

Extremely high polymorphism level in fungi *S. commune*: the cause and the importance for population genomics

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Hypervariable species are of particular interest for population genetics. Indeed, population genetics deals with differences between genotypes and, the higher the differences, the more we can learn about the factors that affect the population. We used next generation sequencing to obtain whole-genome sequences of 12 individuals of fungi *Schizophyllum commune* from the USA and 12 individuals from Russia. The diversity at synonymous sites is 0.20 in the American population of *S. commune*, and 0.13 in the Russian population, and the first of these figures is the highest reported. Hyperdiversity may be caused by high effective population size or high mutation rate. We studied negative selection in the population of *S. commune* to estimate a role of the effective population size. We showed that the amino acid-changing polymorphisms in *S. commune* are more neutral compared to *D. melanogaster* population. It is consistent with higher values of effective population size, leading to a lower proportion of segregating slightly deleterious mutations. We then developed a method to

measure directly the mutation rate in highly polymorphic population. We estimated mutation rate to be rather high $\sim 2.2 \times 10^{-8}$, what is about an order of magnitude higher than the mutation rate observed in *D. melanogaster*. Together these results show that in *S. commune* population high effective population size and high mutation rate play a role in high polymorphism level simultaneously. In addition, we demonstrated that high polymorphism level allows studying negative selection and functional sites with very high resolution.