# Effect of the inoculum characteristics on the first stages of a growing yeast population in beer fermentations by means of an Individual-based Model

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The budding yeast *Saccharomyces cerevisae* has a limited replicative lifespan. The cell mass at division is unequally partitioned between a bigger, old parent cell and a smaller, new daughter (virgin) cell. Industrial fermentation performed to produce beer is the unique within the alcoholic beverage industry in that the yeast is maintained and reused a number of times. At the end of fermentation a portion of the yeast is 'cropped' from the fermentation vessel for 'serial repitching'. Typically this is the centre-top portion of the yeast crop, theoretically comprising middle-aged and virgin cells. However, increasingly yeast is removed early to decrease process time via a 'warm' or 'early' cropping regime and this facilitates removal of the lower portion of the crop, comprising a greater proportion of aged cells. Harvesting yeast may therefore select a population with an imbalance of young and aged individuals. In fact, the output of a bioprocess is strictly dependent on the physiology of each single cell in the population, on the distribution of the cells throughout the cell cycle and on the effects of environmental conditions on the population. Unlike continuous models, Individual-based Modelling (IbM) is a bottom-up approach, meaning that it considers each microbe as an individual, a unique and discrete entity, with more than one characteristic that changes throughout its life. IbMs are in an increasingly established approach to diverse microbial communities and their use is also becoming more widespread in food microbiology. Of those available we have used INDISIM, the simulator developed by our group, and which has already been used to study different features of bacterial growth, providing an ample pool of interesting results [1]. INDISIM-YEAST constitutes the adaptation of INDISIM to study the specific characteristics of the yeast cell cycle and to deal with yeast populations growing in liquid media [2]. The aim of this contribution is, by means of individual-based simulations of INDISIM-YEAST, to explore the effects of inoculum size and cell genealogical age on the dynamics of the yeast fermentation, focusing on: i) the lag phase and the first stages of yeast population growth, ii) the rate of glucose uptake and ethanol production, and iii) biomass and genealogical age distributions, in order to be able to integrate these results and to improve the understanding of the composition of yeast population and its temporal evolution in fermentation. This simulator provides, from a previous simulation of a yeast fermentation, a complete virtual characterization of a pre-inoculum to be used in this study. From this we remove the inocula for the ensuing simulations, combining different inocula sizes (i.e., from 1 to 1000 cells) and genealogical age distributions (i.e., virgin (daughter) cells with 0 scars, young parents cells with 1 to 5 scars and old parent cells with more than 5 scars). Fifty independent simulations of each combination were performed, taking a new inoculum with specified characteristics from the pre-inoculum each time. All these simulation results show there is an influence of these initial features of the inocula on the classic lag parameter, defined at the population level of description and calculated through its geometrical definition, and on the first division time or time until the first budding reproduction appears, defined at an individual level of description. Only slight discrepancies on maximum growth rate (exponential phase) are observed. Also, our simulation results show that the initial conditions of the seed yeast cells influence also the rate of nutrient uptake and ethanol production. Moreover, the evolutions of the biomass and genealogical age distributions during the first stages of growth are dissimilar and depend on the initial configuration of the inocula. In this way, we can compare and contrast both the individual and global properties of yeast cells and populations at chosen time steps during simulated growth. This can offer useful insight to improve understanding of the macroscopic behaviour observed in experimental research. This kind of study highlights one of the benefits of the IbMs.

**Keywords** Yeast population, Yeast inoculum, Fermentation, Individual-based Modelling, Serial repitching

**References**

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