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Background

Lactiplantibacillus pentosus is one of the most frequently isolated lactic acid bacteria from table olives fermentations

(<https://doi.org/10.3390/foods9070948>) and is used as a starter for this and other vegetable fermentations because of its tolerance of salt and phenolics and its ability to ferment a large variety of sugars. We sequenced the genomes of 29 strains obtained from samples of table olives analysed during the METAolive project. In this study we are reporting on the modelling of the effect of NaCl on their growth in MRS broth.

Methods

Stationary phase cultures were used to inoculate MRS with 0-9% NaCl in microtiter plates. Growth curve data were collected at 25°C using a Varioskan multiplate reader with SkanIt software. A R script was used for graphical and statistical analysis using variations of the Baranyi and Roberts D-model. A secondary model (the 2 point cardinal model of the nlsMicrobio package) was then used to model the effect of NaCl on maximum specific growth rate (μ_{max})

Results

The best fitting primary models (selected automatically on the basis of lowest AIC) were the complete D-model or variations of the biphasic model (without lag phase or without stationary phase). The maximum specific growth rate under optimal conditions (usually 0 % NaCl) varied significantly among strains (0.6-1.2 h⁻¹). Most strains were still able to show significant growth at 6% NaCl and some did grow at 9% NaCl, while a few strains were unable to grow at this NaCl concentration. Unfortunately estimates of the maximum NaCl concentration had a high standard error.

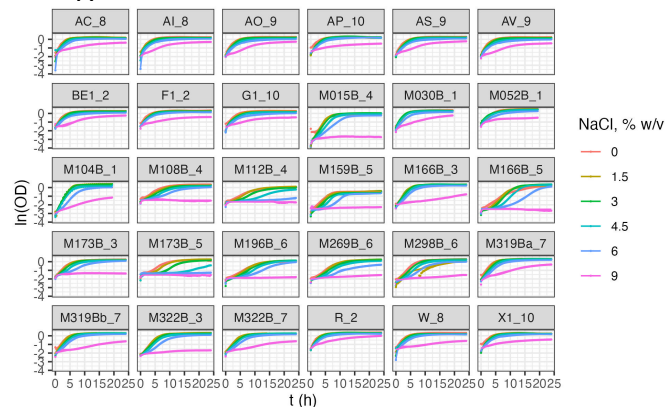


Fig 1. Fitted values for the growth curves of *Lpl. pentosus* strains. For some strains 2 replicates were used.

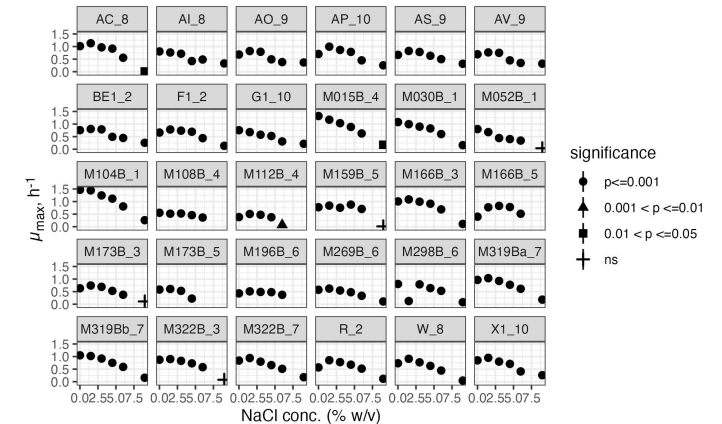


Fig 2. Fitted μ_{max} values as a function of NaCl concentration

Conclusions

We developed a rapid screening method for modelling the growth of *Lpl. pentosus* in microtiter plates. Further work to model the growth in synthetic brines and model green olive brines. As genomic data become available we plan to correlate the results with genes related to osmotic/salt stress response.

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