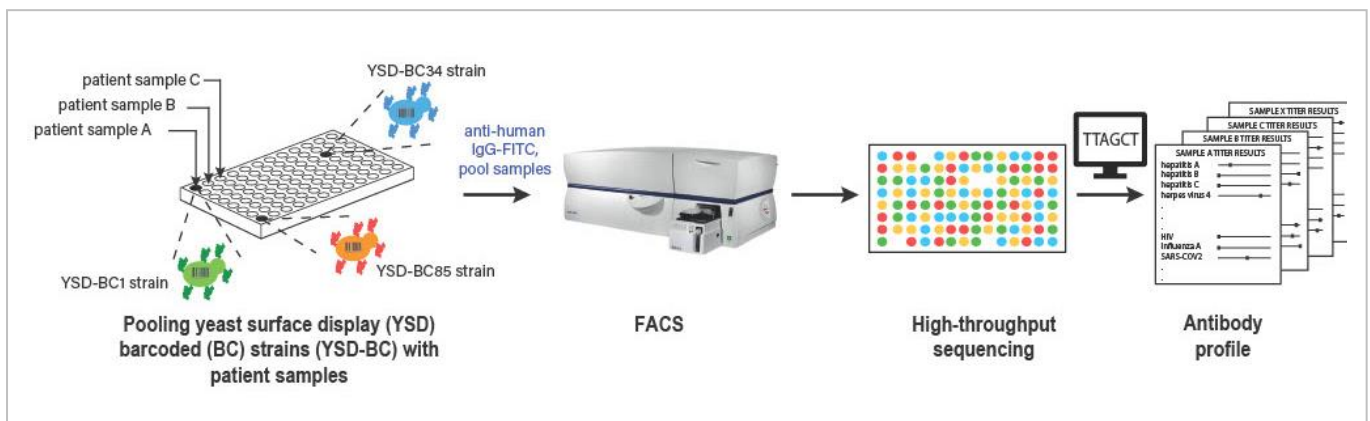




Multiplexed Serology for the quantification of antibodies against antigens of interest

Technology Offer

Ref. No.: 1001-22



Category

Diagnostic, Serology,
Antibody profiling

Keywords

Multiplexed serology,
antibody quantification
and titer determination

Development stage

PoC in vitro

Seeking

Licensing / collaboration

IP status

PCT application pending
(filing date 11.07.2024)

Background

Antibodies are a highly diverse group of Y-shaped proteins that bind and neutralize foreign substances (e.g. bacteria or viruses), constituting one of the most important weapons of the immune system. Moreover, antibodies have been playing a major role in research, industry and medicine for decades. Antibodies are used as diagnostic tools of infections, cancer, and autoimmune diseases, but they also play a central role as therapeutic agents.

Accordingly, there is a great interest in the biomedical field to identify and quantify antibody diversity, also known as antibody profiling, as it can be used to answer immunological research questions, develop novel diagnostic procedures or therapies. Unfortunately, current methods used for antibody profiling including the Luminex Technology, are expensive and time-consuming, as they require the expression, purification and crosslinking of antigens of interest to a specific matrix (e.g. beads).

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Technology

The technology enables a multiplexed serology based on the innovative combination of barcoded yeast-surface-display libraries, cell-sorting and Next-Gen Sequencing. This technology enables the simultaneous quantification of hundreds of antibodies in hundreds of samples in one single run.

The multiplexing capabilities of this technology are achieved by the use of thousands of barcoded yeast strains that are used to encode antigens and patient samples. The quantitative capabilities achieved by this technology are attributed to: a) the physical separation of single yeast cells (cell-sorting) bound to a variable number of antibodies into fluorescence intensity bins, where the antibody concentration in the sample is proportional to the magnitude of the fluorescent signal, and b) the utilization of deep-sequencing technology, enabling the retrieval and deconvolution of DNA barcodes within complex DNA libraries.

Benefits

- Multiplexed capabilities that make possible the simultaneous quantification of antibodies targeting different antigens in one or more samples.
- Antigens are expressed in a eukaryotic environment supporting protein folding and post-translational modifications
- Antigens are exposed at the yeast cell surface, reason why antigens do not need to be purified or cross-linked to any support material (e.g. beads)

Applications

- **Quantitative serology:** quantification of antibody titer for one or multiple antigens in one or more patients (Multiplexed analysis at the sample and/or antigen level).
- **Diagnostic tool:** Screening of patient samples (blood, plasma, serum, etc) for large panels (hundreds up to thousands) of disease-related antibodies (e.g. autoantibodies, antibodies targeting neopeptides or tumour antigens, etc).

Publications

- Meurer, M., Duan, Y.Q., Sass, E., Kats, I., Herbst, K., Buchmuller, B.C., Dederer, V., Huber, F., Kirrmaier, D., Stefl, M., et al. (2018). Genome-wide C-SWAT library for high-throughput yeast genome tagging. *Nat Methods* 15, 598-600.
- Kats, I., Khmelinskii, A., Kschonsak, M., Huber, F., Kniess, R.A., Bartosik, A., and Knop, M. (2018). Mapping Degradation Signals and Pathways in a Eukaryotic N-terminome. *Mol Cell* 70, 488-501.
- Boder, E.T., and Wittrup, K.D. (1997). Yeast surface display for screening combinatorial polypeptide libraries. *Nat Biotechnol* 15, 553-557.
- Khmelinskii, A., Knop, M. (2014). Analysis of protein dynamics with tandem fluorescent protein timers. *Methods Mol Biol.* 1174:195-210.
- Wang, E. Y., Dai, Y., Rosen, C. E., Schmitt, M. M., Dong, M. X., Ferré, E. M. N., Liu, F., Yang, Y., González-Hernández, J. A., Meffre, E., Hinchcliff, M., Koumpouras, F., Lionakis, M. S., and Ring, A. M. (2022). High-throughput identification of autoantibodies that target the human exoproteome. *Cell Rep Methods*, 2(2), 100172.

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