



APR 19, 2023

OPEN ACCESS

Protocol Citation: Katrina M Pollock, Calliope Dendrou 2023.

LEGACY01: INTRODUCTION.
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Protocol status: Working


Created: Jan 10, 2023

Last Modified: Apr 19, 2023

PROTOCOL integer ID:
75045

Keywords: Single-cell sequencing, lymph node, influenza vaccine, ancestry

LEGACY01: INTRODUCTION

 In 1 collection

Katrina M Pollock¹, Calliope Dendrou²

¹NIHR Imperial Clinical Research Facility, ICTEM Building, Hammersmith Hospital Campus, Du Cane Road, London W12 0HS UK;

²Wellcome Centre for Human Genetics, University of Oxford, Oxford OX3 7BN

Katrina M Pollock: Chief Investigator;
Calliope Dendrou: Scientific Lead

Human Cell Atlas Method Development Community



Katrina M Pollock

University of Oxford , Imperial College London

ABSTRACT

This protocol provides introduction to an experimental medicine study of seasonal influenza vaccination responses in Lymph nodeE single-cell Genomics in AnCestrY (LEGACY01).

ATTACHMENTS

[602-1266.docx](#)

GUIDELINES

BACKGROUND

The efficient development of vaccines effective against global and emerging pathogens is complicated by geographic differences in vaccine responsiveness. The relative contribution of genetic and environmental factors to differential immune responses after vaccination remains poorly defined and is complicated by the spectrum of immune cell types involved. The Lymph nodeE single-cell Genomics AnCestrY LEGACY01 study will create an ethnically diverse dataset with a single-cell atlas of lymph node (LN) and blood vaccine responses. Healthy volunteers of African and Asian ancestry who have immigrated to or were born in the UK will be invited to participate. They will be asked to donate blood and lymph node samples at specific timepoints pre- and post-immunisation. LN fine-needle aspirates (FNAs) will focus on the dynamics of germinal centre formation, capturing the interplay between lymphocytes, antigen-presenting cells and the stromal microenvironment. This will generate a curated data-structure of FNA single-cell (sc)RNA-seq, blood transcriptomic, cytometric, and serological analyses, with ethnicity, genetic, demographic and clinical metadata. To facilitate atlas utilisation and enable future international adoption of this approach, data, protocols and training materials will be

made open access.

RATIONALE FOR CURRENT STUDY

Recent infectious disease outbreaks, including the COVID-19 pandemic, have emphasized the critical need for rapid development of effective vaccines.¹⁻⁵ However, recognised variation in immune responses after vaccination across populations in different countries poses a barrier to progress, and it has yet to be determined whether this variation is due to differences in genetic background, in environmental influences including past or persistent antigenic exposure, and/or other poorly defined mechanisms.⁶⁻⁹ Despite this known variation, the majority of mechanistic studies investigating immune responsiveness to vaccines have focused on populations of white European ancestry.^{10,11} In the UK, this underrepresentation of ethnic minorities in vaccine experimental medicine research is at least partly due to vaccine hesitancy amongst these groups.¹²

A further challenge in addressing differences in vaccine response across populations is that studies have traditionally focused on the use of peripheral blood samples, even though inflammatory and germinal centre (GC) responses mounted in the draining LNs likely dictate vaccine priming efficiency and underpin protective efficacy.¹³ Ultrasound (US) guided FNA is a tractable and safe approach for LN sampling, and its use has recently demonstrated a good representation of cell subtypes found in excisional biopsies, including GC cells, thereby opening invaluable new routes for assessing vaccine efficacy in humans in vivo.¹⁴⁻¹⁷

The LEGACY01 clinical study will address this by creating a dataset of unstimulated and stimulated in vivo immune responses to a model, seasonal influenza vaccine, from participants with African and Asian ancestry.

ROLE OF THE PARTNER INSTITUTIONS

Imperial College London is the Sponsor for the study. Recruitment and study visits will be at the NIHR Imperial Clinical Research Facility, Hammersmith Hospital, Du Cane Road, London W12 0HS. Imperial College London and Imperial CRF will manage the study. The University of Oxford will receive and process samples and run laboratory analysis of blood and lymph node tissues led by Dr Calli Dendrou at the Wellcome Centre for Human Genetics. The Uganda Virus Research Institute will support establishment of a framework for delivering single-cell vaccine studies at international sites such as Uganda. Specifically, they will appoint and support the training of a visiting Clinical Research Fellow to the UK at Imperial College London and the University of Oxford. All centres will support the patient and public involvement and engagement activities of the study.

