

# Researchers develop way to calculate speed of bacterial sex

May 15 2007

---

Scientists from the University of California-Davis recently developed a mathematical model of the rate of gene transfer among bacteria in the environment. Researchers believe this new model improves upon existing models by taking into account characteristics of the natural subsurface environments, the typical bacteria hangouts. This model will help scientists to quantify the spread of important bacterial traits.

The swapping of genetic material between bacteria leads to bacterial adaptation and evolution; however, bacterial adaptation is a double-edged sword for the environment. While the genetic exchange among bacteria can lead to positive environmental outcomes, such as improved bioremediation qualities, bacterial adaptation can also create potentially harmful bacteria that are resistant to antibiotics and increase gene flow from genetically modified organisms to native soils. By developing a real-life model of bacterial gene transfer, UC-Davis researchers hoped to gain insight into the rates of bacterial adaptation in the environment. They report their findings in the May 2007 issue of *Vadose Zone Journal* in a special section on soil biophysics.

Researchers believe that one of the major mechanisms for the transfer of genetic information in the environment occurs through a conjugation. According to study co-authors, Timothy Ginn and Arash Massoudieh, donor bacteria cells act like vampires, latching onto nearby unsuspecting non-related bacteria cells. Just as the bite from a vampire leads a victim to be transformed into a vampire, the donor bacteria's "bite" injects genetic material into the recipient, causing the recipient to become a

donor. The controlling rates of conjugative gene transfer and the kinetics of conjugative gene transfer are unknown.

The study of conjugative gene transfer centers on biofilms, a coat formed by colonizing bacterial cells.

"While scientists have studied [conjugation] in the lab, and wondered about its impact in nature, current computer models of conjugation were pretty basic," said Ginn. UC-Davis researchers set out to build a better model that incorporated the experiences of bacteria in nature, such as wait times associated with conjugations, bacterial cell motion and transport in ground water, and the colonization of soil surfaces by bacterial cells.

Using a previously established conceptual framework of conjugation processes in an isolated environment, researchers created a new mathematical model of bacterial transport and conjugation that focused on subsurface bacteria colonizing surfaces, such as sand and soil grains. The UC-Davis research was funded by the National Science Foundation.

The new model was then used to re-interpret previously published conjugation data. The findings revealed that bacterial transport and colonization of surfaces is as important a controlling factor for gene spread as was the rate of conjugation itself.

It is important to consider all natural processes together when trying to predict rates of gene transfer, said Ginn.

"The model gives us a new tool for designing new experiments that reflect gene transfer in the real world, including such things as transport of cells in porous media of soils and aquifers," explained Massoudieh. "It also can be used for 'extrapolative' modeling to predict rates of gene transfer in certain cases, mainly environmental science scenarios, but

also with relevance to some medical scenarios."

Source: American Society of Agronomy

Citation: Researchers develop way to calculate speed of bacterial sex (2007, May 15) retrieved 26 April 2024 from <https://phys.org/news/2007-05-bacterial-sex.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.