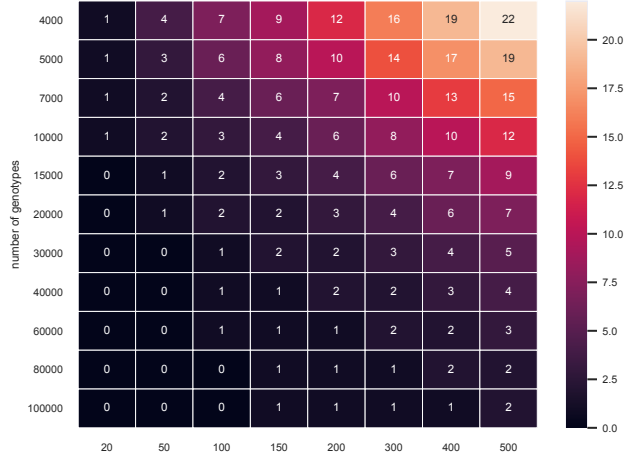
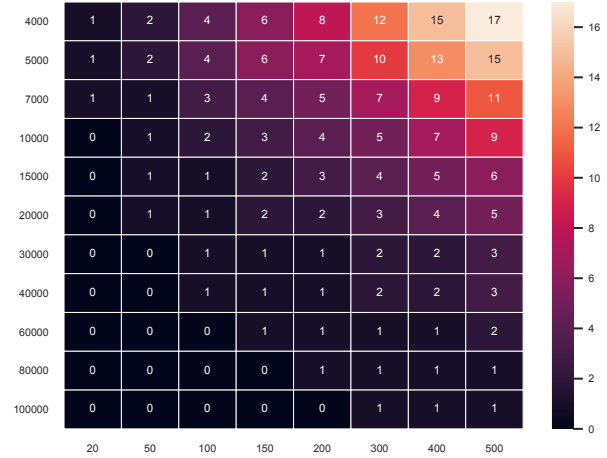


Figure 1: Visualization of the increase in cell numbers of sampled genotypes over 60 days and the resulting number of picked clones. For this model run, 1000 distinct genotypes, a sample size of 20 isolates, and a growth rate distribution with $\mu=0.2$ divisions per day and $\sigma=0.04$ were chosen. Every genotype was assigned a number from 0-999.

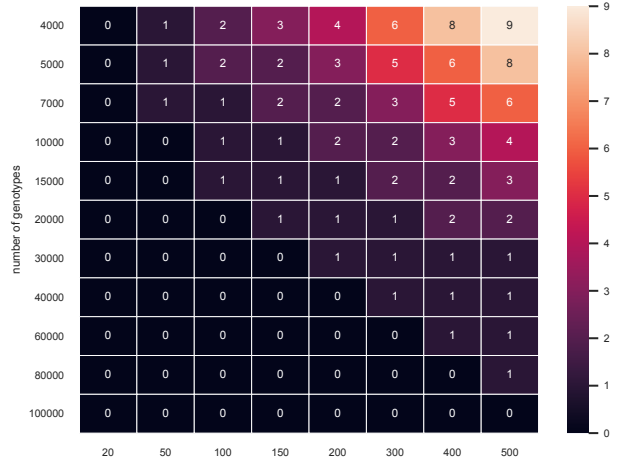
A) $\mu = 0.5$, $\sigma = 0.1$, days = 14, cell = 1



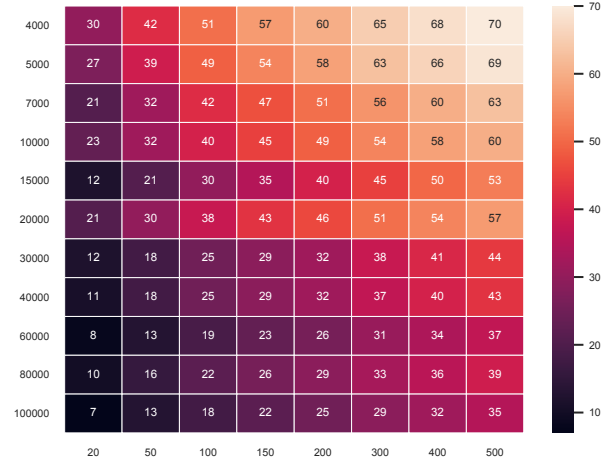
B) $\mu = 0.1$, $\sigma = 0.02$, days = 60, cell = 1