HUMAN CELL ATLAS

LEGACY01 is one of the Ancestry Networks for the Human Cell Atlas funded by the Chan Zuckerberg Initiative. The goal of these networks is to generate single-cell data

from ancestrally diverse tissue samples, which will be uploaded and made available as open access research data for the Human Cell Atlas¹⁸.

STUDY AIM, OBJECTIVES AND OUTCOME MEASURES

The aim of the study is to investigate human immune responses in lymph node cells before and after immunisation with a seasonal influenza vaccine

Primary objective: To generate a single cell atlas of lymph node cells before and after immunisation with seasonal influenza vaccine.

Secondary objective: To compare serum antibody responses before and after immunisation.

Exploratory: To compare immune responses in various immune compartments (e.g., blood and lymph nodes) against antigens including influenza before and after immunisation to help inform vaccine development and testing across different ethnicities.

Capacity building and training: To build capacity with respect to staff expertise and resource between the three partner institutions to support this project and future similar research.

Outcome measures may include but are not limited to the following assays:

1. Single cell RNA sequencing analysis of LNC and matched paired PBMC
2. Binding ELISA specific for influenza/A antigens e.g., haemagglutinin
3. Intracellular cytokine secretion or activation induced marker assay of PBMC and LNC
4. Genotypic assays such as HLA-testing.

REFERENCES

1. Huang C, Wang Y, Li X, et al. (2020) Clinical Features of Patients Infected With 2019 Novel Coronavirus in Wuhan, China. *Lancet* 395:497-506.
2. Petersen LR, Jamieson DJ, Powers AM, Honein MA (2016) Zika virus. *N Engl J Med* 374:1552-1563.
3. WHO Ebola Response Team (2014) Ebola virus disease in West Africa—the first 9 months of the epidemic and forward projections. *N Engl J Med* 371:1481-1495.
4. WHO Disease Outbreak News, <https://www.who.int/emergencies/disease-outbreak-news>
5. Ball P (2021) The lightning-fast quest for COVID vaccines – and what it means for other diseases. *Nature* 589:16-18.
6. Christy C, Pichichero ME, Reed GF, et al. (1995) Effect of gender, race, and parental education on immunogenicity and reported reactogenicity of acellular and whole-cell pertussis vaccines. *Pediatrics* 96:584-587.
7. Kurupati R, Kossenkova A, Haut L, et al. (2016) Race-related differences in antibody

- responses to the inactivated influenza vaccine are linked to distinct pre-vaccination gene expression profiles in blood. *Oncotarget* 7:62898-628911.
8. Haralambieva IH, Salk HM, Lambert ND, et al. (2014) Associations between race, sex and immune response variations to rubella vaccination in two independent cohorts. *Vaccine* 32:1946-1953.
 9. Sharma S, Hagbom M, Svensson L, Nordgren J (2020) The impact of human genetic polymorphisms on rotavirus susceptibility, epidemiology, and vaccine take. *Viruses* 12:324.
 10. D'Souza RS, Wolfe I (2021) COVID-19 vaccines in high-risk ethnic groups. *Lancet* 397:1348.
 11. Peng K, Safonova Y, Shugay M (2021) Diversity in immunogenomics: the value and the challenge. *Nat Methods* doi: 10.1038/s41592-021-01169-5.
 12. Razai MS, Osama T, McKechnie DGJ, Majeed A (2021) COVID-19 vaccine hesitancy among ethnic minority groups. *BMJ* 372:n513.
 13. Liang F, Lindgren G, Sandgren KJ et al. (2017) Vaccine priming is restricted to draining lymph nodes and controlled by adjuvant-mediated antigen uptake. *Sci Transl Med* 9:eaal2094.
 14. Cirelli KM, Carnathan DG, Nogal B et al. (2019) Slow delivery immunization enhances HIV neutralizing antibody and germinal center responses via modulation of immunodominance. *Cell* 177:1153-1171.
 15. Havernar-Daughton C, Carnathan DG, Torrents de la Peña A et al. (2016) Direct probing of germinal center responses reveals immunological features and bottlenecks for neutralizing antibody responses to HIV Env trimer. *Cell Rep* 17:2195-2209.
 16. Havernar-Daughton C, Newton IG, Zare SY et al. (2020) Normal human lymph node T follicular helper cells and germinal center B cells accessed via fine needle aspirations. *J. Immunol. Methods* 479:112746.
 17. Turner JS, Zhou JQ, Han J (2020) Human germinal centres engage memory and naïve B cells after influenza vaccination. *Nature* 586:127-132.
 18. <https://www.humancellatlas.org/>