

# Meta-analysis for Quantitative Microbiological Risk Assessment

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## INTRODUCTION

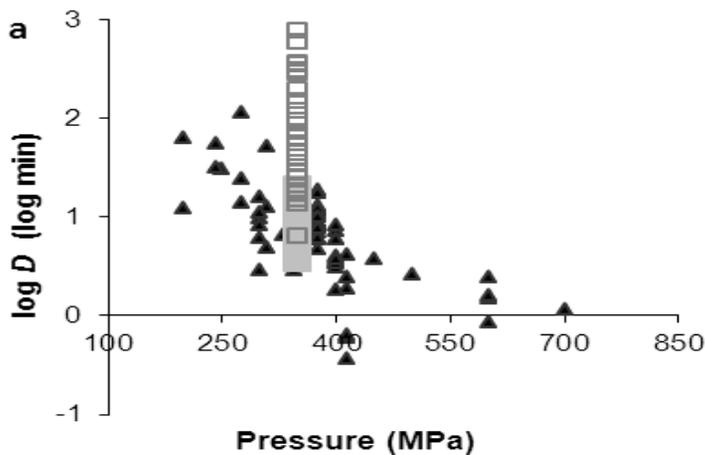
Quantitative Microbiological Risk Assessments (QMRA) are more and more used for food safety legislation, microbiological criteria and specifications, food safety control, justification of measures, and to obtain insight in most important phenomena responsible for the risks of foodborne diseases. QMRAs are very data demanding, and need to be supplied with data that are representative for the cases under study. However, except for the quantitative value of certain properties, also the variability of the data needs to be determined, since most technological, biological and behaviour factors are largely variable. Generally specific studies do not cover broad enough data to be sufficiently generic, therefore meta-analyses might be used to produce sufficiently extensive data. The objective of the study is to describe a method to determine appropriate input data for QMRAs being sufficiently generic and including appropriate measures of the corresponding variability. Apart from supplying this information, the gathered data can also be used very effectively for bench-marking.

## MATERIALS & METHODS

For specific values needed to describe microbial behaviour, a literature search is performed and all quantitative data are entered in a database including relevant quantitative and qualitative descriptors of the specific study. The data are then analysed for main factors and clustered to obtain global parameters (with their variability) and more specific parameters (with their variability). Furthermore the datasets are used to compare newly gathered data under specific conditions, to see the relevance of the effect of these conditions (bench-marking).

## RESULTS & DISCUSSION

Large data sets for irradiation parameter  $D_{10}$  [1] concentration of contaminants in air in various factory environments [2] sedimentation velocities of micro-organisms [2], thermal inactivation parameters [3], and high hydrostatic pressure inactivation parameters [4] were successfully gathered and evaluated. Main influencing factors could be identified and global and more specific estimations of the parameters with their attendant variability could be estimated. Both for thermal inactivation and high hydrostatic pressure inactivation data, new literature information could be easily benchmarked against the data in the database, showing the relevance of the studied effects in these studies. As an example in Figure 1 the decimal reduction time for HHP-inactivation of *Listeria* spp. from literature are shown as function of the pressure, and a new set of data of HHP inactivation of selected variants [5] both from stationary and exponential phase precultures are shown. It is clear that the exponential phase cells have comparable inactivation rates as the data from the literature dataset, while the stationary phase cells clearly have higher D-values and are thus more resistant towards HHP-inactivation.



**Figure 1.** HHP inactivation (350 MPa, 20 °C, ACES buffer) log  $D_p$ -values of HHP resistant variants [5] of *Listeria monocytogenes* LO28, (◻) stationary cells, (◼) exponential cells; and all log  $D_p$ -values corresponding to *Listeria* spp. collected (▲) plotted against pressure.

## CONCLUSION

Meta-analysis is an emerging methodology in the area of food microbiology to systematically and critically collate a large number of individual studies and to quantitatively integrate their findings resulting into global parameter estimates and their corresponding variabilities. The differences between individual studies can contribute to rather high variabilities of parameter estimates, allowing to make conclusive separations of main effects. The data supply generic estimates of values with their attendant variability, very productive as input values for QMRAs. Furthermore data gathered for meta-analysis can be very fruitfully used to benchmark newly gathered data.

## REFERENCES

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