

Early detection of highly pathogenic influenza viruses

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Lack of appropriate drugs and vaccines during the influenza A virus pandemic in 2009, the recent Ebola epidemic in West Africa, as well as the ongoing Middle Eastern Respiratory Syndrome-Coronavirus outbreak demonstrates that the world is only insufficiently prepared for global attacks of emerging infectious diseases and that the handling of such threats remains a great challenge.

Highly pathogenic avian [influenza viruses](#) of the H5N1-type represent one of the most serious threats for the human population. Although the virus has only occasionally been transmitted to humans yet, it results in diseases with a mortality rate of up to 60 percent. There are indications for the H5N1 viruses' mutation towards a more easy transmission to humans. This is especially true for Egypt, which could possibly become a potential epicenter of a new [influenza pandemic](#). A better understanding of the molecular basis of the evolution of IAV is therefore of outmost importance for an early detection of highly pathogenic IAV and the efficient fight and control of possible epidemic or even pandemic outbreaks. A multidisciplinary research team, including scholars from the Institute of Medical Virology at Justus Liebig University Giessen, has recently developed a tool, which is suitable to identify candidate pandemic influenza viruses circulating in animal hosts.

On the basis of a combined application of a computational technique (ISM) and experimental molecular virological methods, the research team from Germany and Serbia was able to develop and validate a new

tool to predict possible biological effects resulting from naturally occurring mutations as they are found for example in H5N1 viruses in Egypt. Thus, the ISM technique can help to identify those influenza viruses circulating in animal hosts that could efficiently transmit to humans and therewith possess a possible pandemic potential. The research team involves the Institute of Medical Virology (JLU), the Georg-Speyer-Haus—Institute for Tumor Biology and Experimental Therapy (Frankfurt am Main), the Robert-Koch-Institute, Division for HIV and other Retroviruses (Berlin) as well as the Centre for Multidisciplinary Research, Institute of Nuclear Sciences VINCA (Belgrade, Serbia).

In spite of various advances in the last years, there are still substantial gaps regarding the genetic information, epidemiology and pathobiology of H5N1-IAV in humans. "Our data opens the possibility to develop a new tool for the assessment of pandemic risks associated with specific influenza viruses", says Prof. Dr. Stephan Pleschka (Institute of Medical Virology at JLU), leading author of the study. "It could thereby provide a better preparation against potential pandemics. This especially concerns the development of a pre-[pandemic](#) vaccine, which might add to the prevention of the negative impacts of newly emerging influenza viruses."

More information: In Silico Prediction and Experimental Confirmation of HA Residues Conferring Enhanced Human Receptor Specificity of H5N1 Influenza A Viruses, *Scientific Reports* 5, Article number: 11434 [DOI: 10.1038/srep11434](https://doi.org/10.1038/srep11434)

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