Characterization of immune cell populations in response to SolaVAX\textsuperscript{TM} vaccine by single cell RNA sequencing

**Abstract**

SARS-CoV-2, the causative agent of COVID-19, is a global pandemic and to date, has caused more than 16.1 million infections and over 645,000 deaths. Therefore, the urgent need for vaccines prompted an international response, with more than 200 candidate anti-SARS-CoV-2 vaccines in development. However, no vaccine is licensed till date for human use. Our team at CSU developed a candidate vaccine, SolaVAX\textsuperscript{TM}, by using Riboflavin and UV light to selectively inactivate SARS-CoV-2 while preserving the integrity and antigenicity of its proteins. The vaccine proved to effectively reduce viral loads and immunopathology in the lungs of vaccinated hamsters. Here, we applied single-cell RNA sequencing (scRNA-seq) to characterize immune cell populations and transcriptional changes in lungs of Syrian Hamsters infected with SARS-CoV-2 after vaccination or not with SolaVAX\textsuperscript{TM} (with and without adjuvant). Our results dissected different immune cell populations, e.g., B cells, effector T cells, Dendritic cells, inflammatory Monocytes, NK cells, Macrophages, and neutrophils in the lungs of different groups. Compared to non-vaccinated hamsters, SolaVAX\textsuperscript{TM} vaccinated groups showed significant differences in the distribution of leukocyte populations infiltrating the lungs. Importantly, inflammatory genes were decreased in SolaVAX\textsuperscript{TM} vaccinated groups along with the SARS-CoV-2 viral loads. Vaccines work by targeting and preparing the immune system to rapidly respond upon exposure to similar antigens. However in the case of coronavirus infections like SARS-CoV-2, vaccines can also result in vaccine-induced immunopathology. Thus, a better understanding of vaccine-elicted protective vs deleterious immune responses is warranted and can be accomplished through the approach described herein.

**Experimental Plan**

- **SARS-CoV-2 infection:**
  - Challenge
- **RiboFlavin + UV light exposure:**
  - 90 min of exposure
- **Single cell RNA sequencing:**
  - scRNA-seq
- **Flow Cytometry Pathology:**
  - Annexin 1

**Results**

- **UMAP for different clusters**
- **Genes for identification of cell types for each cluster**
- **Percentage of cells in each cluster**

**Average log fold change gene expression of selected genes and SARS-CoV2 in non vaccinated and vaccinated groups**

**Summary**

- Inflammatory Monocytes, NK T cells and dendritic cells are significantly reduced in SolaVAX + CpG-1018 adjuvant group compared to non vaccinated group and vaccinated group without adjuvant.
- Genes for inflammasome, CCL4 and granzyme B is significantly reduced in group SolaVAX + CpG-1018 adjuvant compared to non vaccinated group.
- Annexin 1 is upregulated in SolaVAX + CpG-1018 adjuvant compared to non vaccinated group.
- CCR10 is highly upregulated in non vaccinated group compared to all other groups.
- IFITM complex genes are highly upregulated in SolaVAX + CpG-1018 adjuvant/ODN-1668 adjuvant group compared to non vaccinated and vaccinated non adjuvant in CD8\textsuperscript{T} cells.

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**References**