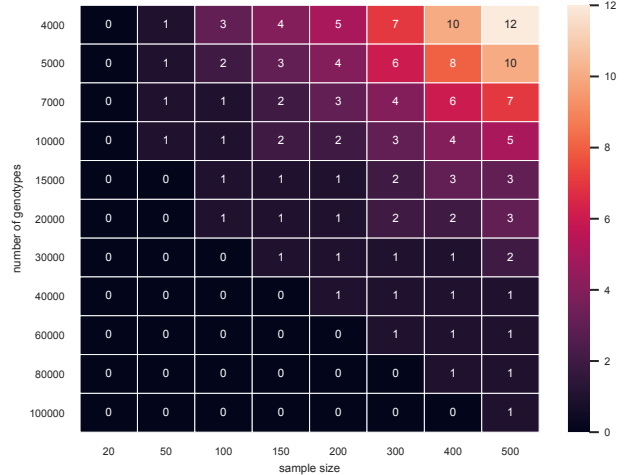
C) $\mu = 0.5$, $\sigma = 0.05$, days = 14, cell = 1



D) $\mu = 0.1$, $\sigma = 0.05$, days = 60, cell = 1



E) $\mu = 0.5$, $\sigma = 0.05$, days = 14, cell = 1-10000



F) $\mu = 0.1$, $\sigma = 0.05$, days = 60, cell = 1-10000

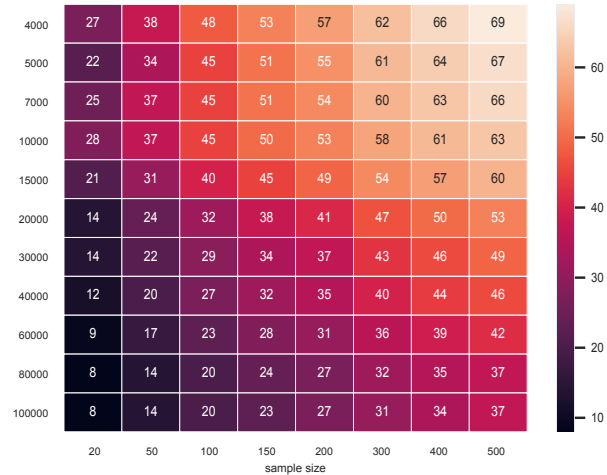


Figure 2: Heatmaps illustrating the probability of picking clones and the impact of intraspecific variability in growth rates (σ) in two ideal model species characterized by high and low average growth rates (μ), and different amount of initial cell concentrations per genotype (cell). A) Fast growing species with intermediate intraspecific variability and initially one cell per genotype. B) Slow growing species with intermediate variability and initially one cell per genotype. C) Fast growing species with low intraspecific variability and initially one cell per genotype. D) Slow growing species with high intraspecific variability and initially one cell per genotype. E) Fast growing species with intermediate intraspecific variability and heterogeneous initial cell number per genotype. F) Slow growing species with intermediate variability and heterogeneous initial cell number per genotype.

