



Contents lists available at ScienceDirect

## International Journal of Food Microbiology

journal homepage: [www.elsevier.com/locate/ijfoodmicro](http://www.elsevier.com/locate/ijfoodmicro)



# Individual cell heterogeneity in Predictive Food Microbiology: Challenges in predicting a “noisy” world



Konstantinos P. Koutsoumanis\*, Zafiro Aspidou

*Laboratory of Food Microbiology and Hygiene, Department of Food Science and Technology, School of Agriculture, Forestry and Natural Environment, Aristotle University of Thessaloniki, Thessaloniki 54124, Greece*

### ARTICLE INFO

#### Article history:

Received 10 March 2016

Received in revised form 13 June 2016

Accepted 19 June 2016

Available online 21 June 2016

#### Keywords:

Gene expression

Noise

Single cell

Time lapse fluorescence microscopy

Predictive Microbiology

Complexity

### ABSTRACT

Gene expression is a fundamentally noisy process giving rise to a significant cell to cell variability at the phenotype level. The phenotypic noise is manifested in a wide range of microbial traits. Heterogeneous behavior of individual cells is observed at the growth, survival and inactivation responses and should be taken into account in the context of Predictive Food Microbiology (PMF). Recent methodological advances can be employed for the study and modeling of single cell dynamics leading to a new generation of mechanistic models which can provide insight into the link between phenotype, gene-expression, protein and metabolic functional units at the single cell level. Such models however, need to deal with an enormous amount of interactions and processes that influence each other, forming an extremely complex system. In this review paper, we discuss the importance of noise and present the future challenges in predicting the “noisy” microbial responses in foods.

© 2016 Elsevier B.V. All rights reserved.