A new filovirus discovered from bats in China

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The family Filoviridae is divided into three genera: Ebolavirus, Marburgvirus and Cuevavirus. This classification is based on antigenic cross-reactivity, genome similarity, overlapping genes (number and patterns), and glycoprotein transcription process editing strategy.

In turn, Ebolavirus genus includes five viruses: Bundibugyo (BDBV), Ebola (EBOV), Reston (RESTV), Sudan (SUDV) and Taï Forest (TAFV). The genus Marburgvirus contains Marburg virus (MARV) and Ravn virus (RAVV). A single virus, Lloviu virus (LLOV), has been assigned to the genus Cuevavirus. Finally, two fish filoviruses were recently discovered.

Bats are known reservoirs of MARV and RAVV, whereas they are suspected reservoirs of ebolaviruses based on serology and viral genome detection.

Some scientists from China recently discovered and characterized a phylogenetically distinct bat filovirus, named Mènglā virus (MLAV). The coding-complete genome of MLAV shares 32–54% nucleotide sequence identity with known filoviruses. Phylogenetic analysis places this new virus between EBOV and MARV, suggesting the need for a new genus taxon.

The scientists analysed the cell tropism of this new filovirus by conducting infection studies with MLAV pseudo-types in cells originating from various mammalian species, in order to determine spillover and/or zoonotic potential. Primary and continuous cell lines derived from bats (Myotis davidii, Rousettus leschenaultia and Eonycteris spelaea), humans, monkeys, hamsters and dogs were tested for susceptibility with vesicular stomatitis virus (VSV)-based pseudo-types. MLAV glycoprotein-typed pseudo-types transduced cell lines derived from humans, monkeys, dogs, hamsters and bats, implying a broad species cell tropism with a high risk of interspecies spillover transmission.

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