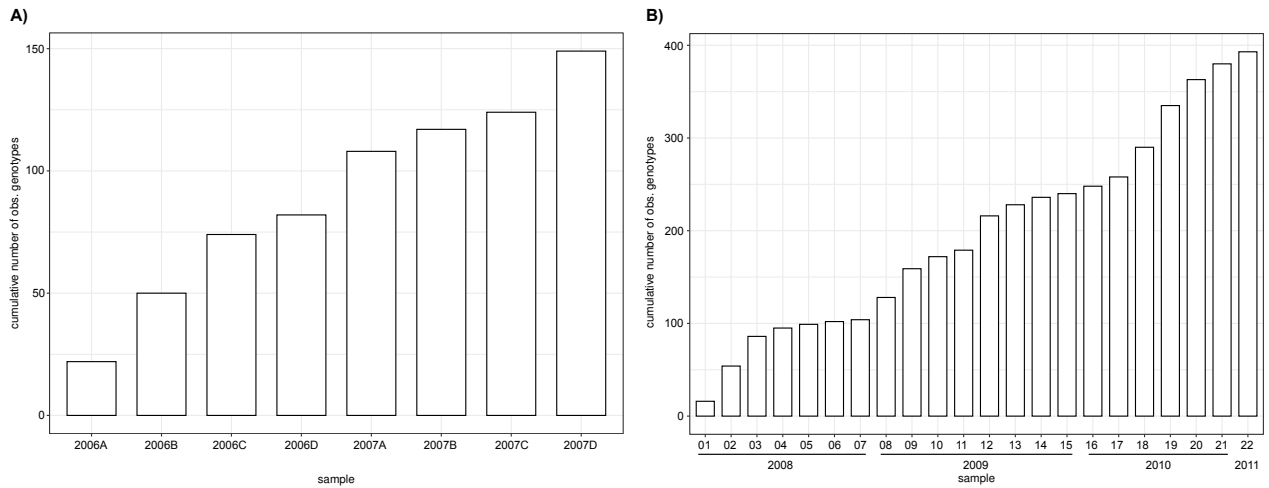


Figure 3: Cumulative number of observed genotypes in *Alexandrium catenella* (A) and *Pseudo-nitzschia multistriata* (B) across samples.

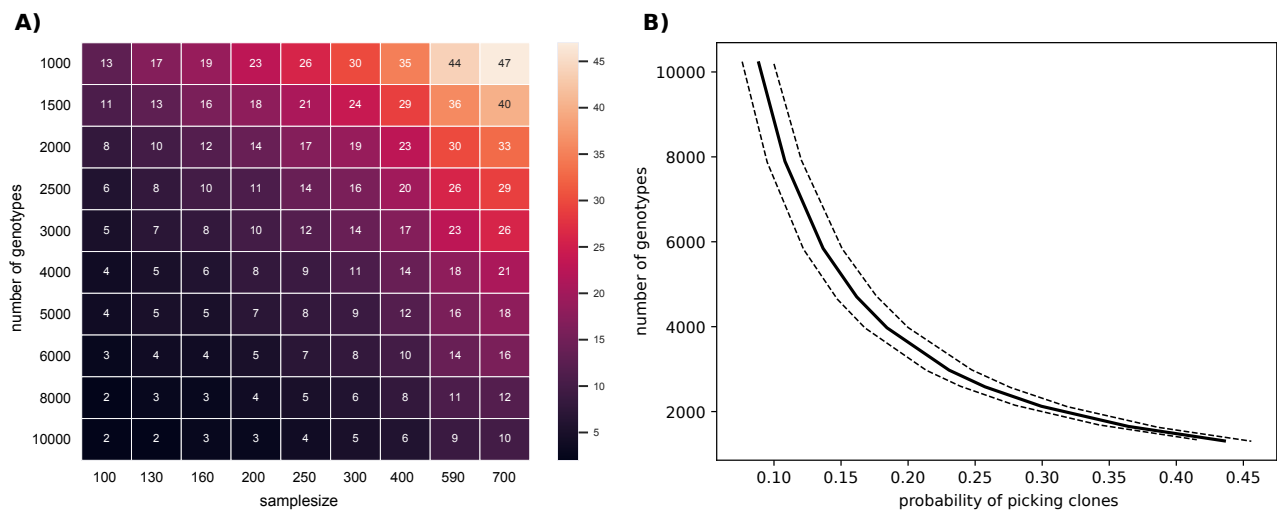


Figure 4: A) Heatmap visualizing the probability of picking clones of *Ditylum brightwellii* depending on number of initial genotypes and sample size. $\mu = 0.18$, $\sigma = 0.05$, initial cell number per genotype = 1-100, exponential growth period = 20 days. B) Number of *D. brightwellii* genotypes as a function of the modeled probability to pick clones, assuming a sample size of 590 isolates and an average growth rate of 0.18 with a standard deviation of 0.05. Solid line indicates the mean ($R^2=0.99$), while dashed lines indicate upper and lower confidence intervals (σ).

