# Establishing single cell sequencing capacity in Bangladesh to build a pediatric nasal mucosa atlas

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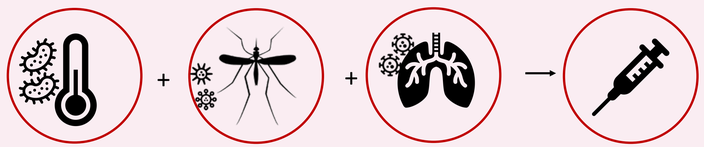
Child Health Research Foundation
CHRF Prevent Infections, Save Lives

## Child Health Research Foundation

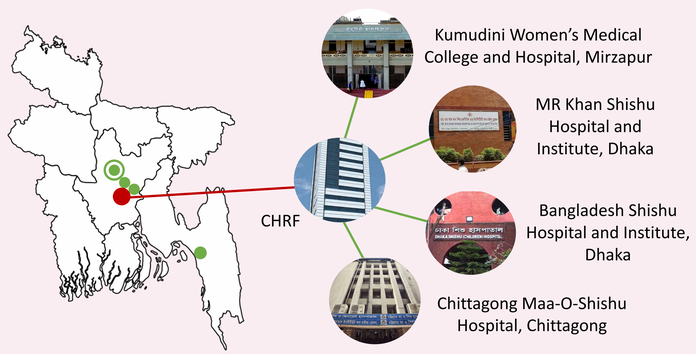


**Fever Investigation**
Sepsis, typhoid, paratyphoid, AMR...

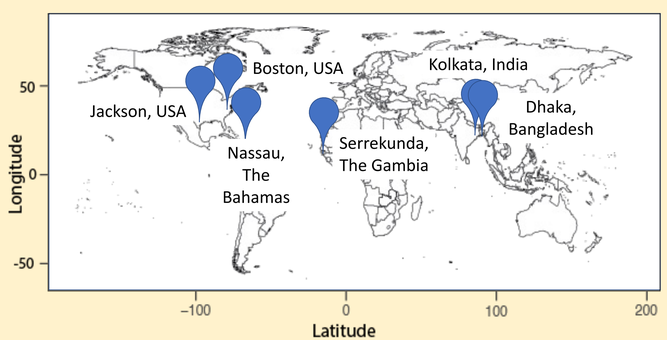
**Outbreak Investigation**
Dengue, Chikungunya, SARS-CoV-2

**Neurological & Respiratory infections**
Pneumococcus, Influenza, RSV
UNKNOWNS..

**Vaccines**
Facilitated Hib & pneumococcal vaccine introduction

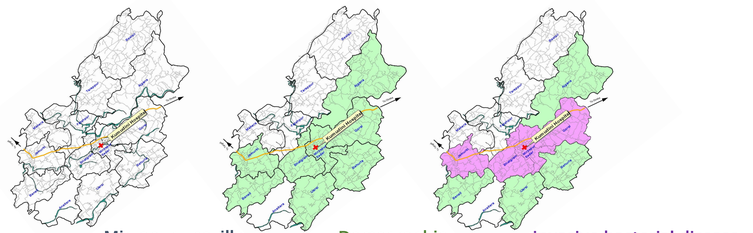



## A Global Pediatric Cell Atlas of Nasal and Oral Mucosa




## Sample collection at a rural community surveillance site at Mirzapur, Bangladesh

Mirzapur upazilla is a semi-urban area, 60 km north of Dhaka, where CHRF has been running a community surveillance since 2013



Mirzapur upazilla, Tangail District | Demographic Surveillance Site (DSS) | invasive bacterial disease-Vaccine preventable - surveillance (IB-VPD)

| Population | Mirzapur | DSS | IB-VPD |
|---|---|---|---|
| Total | 428,170 | 263,079 | 130,416 |
| Birth Cohort | 7,714 | 4,954 | 2,500 |
| <5 y | 38,953 | 26,116 | 13,342 |
| Union | 13 | 8 | 4 |

## Design of sample collection

- ❑ Village Health Workers identify children with symptoms of suspected respiratory infection
- ❑ Two nurses visit next day & collect nasopharyngeal sample
- ❑ Age/sex/geography matched health controls are selected by a biostatistician enrolled, and samples are collected collected
- ❑ Data regarding health condition, household information are collected from all
- ❑ All samples re stored in -70 $^{0}$C for processing at CHRF HQ

WHO case definition for community-based surveillance for RSV infections:
- shortness of breath; cough and/or
- sore throat and/or
- coryza

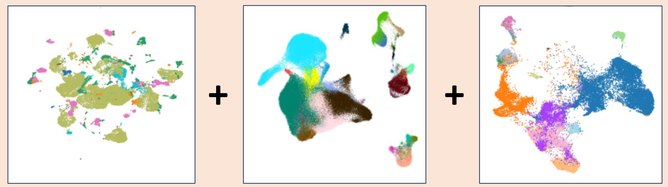
## Building computational capacity @CHRF

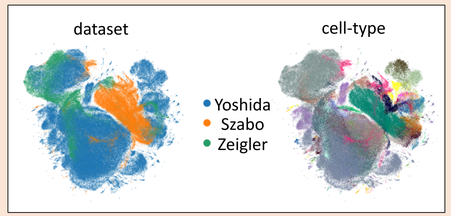
- Single-cell analysis requires robust computational skills; building on the genomic sequencing and analysis capacity @CHRF≈

Szabo et al, Immunity 2021
55,218 cells

Yoshida et al, Nature 2022
236,977 cells

Zeigler et al, Cell 2021
32,588 cells






Merged dataset = 324,783 cells (BBKNN, Polanski et al 2019)

## Next steps

- Complete sample collection (n=48) by November 2023 (n = 100)
- Undertake single cell capture and sequencing in-house using the Honeycomb HIVE kit and Nextseq2000
- Analyze data and compare with other sites, published datasets to build an atlas of nasal swabs
- The biggest challenge: Acquisition and price of reagents

## Acknowledgements


- Senjuti Saha & team, Child Health Research Foundation
- José Ordovas-Montanes & team, Boston Children's Hospital
- Bruce Horwitz & team, Boston Children's Hospital
- Alex Shalek & team, Massachusetts Institute of Technology
- All of other sites of the consortium

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