# New PCR primer database to combat RNA viral epidemics

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Scientists at Korea's Daegu Gyeongbuk Institute of Science and Technology (DGIST) scientists have compiled a comprehensive new public database of genetic information to enable the detection and

identification of RNA viruses using the polymerase chain reaction (PCR) assay. The database should prove invaluable in combating potential future epidemics.

RNA viruses, which contain ribonucleic acid as their genetic material, cause many infectious diseases including influenza, polio and measles. In recent years, new and fatal diseases due to RNA viruses have emerged, notably severe acute respiratory syndrome (SARS) and Middle East respiratory disease (MERS), both of which had severe health and economic impacts.

The SARS epidemic emerged in southern China 2002. It killed 774 people in 37 countries, before its eventual control, while last year's MERS outbreak in Korea resulted in an estimated 40% reduction in foreign tourism, adversely impacting the national economy.

In both cases, the disease spread rapidly due to the slow and unreliable diagnosis of the responsible virus. When such outbreaks occur, accurate pathogen detection and identification is essential, in order to understand and control the disease, thereby minimizing its effects on public health.

PCR, which involves amplifying a section of DNA to generate thousands or millions of copies of a particular DNA sequence, is widely used for rapid and accurate viral identification, thanks to its low cost but high sensitivity and specificity.

PCR uses 'thermal cycling,' which entails repeated heating and cooling of the reaction for DNA melting and enzymatic (polymerase) DNA replication. Primers comprising a short strand of DNA, usually 18-22 nucleotide bases long, serve as a starting point for DNA synthesis, with the enzyme DNA polymerase enabling selective, repeated amplification.

However, very few online databases have compiled high-quality PCR

primers for RNA viruses and those that are available have certain limitations that restrict their usefulness.

To address this need, a research team led by Min-Soo Kim (Department of Information and Communication Engineering) and JaeHyung Koo (Department of Brain and Cognitive Sciences) at DGIST, have compiled a comprehensive new database of PCR primers, to enable the detection and identification of RNA viruses more rapidly and effectively. They reported their results in the November 29, 2016, edition of *Nucleic Acids Research*.

The new DGIST reference resource, the MTPrimerV database, contains 152, 380, 247 PCR primer pairs for the detection of 1,818 viruses, covering 7,144 gene-coding sequences or CDSs (from coding DNA sequence), which are the portion of a gene's DNA or RNA that codes for a protein.

These in silico primers are capable of detecting 100% of the RNA viruses included in the latest U.S National Center for Biotechnology Information Reference Sequence (NCBI RefSeq) database, an open access curated collection of DNA and RNA nucleotide sequences and their protein products.

Due to rigorous similarity testing against all human and viral sequences, every primer included in the MRPrimerV database (MRPrimerV.com) is extremely target-specific.

"We believe that the public availability of MRPrimerV will facilitate viral metagenomics studies aimed at evaluating the variability of viruses, as well as other scientific tasks, facilitating effective responses to potential epidemics," the DGIST researchers conclude.