

Single cell biotechnology to shed a light on biological 'dark matter' in nature

Wei E. Huang,^{1*} Yizhi Song² and Jian Xu³

¹Department of Engineering Science, University of Oxford, Parks Road, Oxford OX1 3PJ, UK.

²Kroto Research Institute, University of Sheffield, Broad Lane, Sheffield S3 7HQ, UK.

³Single-Cell Center, CAS Key Laboratory of Biofuels and Shandong Key Laboratory of Energy Genetics, Qingdao Institute of Bioenergy and Bioprocess Technology, Chinese Academy of Sciences, Qingdao 266101, China.

It is estimated that over 99% of microorganisms have not as yet been cultivated (Whitman *et al.*, 1998). These uncultured microbes are the 'dark matter' of the microbiological world and play important roles in natural ecosystems and the human microbiome (Lagier *et al.*, 2012; Rinke *et al.*, 2013); however, their ecological role and function remain largely elusive (Lasken, 2012; Li *et al.*, 2012a,b). Furthermore, these uncultured bacteria represent a significant, yet largely untapped, genetic resource for use in synthetic biology for the provision of novel bioparts or biobricks, in medicine for new drug biosynthesis, in industry for robust biocatalysts and biofuel synthesis, and in environmental bioremediation for new biodegradation genes.

Metagenomics circumvents the cultivation issue by extracting the total DNA from an environmental sample, and directly sequencing it (Handelsman, 2004), and this approach has revealed an unprecedented view of the diversity and complexity of microbial communities. However, such approaches are usually unable to define or validate the specific role of individual members of the usually complex microbiota. Single cell biotechnology, which characterizes microbial cells in their native microbiota one by one, offers a new approach to study uncultured bacteria. An ideal platform is to integrate accurate and 'contamination-free' single cell sorting tools with powerful next-generation DNA sequencing. This will usher

in a new area of single cell omics (genomics, transcriptomics, proteomics and metabolomics).

For single cell biotechnology, there are a number of key challenges: non-invasive and *in-vivo* cell analysis, the linking of cell phenotypes to specific ecological functions (e.g. substrate metabolism), overcoming limitations in measurement parameters, systematic differentiation of the given 'state' or phenotype of a cell and isolation of live single cells from complex samples *in-situ*.

Among the various single cell sorting techniques (Lasken, 2012; Li *et al.*, 2012a,b), an emerging approach is Raman-activated cell sorting (RACS), which overcomes the requirement for external labelling. Single cell Raman spectra (SCRS) provide a label-free, non-invasive and intrinsic phenotypic profile of individual cells which can be used to characterize cell type, physiological state and cell functionalities (Huang *et al.*, 2004; 2007a,b,c; Harz *et al.*, 2009; Li *et al.*, 2012a,b; Wang *et al.*, 2014). A typical SCRS provides an intrinsic chemical 'fingerprint' of a single cell, and usually contains multi-parameter (> 1000 readings) including rich information on nucleic acids, protein, carbohydrates and lipids (Li *et al.*, 2012a,b). Since SCRS measures the vibration of molecular bonds, it is sensitive to stable isotope compounds and SCRS undergoes Raman shift when cells incorporate stable isotope compounds (e.g. ¹³C-, ¹⁵N-substrates or ²H from heavy water D₂O) into the cell's building blocks (e.g. DNA, lipids, protein or carbohydrate) (Huang *et al.*, 2004; 2007a,b,c; Wang *et al.*, 2013). SCRS offers a unique way to link cells to specific functions (e.g. C/N metabolism and metabolic activity) and to define cells of interest at a single cell level. A RACS system consists of a SCRS detection system and a cell isolation system that can be optical tweezers (Huang *et al.*, 2009), a microfluidic device (Li *et al.*, 2012a,b) or a single cell ejection system (Wang *et al.*, 2013).

RACS would identify cells of interest and isolate them for downstream single cell omics analysis. The isolated single cells would be processed on microfluidic chips for DNA/RNA extraction and amplification. The DNA/RNA can then be quantified or sequenced to decode the genomes or transcriptomes of the particular cells. Such a platform directly establishes the links between genotype and phenotype of individual cells, thus offering unprecedented opportunities to study how variability of environmental and genetic impacts on the phenotype of single cells.

Received 4 November, 2014; accepted 4 November, 2014. *For correspondence. E-mail wei.huang@eng.ox.ac.uk; Tel. 01865 283786; Fax 01865 374992.

Microbial Biotechnology (2015) 8(1), 15–16
doi:10.1111/1751-7915.12249

Funding Information This work is funded by EPSRC flashlight of Synthetic Biology EP/H-4986X/1 and EPSRC Fellowship EP/M002403/1.

