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Japan supports precision prediction model for COVID-19 outcomes

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RIKEN's precision model algorithms designed to predict COVID-19 outcomes using THL's patient data and BCP's BC|INSIGHT

BC Platforms, a global leader in clinical and genomic data management, analytics and access, has announced that it has joined forces with Japan's RIKEN research institution and the Finnish Institute for Health and Welfare (THL), in an international research effort to support development of a precision prediction model to identify those most at risk from COVID-19.

RIKEN and THL play significant roles in Japan and Finland, respectively, in the fight against COVID-19, improving society's resilience to the coronavirus pandemic.

RIKEN has developed precise disease stratification algorithms using information geometry and artificial intelligence which is applicable to determine which people are at risk of mortality and aggravation from COVID-19.

THL leads a nationwide research project, COVIDprog, which collects samples and data from patients with positive COVID test results to support the identification of individual characteristics, including underlying genetic causes, which affect outcomes.

BC-Platforms is providing its BC|INSIGHT platform to enable the curation, integration and analysis of THL's clinical data of 300 to 1,000 Finnish COVIDprog research subjects using RIKEN's algorithms. This is to identify a 'COVID-19 prediction procedure' that can estimate symptoms and outcomes of COVID-19 based on health records of infected patients obtained before SARS-CoV-2 infection.

Other factors like, susceptibility and resistance to virus, role of innate and acquired immunity, influences of previous vaccinations, infections from other coronaviruses, the role of gut microbiota in the immune system, damaged by inappropriate use of antibiotics can also be identified. Multiple associations observed between outcomes and hypertension, diabetes, obesity and cardiovascular disease. Several genes have been identified from research on other coronaviruses, including ACE2 and TMPRSS2, which are directly involved in viral infection. This international collaboration aims to unpick these phenotypic and genetic associations to provide a better understanding of specifically why and how COVID-19 leads to mortality in some patients.