Towards an image-based analysis and separation of neutrophils from whole blood

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In life science, the processing and analysis of cells in microfluidic systems is a well-established field. Nevertheless, sensitive or precious cell samples suffer serious drawbacks when sorted by standard high throughput cell sorting techniques associated with high shear stresses, biochemical perturbations or low recovery rates.

Of importance is the case of neutrophiles, which represent a heterogeneous cell population that is inherently unstable ex vivo and is rapidly activated by many common methods of sample preparation and sorting. These factors hamper the progress in understanding this subset of circulating leukocytes[1,3].

Here we present a microfluidic system for a gentle, image- based processing of neutrophiles of human origin based on dielectrophoresis (DEP) [2,4] from a single human drop of blood as loading sample. The aim of this work is to maximize two key parameters: the neutrophil viability after sorting from a heterogenous leukocyte population in comparison with unprocessed cells, and the final total target cell recovery. To achieve this, we abstain from labeling the neutrophiles with fluorescent labeled antibodies to mitigate neutrophile activation[1,3]. Instead we use sorting protocols based on negative selection and – in future - also morphological patterns. Furthermore, we optimize sheath flow velocity, exposure time, DEP-electrode controls and voltage and use a mild sample preparation to decrease neutrophil perturbation. In future, this will lead to a simple and robust system that enables analysis and sorting of this cell population comparable to other commercial techniques.

Words: 234

References:

[1]Ashley N. Connelly et al., Scientifc Reports | (2022) 12:3667

[2] N. Godino et al., Lab Chip, 2019, **19**, 4016–4020.

[3] Andrea Cossarizza et al., Eur. J. Immunol. 2019. 49: 1457–1973

[4] Tobias Gerling et al., Lab Chip, 2023, 23, 3172