Single cell biotechnology will not only be a powerful tool to microbiology, but also herald single cell biology as a new frontier of cell biology. A single cell is the basic functional unit of life and all living organisms start from single cells. Learning how cells work by studying the individual cell is an important component of cell biology and single cell technology promotes a deeper understanding of cell biology. Recent research from the studies of single cells reveals that individual cells within the same population may differ dramatically in function, and these differences have profound biological implications, ranging from bacterial physiology to embryonic cell development, tissue differentiation, cancer cell formation and evolution.

In summary, during the next decade, just like DNA sequencing, single cell biotechnologies are expected to rapidly move into bench tops of biology laboratory, and to permeate all branches of life sciences and biotechnology. They promise to uncover fundamental biological principles and ultimately improve the diagnosis and treatment of diseases, unravel the ecological role of bacteria in soils, plants and humans, and promote the discovery of new gene functions for use in industry.

Conflict of interest

None declared.

References

- Handelsman, J. (2004) Metagenomics: application of genomics to uncultured microorganisms. *Microbiol Mol Biol Rev* **68**: 669–684.
- Harz, A., Rosch, P., and Popp, J. (2009) Vibrational spectroscopy – a powerful tool for the rapid identification of microbial cells at the single-cell level. *Cytometry A* **75A**: 104–113.
- Huang, W.E., Griffiths, R.I., Thompson, I.P., Bailey, M.J., and Whiteley, A.S. (2004) Raman microscopic analysis of single microbial cells. *Anal Chem* **76**: 4452–4458.
- Huang, W.E., Bailey, M.J., Thompson, I.P., Whiteley, A.S., and Spiers, A.J. (2007a) Single-cell Raman spectral profiles of *Pseudomonas fluorescens* SBW25 reflects in vitro and in planta metabolic history. *Microb Ecol* **53**: 414–425.
- Huang, W.E., Stoecker, K., Griffiths, R., Newbold, L., Daims, H., Whiteley, A.S., and Wagner, M. (2007b) Raman-FISH: combining stable-isotope Raman spectroscopy and fluorescence in situ hybridization for the single cell analysis of identity and function. *Environ Microbiol* **9**: 1878–1889.
- Huang, W.E., Ude, S., and Spiers, A.J. (2007c) *Pseudomonas fluorescens* SBW25 biofilm and planktonic cells have differentiable Raman spectral profiles. *Microb Ecol* **53**: 471–474.
- Huang, W.E., Ward, A.D., and Whiteley, A.S. (2009) Raman tweezers sorting of single microbial cells. *Environ Microbiol Rep* **1**: 44–49.
- Lagier, J.C., Armougom, F., Million, M., Hugon, P., Pagnier, I., Robert, C., et al. (2012) Microbial culturomics: paradigm shift in the human gut microbiome study. *Clin Microbiol Infect* **18**: 1185–1193.
- Lasken, R.S. (2012) Genomic sequencing of uncultured microorganisms from single cells. *Nat Rev Microbiol* **10**: 631–640.
- Li, M., Xu, J., Romero-Gonzalez, M., Banwart, S.A., and Huang, W.E. (2012a) Single cell Raman spectroscopy for cell sorting and imaging. *Curr Opin Biotechnol* **23**: 56–63.
- Li, M., Ashok, P.C., Dholakia, K., and Huang, W.E. (2012b) Raman-activated cell counting for profiling carbon dioxide fixing microorganisms. *J Phys Chem A* **116**: 6560–6563.
- Li, M., Canniffe, D.P., Jackson, P.J., FitzGerald, S., Dickman, M.J., Davison, P.A., et al. (2012b) Rapid resonance Raman micro-spectroscopy to probe carbon dioxide fixation by single cells in microbial communities. *ISME J* **6**: 875–885.
- Rinke, C., Schwientek, P., Szyrba, A., Ivanova, N.N., Anderson, I.J., Cheng, J.-F., et al. (2013) Insights into the phylogeny and coding potential of microbial dark matter. *Nature* **499**: 431–437.
- Wang, T., Ji, Y., Wang, Y., Jia, J., Li, J., Huang, S., et al. (2014) Quantitative dynamics of triacylglycerol accumulation in microalgae populations at single-cell resolution revealed by Raman microspectroscopy. *Biotechnol Biofuels* **7**: 58.
- Wang, Y., Ji, Y., Wharfe, E.S., Meadows, R.S., March, P., Goodacre, R., et al. (2013) Raman activated cell ejection for isolation of single cells. *Anal Chem* **85**: 10697–10701.
- Whitman, W.B., Coleman, D.C., and Wiebe, W.J. (1998) Prokaryotes: the unseen majority. *Proc Natl Acad Sci USA* **95**: 6578–6583.