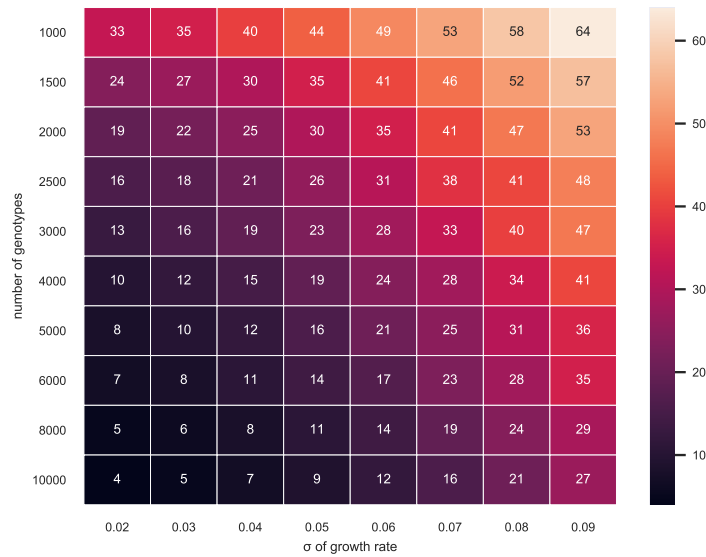


Figure 5: Heatmap visualizing the probability of picking clones of *Ditylum brightwellii* depending on number of initial genotypes and intraspecific variability in growth rates (σ). $\mu = 0.18$, sample size = 590 isolates, exponential growth period = 20 days, initial cell number per genotype = 1-100.

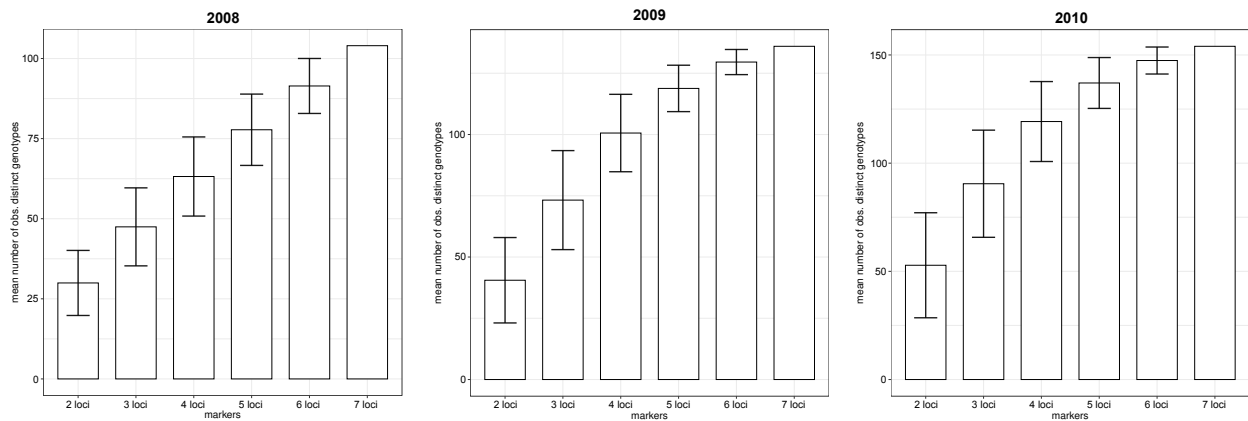


Figure 6: Mean number of observed distinct genotypes of *Pseudo-nitzschia multistriata* (Tesson et al. 2014) depending on the number of applied genetic markers. Error bars indicate standard deviation from the mean calculated from all possible combinations of the number of selected microsatellites.