



isirv

**International Society for
Influenza and other
Respiratory Virus Diseases**

ISIRV Symposium at the 9th ESWI Conference, Valencia

**7.45am - 8.30am
Tuesday 19 September**

How Much Respiratory Viral Genome Sequencing Do We Need?

An open discussion session hosted by ISIRV

The 2020 global pandemic of SARS CoV2 resulted in significant progress in production of timely viral genomic data, requiring implementation of advanced laboratory technical capabilities. Over 170 countries developed whole genome sequence data, with close to 15 million viral sequences being made available for analysis through publicly accessible databases. The use of this data was important for understanding viral variation, but also provided challenges for data handling and quality assessment.

With de-escalation of the pandemic, it is an appropriate time to consider how much sequence data is needed on a regular basis to track changes in circulating respiratory viral pathogens of public health importance to support disease control measures. Affordability, sampling bias and data quality are issues which need consideration as we settle into 'new normal' national and international genomic surveillance programmes for seasonal influenza, SARS-CoV-2 and RSV.

Panel Chair | Maria Zambon, UK Health Security Agency

Panel | Each speaker will provide insights to stimulate a discussion and generate active engagement from the audience.

SARS CoV 2

John Paget, NIVEL Institute, Netherlands

INFLUENZA

John McCauley, The Francis Crick Institute, UK

RSV

Fernando Couto Motta, on behalf of WHO / Instituto Oswaldo Cruz, Brazil (recording)