1. What percetage of possible alleles are present in the initial population, that is, population P(0)?

Since the entire population are exact clones at the start, there are exactly 50% of possible alleles present. Since each allele is a bit (either 0 or 1), then one individual always has 50% of all possible alleles. Since there’s only one genotype present at the start, there’s 50% of all possible alleles in the entire population.

1. What percetage of possible alleles would you expect there to be in the population after one generation, that is, in population P(1)?

Since each locus has a 1% mutation rate, and there are 100 locii per chromosome/individual, a single cloning reproduction would result in, on average, a mutation to a single allele. Since each of the 100 individuals clone themselves, the resulting 100 all have, on average, one allele different from the original genotype. Theoretically, if everything lined up perfectly, the population could have 100% of all possible alleles, but that is unlikely. I would guess 75%, but at this point it gets a little more complicated and I think an empirical answer would provide the best insight.

After writing the code to provide a simulation of this population reproduction, it begins with 50% of all possible alleles as expected. The first generation provides enough mutations to bring that number around 80% most of the time, but since it is random this value does change on each run. It is usually anywhere between 78% and 86%, but occasionally it’s even more or less than that.

In the same way the second generation typically brings the population to over 90% of possible alleles. And once again there’s variation so it can be even higher or lower, but is typically between 90 and 95. After this it is just approaching 100% and usually gets closer with each generation, often getting there between generation 4 and 7 or so. In some cases I have seen it get to 100% around 4 or 5, but then it would go back down to over 99% for a few generations, before getting back to 100 again. This makes sense because there was apparently 1 allele that existed for a generation, and either that one or another one reverted back to the same allele all other individuals had. Then it took a few more generations for one individual to happen to mutate it back.

1. After 10 generations/P(10)?

By the time 10 generations was reached, there was almost never *not* 100% of potential alleles present. And same it would never revert either, because by this point all loci had mutated sufficiently where there was enough variation in the population where an allele wouldn’t disappear again.

1. After 100 generations/P(100)?
2. After 200 generations/P(200)?

Same goes for any further generation. The percentage of possible alleles present remained at a constant 100% after it reached that threshold. The amount of diversity overwhelmed any potential for mutation eliminating an allele.