RNA editing has evolved multiple times independently, and some have suggested that it may have been a feature of early low fidelity biological systems. Covello and Gray proposed a 3-step model for the evolution of RNA editing. However, this model has yet to be tested experimentally. In this model, RNA editing activity pre-exists but there is no substrate for it to act upon. Subsequently, mutation creates editable nucleotide sites, which may be fixed by genetic drift. RNA editing is now required for function, and thus becomes indispensable for gene expression. We sought to test this model by asking whether slippage-type editing can evolve under lab conditions favoring genetic drift. Our previous work on Buchnera, an endosymbiont of aphids, showed that RNA polymerase slips upon encountering poly(A/T) tracts, leading to stochastic incorporation or removal of As or Us in the nascent messenger RNA. This results in a heterogeneous population of mRNAs. Slippage-type editing can restore the open reading frame at the mRNA level where frameshift mutations have been acquired at the DNA level. This in turn leads to the expression of functional proteins but may also reduce expression efficiency of in-frame genes. To establish whether slippage-type editing emerges under conditions of genetic drift, we propagated 10 E. coli lines through daily single-cell bottlenecks. After 50 days, one line showed a decrease in growth rate and genome sequencing revealed the emergence of 38 frameshift mutations. In this turn suggests that RNA editing could well have been a feature of early biological systems.

**Whole Genome Sequencing**

Whole genome sequencing (Illumina’s HiSeq) was carried out at 10-day intervals for a single lineage that showed a marked decrease in growth rate.

- Increase in number of SNPs and poly (A/T) tracts in the bottlenecked population

**References**