Sputum-Derived Cellular Profiles Produced by Flow Cytometric Analysis

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Squamous epithelial cells excluded from analysis via viability dye staining

- Sputum liquefaction using warmed NAC and DTT
- Nylon strainer filtration to collect single cell suspension
- Average cell yield per sputum sample: \(20 \times 10^6\) total cells
- Average cell viability per sample: 65%
- Average squamous epithelial cell (SEC) contamination: 20%

L. Bederka, et al., CYTO, 2020
Sputum-derived cellular profiles split into two lineages: leukocytes (CD45\(^+\)) and non-leukocytes (CD45\(^-\))

- Live cells
- Single cells
- CD45\(^+\) cells
- CD45\(^-\) cells

Sorted CD45\(^-\) population
- Bronchial epithelial cells

Sorted CD45\(^+\) population
- Alveolar macrophages

L. Bederka, et al., CYTO, 2020
We chose to investigate whether sputum can be analyzed on a flow cytometry platform analogous to its use for the diagnosis of hematologic malignancies.

Sputum donors used the acapella® airway assist device (Smiths Medical) to collect sputum over a 3-day period.

Samples were processed into a single cell suspension and analyzed efficiently by flow cytometry.

Reproducible profiles of sputum for both the leukocyte and non-leukocyte lineages were obtained.

The presence of both alveolar macrophages and bronchial epithelial cells indicate that the sputum sample represented the environment of the lung.

Our data reveals that flow cytometers can analyze samples isolated from sputum in a high-throughput manner that can be developed for diagnostics of lung health.