Tail Fiber Cross

Article Overview

Tail Fiber Cross refers to the recombinant formation of bacteriophage tail fibers, such as in lambda phage, where fibers from different strains combine to alter host specificity and adsorption efficiency.

Overview of Tail Fibers

Tail fibers are elongated, flexible proteins attached to the distal end of bacteriophage tails, playing a critical role in host recognition and attachment. They bind reversibly to host receptors, such as outer membrane proteins, exopolysaccharides, or flagella, allowing the phage to position its tail tip for DNA injection into the host cell . Typically, a phage virion carries multiple fibers; for example, lambda phage has about six fibers per virion, each approximately 35 nm long .

Tail Fiber Cross in Lambda Phage

The term "Tail Fiber Cross" is often associated with the recombinant laboratory strain lambdaPaPa, which originated from a cross between lambda Pasadena (Caltech) and lambda Paris (Institut Pasteur) . This cross introduced frameshift mutations relative to the original K12-derived Ur-lambda strain. As a result:

o Ur-lambda virions have thin, jointed side tail fibers absent in wild-type lambda.
o These fibers expand receptor specificity and allow faster adsorption to E. coli cells.
o The cross demonstrates how genetic recombination can modify tail fiber structure and host range, providing a model for studying phage evolution and engineering.

Structural and Mechanical Insights

Modern studies using AlphaFold2-multimer and ESMFold have revealed that tail fibers are trimeric, modular proteins with distinct domains that can undergo domain swapping and horizontal gene transfer, contributing to diversity in host recognition . Mechanical studies on T4 phage fibers (gp37) show that three fibers provide sufficient mechanical strength to maintain attachment under Brownian motion, with a Young's modulus of ~20 MPa and breaking force ~120 pN . This explains why specific fiber numbers are evolutionarily conserved.

Evolutionary and Functional Implications

Tail fiber genes evolve rapidly due to high selective pressure and can be exchanged between phages, crossing host phylogenetic boundaries . This modularity and recombination allow phages to adapt to new hosts, expand their host range, and are exploited in phage therapy and synthetic biology.

Summary

Tail Fiber Cross

A Tail Fiber Cross represents both a historical genetic recombination event (as in lambdaPaPa) and a broader concept of modular exchange in phage tail fibers, affecting host specificity, adsorption kinetics, and mechanical stability. Understanding these crosses provides insights into phage evolution, structural biology, and potential therapeutic applications.

Extracellular contractile injection systems (eCISs) are bacteriophage tail-derived toxin delivery complexes in

The complicated nature of fiber structures necessitates the participation of intra- or intermolecular chaperones for their

The cross-correlation of the map against the full RBPseg model is shown 715 in "sky blue" (dash-dot line), while the

Checking your browser before accessing pmc.ncbi.nlm.nih.gov ...

After addition of tail completion protein (TCP gpZ), tail assembly is finished and the tail subsequently binds to head-tail

The crystal structure of a complex between the tail fibre and tail fibre assembly (Tfa) protein of Escherichia coli phage

Why cross-over Fiber Cables? Occasionally, there will be instances in which you need to cross over fiber optics

Bacteriophages use receptor-binding proteins (RBPs) to adhere to bacterial hosts. Understanding the structure of

Tail fibers are responsible for the specific, albeit reversible primary attachment to host cell. Due to high

Viral fibers play a central role in many virus infection mechanisms since they recognize the corresponding host and establish a

This process is mediated by interactions between phage receptor-binding proteins (RBPs), such as tail fibers, and

Hier sollte eine Beschreibung angezeigt werden, diese Seite lässt dies jedoch nicht zu.

We demonstrate that Tfa forms a stable complex with the tail fibre, and present a 2.1 Å resolution X-ray

crystal

Here, we introduce RBPseg, a method that combines monomeric ESMFold predictions with a structural- based domain identi cation

A variable number of fibers are attached to the distal part of the tail of caudovirales bacterial viruses. Tail

Here, we discuss the molecular mechanisms and models of the tail fibers of the well-characterized T4 phage"s

Web: https://www.kremgroup.co.za