

Influenza coinfection...could it be the next to instigate a pandemic influenza outbreak?

When RNA viruses replicate, they tend to make some mistakes (aka mutations) along the way. In fact, it is estimated that an RNA virus makes, on average, one mistake each time it replicates...much higher than what is observed in DNA viruses. This is, in large part, due to the limited proof-reading capacity of proteins responsible for RNA replication. These mistakes can either benefit the virus, making it more adapted to the host or it can be detrimental, resulting in a virus that is less fit. Either way, these mutations cause the virus to change over time (or evolve) resulting in viruses that can be quite different from parental/original strains. For RNA viruses like influenza (“flu”), different strains can infect the same cell...when this happens, entire portions of the genome can be swapped between the infecting viruses in a process called reassortment further contributing to viral evolution. But what do these mistakes and gene swappings mean for you and I?

Well...in any given flu season, there are many strains of influenza in circulation (in many different species), yet the annual flu vaccine generally contains components from only 3-4 different strains. Thus, it is possible that you or I could become infected with multiple influenza subtypes at the same time (“coinfection”). Although the frequency of coinfection is inconsistent in the literature, there were reports of a spike in incidence in the 2015-2016 flu season(1, 2). Since influenza coinfection can lead to reassortment, which is responsible for generating novel strains that have fueled epidemics and pandemics in the past, it remains important to define the conditions that enable reassortment to occur in vivo.

These pandemic strains arise when human and animal (i.e. bird and swine) influenza viruses infect the same cell and genomic parts are swapped between the two...but what controls whether or not this can/will happen? Well, most seasonal influenza strains are generally restricted to the upper respiratory tract (i.e. trachea, upper airways, and nasopharynx) (3), while avian and swine flu strains tend to prefer the lower respiratory tract. Thus, there are already safeguards in place to prevent the mixing between these species-specific strains. But, we know it can happen (think Swine Flu of 2009), so the authors in a recent study sought to determine whether location of infection played a role in reassortment (4). The researchers coinfecting ferrets with two genetically distinct influenza A viruses in the same anatomical site (both intranasal) versus two separate sites (intranasal and intratracheal). Reassortant viruses were only recovered when viruses were introduced at the same site. This study suggests that, although influenza coinfections may be more commonly detected (likely due to improvements in sequencing technology), the culprits are most likely human influenza

viruses. Thus, in conclusion, although the authors did not attempt to infect with two species-specific strains at the same time in the same location to determine the likelihood of reassortment under these conditions, the chances that you are the breeding ground for the next influenza pandemic is relatively low thanks to the fact that animal and human influenza viruses prefer different cell types (and thus different locations). And we have Mother Nature to thank for that!

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References

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