1:**

The final model for the **B8 attached amoebae** was as follows: model.nb<-glm.nb(attached\_amoebae ~ temperatureF \* day, data = taskA, link="log", while the best fitting model for the **B8 un-attached amoebae** count data included the interaction term and the quadratic term (turning a linear regression model into a curve) as follows: model4.nb<-glm.nb(unattached\_amoebae ~ temperatureF \*( day + I(day^2) ), data = taskA, link="log").

Final model for the **CE6 attached and un-attached amoebae**: model4.nb<-glm.nb(amoebae ~ temperatureF \*( day + I(day^2) ), data = taskA, link="log". Based on the attached CE6 amoebae count data, the model output showed significant differences in population growth between the two temperatures (10°C and 15°C) over 21 days, also including the day quadratic term of a non-linear relationship (p ≤ 0.001, n = 128). The best fitting model for the CE6 un-attached count data showed a significant difference between the two temperatures not only over time (p ≤ 0.001, n = 128) but also in the model output which included a single temperature parameter (p ≤ 0.001, n = 128). Moreover, the interaction term and the day quadratic term were also significantly different in both model outputs (p ≤ 0.001, n = 128).

The best model for both the **attached and un-attached G (polyclonal) culture** count data included the interaction term and the day quadratic term of a non-linear relationship as follows: model4.nb<-glm.nb(amoebae ~ temperatureF \*( day + I(day^2) ), data = taskA, link="log").

**Difference in growth among B8, CE6 and G cultures at 10°C and 15°C over 21 days.** The best fitting model for all these analyses resulted in a negative binomial distribution which included the interaction between the two temperatures and the quadratic term for a non-linear relationship, as follows: model4.nb<-glm.nb(amoebae ~ clone \*( day + I(day^2) ), data = taskA, link="log"). The model output for 10°C attached amoebae count data showed that B8 and CE6 growth rates were significantly different (p ≤ 0.01, n = 128), CE6 and G growth rates were significantly different (p ≤ 0.001, n = 192) including also the interaction between the two cultures over time (p ≤ 0.01, n = 192) and the quadratic term (p ≤ 0.05, n = 192), and B8 and G growth rates were significantly different over time (p ≤ 0.01, n = 192). At 15°C attached amoebae count data showed a similar trend for B8 and G cultures which increased over time even if at a different magnitude, while CE6 count data numbers started to decrease after 15 days. The model output for 15°C attached amoebae count data showed significant differences between the CE6 and G count data and between the G and B8 count data (p ≤ 0.001, n = 192), while the B8 and CE6 count data showed a significant difference only over time, including also the quadratic term (p ≤ 0.001, n = 192). Un-attached amoebae count data showed an increasing trend at 10°C over time for all cultures with significant differences among the different cultures (p ≤ 0.001 between B8 and CE6 count data and between B8 and G count data, p ≤ 0.01 between CE6 and G count data, n = 192), while at 15°C un-attached count data numbers started to decrease after 10 days in all the different cultures. The model output for 15°C un-attached amoebae count data showed a significant difference between the G and CE6 count data (p ≤ 0.001, n = 192) and between the G and B8 count data (p ≤ 0.001, n = 192), whereas the difference between the CE6 and B8 count data was significant only over time and also including the quadratic term (p ≤ 0.001, n = 192).