

Brownian Motor Based Virus Detection

Rendicontazione

Informazioni relative al progetto

MoViD

ID dell'accordo di sovvenzione: 825794

DOI 10.3030/825794

Progetto chiuso

Data della firma CE 15 Novembre 2018

Data di avvio 1 Gennaio 2019 Data di completamento 30 Giugno 2020 **Finanziato da** EXCELLENT SCIENCE - European Research Council (ERC)

Costo totale € 150 000,00

Contributo UE € 150 000,00

Coordinato da IBM RESEARCH GMBH Switzerland

Periodic Reporting for period 1 - MoViD (Brownian Motor Based Virus Detection)

Periodo di rendicontazione: 2019-01-01 al 2020-06-30

Sintesi del contesto e degli obiettivi generali del progetto

The detection of dilute populations of nanoparticles in microfluidics is difficult due to diffusion as the time limiting step to reach the sensor. Using active transport, we propose to build a proof of concept microfluidic device that reaches sub-attomolar detection sensitivity within an hour and at a device footprint of 1 cm. The active transport enables size separation of the particles into multiple channels and up-concentration in detection reservoirs for label free detection. At the end of the process the

size-separated particles can be easily extracted for further downstream processing.

The applied use case is the detection and quantification of virus in drinking water, a global healthcritical challenge. A viral concentration of 10-100 particles is infectious in 2l of water consumed by a person, corresponding to a concentration of 10^(-22) molar. Traditional methods rely on multiple concentration steps followed by detection using molecular and/or culture based methods. Most common are adsorption/elution assays which co-concentrate and add contaminations that interfere with the downstream detection analysis. The detection methods are also often specific for the viral type and require a priori identification of the target virus. Metagenomic sequencing allows for general identification but lacks sensitivity.

The proposed method will simplify and improve the process significantly. The viruses will be concentrated without damage of the virus shell and with a high rejection of the contamination present in the sample. All virus particles will be separated and sorted according to predefined size ranges into detection compartments on the chip, allowing for a parallel and quantitative marker-less detection on a single particle level. Specific identification is possible for future devices using (integrated) molecular methods with reduced cross-contamination and without a priori virus identification.

Ultimo aggiornamento: 6 Maggio 2024

Permalink: https://cordis.europa.eu/project/id/825794/reporting/it

European Union, 2025