

Heterogeneous Diversity of Spacers within CRISPR

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Clustered regularly interspaced short palindromic repeats (CRISPR) in bacterial and archaeal DNA have recently been shown to be a new type of anti-viral immune system in these organisms. I will discuss the diversity of spacers in CRISPR under selective pressure. I will propose a population dynamics model that explains the biological observation that the leader-proximal end of CRISPR is more diversified and the leader-distal end of CRISPR is more conserved. I will show this result to be in agreement with recent experiments. The results show that the CRISPR spacer structure is influenced by and provides a record of the viral challenges that bacteria face [1].

- [1] I. J. He and M. W. Deem, "Heterogeneous Diversity of Spacers within CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats)," *Phys. Rev. Lett.* 105 (2010)