Outline

- COVID-19 globally and in Africa
- COVIGen-SA update
- Challenges & Next steps
COVIGEN-SA
Coronavirus Host Genomics Study – South Africa

Total cases per country (as of 21 September 2021)

South Africa (28 October 2021)
2,921,114 cases
89,104 deaths
Case total by continent

Tests per thousand

- Africa
- Asia
- Europe
- North America
- South America
- UK
- USA
- South Africa
- Other African countries
Africa’s low burden

- Young demographic: Median age < 20 years old
- Warmer climate: Unfavorable conditions for viral spread
- Lower urban density: Numerous rural communities
- Trained immunity: From other vaccines like BCG
- Natural Selection: Increased frequency of protective alleles
- Past experience: Established infection control measures
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Aim

A platform for COVID-19 research that accounts for individual variability in the genetics and health backgrounds of Black South Africans, in line with a precision medicine approach.

Objectives

1. Establish a research resource of harmonised clinical and genetic data for a large sample of SARS-CoV-2 positive Black South Africans
2. Conduct a multi-approach investigation into host genetic factors affecting COVID-19 susceptibility and severity
Methodology

1. Network of partners
   - SBIMB
   - WCGMO
   - AHRI
   - Ezintsha
   - CRDI
   - PHRU
   - RHHT
   - VIDA

2. Participant recruitment
   - Study survey on clinical and demographic variables

3. COVIDen-SA research resource
   - DNA extraction from whole blood
   - Biobanked aliquots of DNA
   - Curated REDCap database

4. Planned host genetic studies on stratified participant groups
   - Exploratory genome-wide analyses
   - Targeted, whole exome, and whole genome sequencing
   - Critical COVID-19 illness
   - Moderate to severe illness
   - Reported infection (asymptomatic to mild illness)

Governance framework
- Cross-disciplinary collaborations
- Transparent and complete ethical adherence
- Data and sample sharing
- Public data accessibility
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- Total records: **1707**
- SARS-CoV-2 positive: **1080** (63%)
- Severe COVID-19: **221** (20%)
  (supplemental oxygen, ICU admission and/or ventilation)
- Asymptomatic or mild symptoms: **859**
- Genotyped: **576**
- Additional funded genotyping: **576**
Genotyping: Principal Component Analysis

572 individuals
1 517 137 SNPs following QC cutoffs:
• Missingness per SNP: 0.1
• Missingness per individual: 0.1
• Minor allele frequency: 0.05
• Hardy-Weinberg threshold: 0.0000001
• Autosomal markers only
Challenges and Next Steps

- Integrating phenotype data
- Increasing number of severe COVID-19 cases
- Resources for further genotyping
- Focus on partnerships and recruitment
- Publish cohort paper
- Analyze preliminary data
- Partner with other host genomics studies