IDENTIFICATION AND EVOLUTION OF NOVEL CRISPR-CAS SYSTEMS FROM THE HUMAN MICROBIOME

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CRISPR technologies are transforming the bio-medicine field by providing new therapeutic concepts for the treatment of diseases through genetic repairs and deployment of disease protecting factors. Nonetheless, the currently available CRISPR nucleases and derived technologies do not address the hurdles related to genome modification in gene therapy applications. Challenges are imposed by specific properties of CRISPR tools which includes high molecular weight limiting their compatibility with most commonly delivery vectors including lipid nanoparticles, target sequence constraints, immunogenicity and heterogeneous efficiency and precision throughout the genome. We recently focused on the development of new technologies by retrieving CRISPR systems from a large databank of the human microbiome and through a directed evolution approach to enhance the activity of the prokaryotic enzymes to eukaryotic environment. This work led us to the discovery of new CRISPR systems and the enhancement of Cas nucleases with compelling features for genome editing applications.