



## Abstract Submission

Submission-1785

**Topic :** / Biochemical Engineering / ECAB3 / Modeling and control

### **NEW APPROACHES TO DETERMINE THE HETEROTROPHIC YIELD ( $Y_H$ ) IN BIOLOGIC WASTEWATER TREATMENT**

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**Submit your abstract below (400 words):** Since the first publication of the ASM (activated Sludge Modeling) task group, the research on wastewater treatment and modeling has known huge progresses thanks to the organizing effect of working with common nomenclature and model. Nevertheless, the main weakness of ASM models is their lack of usefulness in the wastewater treatment industrial sector. In this context, the MOCOPEE project run by the SIAAP, offers a new framework for academics and industrials to work together and focus on the operational aspects of the topic. The aim of this study is to address the issue of the heterotrophic yield ( $Y_H$ ), which is used as both an operational parameter for scaling and control in WWTP (Waste Water Treatment Plants) and a model parameter for ASM. Indeed the common use of the value  $Y_H=0.67$  for modeling WWTP's processes compared to variations observed in laboratory measured values raises the ambiguity of this useful parameter. For instance, the literature shows that the  $Y_H$  appears to be substrate-dependant. The value 0.67 has been identified with acetate as a substrate whereas other values are obtained in similar conditions for other substrates. Consequently, this study offers different approaches of "measuring" the  $Y_H$  using a homemade batch respirometer.

The first approached was to use the reactor's oxygen mass balance by integrating the OUR curve over the time of a single substrate degradation. This method was used to calibrate the system by checking that the value 0.67 was obtained for acetate. The second approach was to consider the  $Y_H$  as a model parameter. The chosen hypothesis was to consider that the storage process could influence its identification. In fact, when storage is considered, several yield coefficients are used in ASM based models. Consequently values vary during the different steps of the degradation. The value obtained with the first method for the overall degradation has been compared with a combination of the ones identified for the different processes, with different models complexity, thus allowing us to assess the adequacy of a model to a specific condition. The last approach consists in questioning the influence of the universally used COD unit. TIC/TOC analyses, pH and the off-gas  $CO_2$  measurement were used to obtain a carbon mass balance of the system in order to have a direct access to the substrate's carbon that was not integrated in cell mass growth.

To conclude, this study offers new approaches of the  $Y_H$  by comparing a very simple and cost effective mass balance method to the identification of yield coefficients for different models. Several clues were obtained to explain the variations of the  $Y_H$  observed throughout the literature by considering different process complexities. Using other substrates also emphasized its substrate dependency, for instance  $Y_H=0.76$  was obtained for glycerol.

**Type of presentation ::** Oral

**Highlight 1:** Traditional and non-traditional approaches were confronted for  $Y_H$  determination



**Highlight 2:** Substrate dependency of the YH was emphasized

**Highlight 3:** Several way of considering the storage process were compared for YH determination

**Keywords:** Bacteria, Bioprocess, Methodology, Modelling, Water treatment