

Standing Genetic Diversity and Transmission Bottleneck Size Drive Adaptation in Bacteriophage Q β

In order to study the relative contribution of the **initial standing genetic diversity versus that generated de novo**, which is a critical issue to understanding **how populations adapt to new selective pressures**, two RNA bacteriophage Q β populations differing in their degree of heterogeneity were propagated at non optimal temperature (43 °C) at different bottleneck sizes ($10^3 - 10^7$ infecting units).

The growth rate achieved by populations with origin in the less heterogeneous ancestor (Q β -t0) did depend on the transmission bottleneck size.

In contrast, evolved populations with origin in the most heterogeneous ancestor (Q β -t25) reached similar growth rates, regardless of their population size. However, the adaptive pathways depended on the frequency of the standing mutations (which were identified through deep sequencing) and the transmission bottleneck size.

The findings illustrate the **advantages for the adaptation of the preexistent genetic diversity in RNA viruses**. In **high heterogeneous** populations, **standing diversity** speeds up adaptation, while **low heterogeneous** populations must resort to **newly generated mutations**.

