**WHO consultation on COVID-19 new variants Knowledge gaps and research priorities; 12.01.2020**

**Agenda:**   
**-Plenary Sessions: Presentations**(1) Prof. Heyman: Objectives of the meeting  
(2) Oliver Morgan: Understanding the global spread of emerging SARS-CoV-2  
(3) Mark Perkins: SARS-CoV-2 and the pressures on the virus to evolve: what is known?  
(4) Maria von Kerkhove: Ongoing strategies for the monitoring and control of spread of emerging variants of SARS-CoV-2  
(5) Adolfo Garcia-Sastre: Animal models  
(6) Jake Dunning: Evidence on changes on disease severity and treatment approaches for pts infected with new variants  
(7) Phil Krause, WHO: vaccines and variants

**-Parallel Sessions: Working Groups**1/Epidemiology & mathematical modelling   
2/ Evolutionary biology   
3/ Animals models  
4/ Assays & Diagnostics  
5/ Clinical management & therapeutics  
6/ Vaccines

comment: WHO is planning to establish a biohub for international research, hosted by Switzerland.

| **Presenter; notes** | **slides** |
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| **Prof. Heyman: Objectives of the meeting** |  |
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| **Oliver Morgan:** **Understanding the global spread of emerging SARS-CoV-2** |  |
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| Over time: Predominance of G614 |  |
| No additional cases, no spread despite good surveillance, has disappeared from human population in Denmark |  |
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| VOC 202012/01:  Coinciding new mutations and S-deletions (useful for diagnostics) |  |
| Continuous spread in UK |  |
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| SAR in different counties: mostly elevated and in all age groups |  |
| No difference in hosp admission or case fatality |  |
| Reports from 46 countries by 11.01.2021 |  |
| In Denmark:  B.1.1.7 has become dominant |  |
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| 501Y.V2 1,5 times more transmissible, perhaps also due to immune evasion.  Severity issue not resolved yet. |  |
| 18 countries affected |  |
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| **Mark Perkins:**  **SARS-CoV-2 and the pressures on the virus to evolve: what is known?** |  |
| From February **2020:** |  |
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| Perhaps from i-compromised pt or undetected population |  |
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| **Maria von Kerkhove: Ongoing strategies for the monitoring and control of spread of emerging variants of SARS-CoV-2** |  |
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| Example of roll-out in Africa |  |
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| Recommendation for prioritization of sequencing |  |
| Platforms: nextrain, GISAID, pangolin |  |
| Standard nomenclature is needed and being worked on 🡪 working group this p.m. |  |
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| Working with R&D blueprint |  |
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| **Adolfo Garcia-Sastre:  Animal models** |  |
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| **Jake Dunning: Evidence on changes on disease severity and treatment approaches for pts infected with new variants** |  |
| SGTF = S-Gene target failure |  |
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| Brazil variant |  |
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| **Phil Krause, WHO:  vaccines and variants** |  |
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| **Breakout sessions** | **WORKING GROUPS** |
| **Group 1** | **Epi & Modelling** |
| **John Amuasi (chair)** | Neil Ferguson: “my greatest concern is the E484K – variant in Brazil. To be precise - B.1.1.28(K417N/E484K/N501Y)” <https://virological.org/t/spike-e484k-mutation-in-the-first-sars-cov-2-reinfection-case-confirmed-in-brazil-2020/584>  Andrew Hayward: “it is important to try to make and make sure the samples that are sequenced are representative of different settings e.g.- community, hospital, nursing homes - rater than biased towards outbreaks”  Oliver Morgan: 2 entry points to detect a VOC: sequencing detects an increasing proportion of a variant 🡪 what is the epi? --- OR: (as happened in the UK): unusual epi 🡪 is there a VOC behind?  Maria Clara Padovec: “The understanding of drivers of mutation leading to VOC is a priority to identify potential for stopping it” |
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| TOP priority: | National databases; longitudinal epi studies for cohorts (infected, never infected, …) |
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| **Group 2** | **Clinical characterization and management and therapeutics** |
| **John Marshall,**  **Lydon Patrick** |  |
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| TOP priority: | Future clinical trials, specific therapies |
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| **Group 3** | **Animal models** |
| **Dan Barouch** |  |
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| TOP priority: | Distribute viruses quickly around the world; resistance studies |
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| **Group 4** | **Assays and Diagnostics** |
| **Florian Krammer** |  |
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| TOP priority: | To get serum samples very rapidly |
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| **Group 5** | **Evolutionary biology** |
| **Malik Peiris**  In short order evolution of several new variants of relevance |  |
| Long branch length of some variants, e.g. UK variant, could suggest evolution under unusual condition.  First signal is mostly: epi or routine sequencing. How to standardize sampling? How putting together epi and sequence data?  Risk assessment: e.g. TIPRA (WHO), or IRAT (CDC).  Nomenclature: should not have a country’s name, but should be easy to capture for the public. |  |
| Sampling: might need something similar as the Global Influenza Surveillance Network. |  |
| TOP priority: | (1)establish GLOBAL surveillance system to monitor variants (use Influenza as model)  (2)nomenclature |
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| **Group 6** | **Vaccines** |
| **Phil Krause**  Many epitopes of vaccines might prevent drop of efficacy |  |
| Ecological studies: e.g. sewage.  Effectiveness might decrease gradually. |  |
| Global surveillance of high importance |  |
| TOP priority: | Global research agenda |

Last