mosquitos, matching the hospital-reported cases. This gave new insights for the researchers to create new and improved models that are more reliable and accurate for the complex dynamics of infectious disease.

Reference

Running Hot and Cold on the Trail to Measuring Adaptation in Fruit Flies

How does species adaptation occur at the genomic level? With the ability to rapidly sequence whole genomes at low cost, next-generation sequencing has ushered in a new era of excitement in experimental evolutionary biology. The ability to manipulate model organisms and sequence whole genomes to pinpoint which genes are responsible for adaptation within a given population—dubbed “evolve and resequence”—now aims to fill in the gaps.

Tobler et al. (2013) used an experimental genetic workhorse, the fruit fly Drosophila melanogaster, and subjected a population to two different environments, one hot and one cold, and asked whether they could quantify the genetic response in each. Wild flies were collected and expanded to a population of 1,000, grown in the hot and cold environments for at least 15 generations, and then subjected to whole-genome sequencing.

Identifying a large number of variants involved in the adaptive response (called candidates), the authors provide convincing evidence that their candidates include loci with functions specific to either the hot or cold environment. Nevertheless, they also deduced that the number of candidate loci was greatly overestimated due to a lack of independence among them that was previously unrecognized. The authors outline how this problem, which severely limits the ability to reliably fine-map such sites, could be ameliorated by modifications to the design of such studies.

References

Staying a Step Ahead of Influenza

Every fall, the latest batch of flu vaccines attempts to keep society a step ahead of the evolution of flu virus. Heroic worldwide surveillance efforts have avoided a repeat of the 1918 flu pandemic, but as shown in the recent H1N1 outbreak, viruses can still outwit even the best public health efforts.

During the H1N1 outbreak, antiviral drugs offered the only hope against emergent flu strains. Two drug classes: adamantanes (FDA approved in 1966) and neuraminidase inhibitors (oseltamivir, FDA approved in 1999) represent two classes of drugs that target a viral anion channel and cell surface antigen, respectively, thereby preventing or treating infection. In an ambitious study, the authors attempt to trace drug resistance against all strains of the flu by using an extensive influenza virus database containing all known genetic sequence information (70,000 complete nucleotide sequences) for influenza strains. Using a phylogenetic approach, Garcia and Aris-Brosou (2013) examined the evolutionary history of antiviral drug resistance. “Although the approaches employed in our study are not novel in themselves, the scale of the analyses is unprecedented and allowed us to track in public databases the dynamics of all known mutations involved in drug resistance,” reported Aris-Brosou.
How does the virus outwit two leading antiviral therapies? Widespread use of these drugs has led to the emergence of drug resistance. Most disconcerting, recent “dual resistance” viruses dodge both drugs, leaving us defenseless against the virus. Although adamantane resistance mutations appeared readily, they took 15–38 years after FDA approval to emerge, but emerged three times, whereas the less spontaneous oseltamivir mutations took at most 7 years, serving as a public health cautionary tale. The authors support the judicious use of antiviral drugs as a last line of defense against influenza to avoid the spread of dual resistance, which is already circulating in H1N1 viruses in humans. “Our results also suggest that most of the mutations leading to influenza drug resistance are on the wane, so that recent efforts in controlling drug use are paying off, but we should remain vigilant,” commented Aris-Brosou.

Reference

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Plants Found to Aid Their Enemies

Throughout the evolution of life on earth, bits of genetic material are routinely swapped among different species of bacteria to give them a competitive advantage. However, rarely do such gene transfers happen between bacteria and higher organisms.

Currently, Prof. Nikolaidis et al. (2013) report on a rare case where plant genes called expansins, which are responsible for loosening or weakening protective cell wall, were transferred from plants to bacteria, fungi, and amoeba, which are known plant pathogens that live nearby in the soil.

“Our study reveals a rare phenomenon in molecular evolution where plant genes have been transferred to simpler organisms like fungi and bacteria,” said Nikolaidis. “The protein products of these genes are weakening the plant cell wall allowing plants to grow. In the case of bacteria and fungi, these proteins are related with the ability of these species to colonize plant roots and their virulence as plant pathogens. Our study suggests that by using proteins acquired from their hosts bacteria and fungi have found new adaptive ways to utilize their hosts resources and maybe become more advanced pathogens.”

The research team found two independent instances of such horizontal gene transfers that occurred from plants to bacteria and fungi. These events were followed by gene swapping among bacteria and fungi to refine their evolutionary fitness. The authors also looked at the details of gene swapping at the molecular level and found fused DNA segments that point to a similar gene function, binding to plant and bacteria cell walls.

The evolution of these nonplant expansins represents a unique case in which bacteria and fungi have found innovative and adaptive ways to interact with and infect plants. This evolutionary paradigm suggests that, despite their low frequency, such rare events have significantly contributed to the evolution of prokaryotic and eukaryotic species.

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Avoiding Poisons: A Matter of Bitter Taste?

In most animals, taste has evolved to avoid all things bitter to prevent from eating something typically poisonous. The taste sensation is mediated by the binding of taste receptors, known as Tas2rs, with bitter compounds. Because plant tissues contain more toxins than animal tissues do, one may hypothesize that herbivores need more Tas2r genes than