Medical Xpress

Viral marker of human migration suspect

October 24 2006

A benign virus previously used as a marker in tracing human migration may be unreliable, according to researchers at Penn State. Results of this study also suggest that some viruses might be undergoing much higher rates of evolution than previously thought.

"The most genetically divergent human populations are in Africa," said Laura Shackelton, a postdoctoral researcher at Penn State's Center for Infectious Disease Dynamics. "But, in the case of this virus, strains from European communities appear to be the most divergent."

The human polyomavirus, or JCV, is a small double-stranded DNA virus that is thought to be primarily transmitted from parents to their children. Infection is usually asymptomatic unless a person has a weak immune system, in which case the virus can cause neurological disease.

There are more than 14 subtypes of the virus, each primarily associated with different human populations such as African, Japanese, South Asian, and European. Population geneticists have assumed that the virus has been with humans since their emergence from Africa.

"Because of this presumed codivergence with human populations, JCV has been widely used as a genetic marker for human evolution and migration," explained Shackelton, whose findings appear this month (October) in the *Journal of Virology*.

The researchers note that while previous studies of genetic variation have observed some differences between the distribution of JCV and

human populations, the extent of the differences in their evolutionary histories has never been fully tested.

Shackelton and her colleagues analyzed 333 genetic sequences of the virus and reconstructed their evolutionary history. They then compared this history to the reconstructed history of human populations, based on mitochondrial DNA.

"If the virus had been with humans since we were a single population, and we have almost strictly transmitted it to our children, you may expect that as populations became isolated, the virus lineages diverged as well," Shackelton noted.

However, though both sets of data indicate a period of relatively constant population size followed by a rapid increase, a closer look reveals that while human populations started to expand considerably about 50,000 years back, the viral population expanded only in the last few hundred years.

"Besides, there are several instances of one population group harboring a subtype typically associated with another group," she said. "For example one finds viruses from the Japanese and Korean subtype in the European subtype group -- another incongruency."

If the virus had been strictly passed down from parent to child and had kept step with human migration, one would expect the various subtypes to group together geographically, she explains.

Shackelton added that if the co-evolution of the virus and human populations were as strict as previously thought one would not find so many differences in the family trees of the virus and humans.

Researchers also said that this study and others by the group suggest that

DNA viruses may not have a slow rate of evolution as previously thought, and that the viruses like JCV might in fact be evolving twice as fast.

Other researchers of the paper include Edward C. Holmes, Penn State University; Andrew Rambaut; and Oliver G. Pybus, University of Oxford, UK.

Source: Penn State