PREDICTING THE DISTRIBUTION OF A WHEY PROTEIN FOULING IN A CORRUGATED PLATE HEAT EXCHANGER USING THE KINETIC PARAMETERS OF THE BETA-LACTOGLOBULIN THERMAL UNFOLDING/AGGREGATION PROCESS

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ABSTRACT

Protein fouling of plate heat exchangers (PHEs) in the dairy industry is a severe issue which requires frequent cleaning-in-place procedures. At the present time few investigations have been able to relate closely the dry deposit mass distribution along a corrugated PHE to a reaction fouling approach based on the thermal denaturation process of beta-lactoglobulin (BLG, the major whey protein responsible for fouling in pasteurization processes). We propose here to predict the BLG fouling distribution along the PHE by means of the ratio between the unfolding reaction rate constant (noted k_{unf}) and the aggregation reaction rate constant (noted k_{agg}) calculated in the bulk solution. Knowing the bulk temperature profile along the PHE, the ratio $R = k_{unf}/k_{agg}$ was calculated at a temperature corresponding to the middle point of each channel. R corresponds to the degree of progress of the heat-induced denaturation reaction, which is a partial representation of the physicochemical environment and of the physicochemistry influence. Experiments have been conducted at pilot scale in a PHE in countercurrent configuration and supplied with a holding section, and whey protein fouling deposits were generated using a model BLG fouling solution which was made using a whey protein isolate powder (89 wt.% in BLG) and a known amount of ionic calcium. Temperature profiles within the PHE were imposed with four degrees of freedom (two temperatures, two flow rates). In parallel the kinetic parameters (activation energy, reaction rate constant) for both the unfolding and the aggregation reactions of BLG were identified at laboratory scale in static conditions and then used to predict fouling. Various temperature profiles along the PHE were generated as a function of the operating conditions, which allowed us to derive the concentration profile of the different BLG species (that is, native (N), unfolded (U) and aggregated (A) BLG) into the bulk of the proteinaceous fouling solution. The comparison between the BLG concentration profiles and the BLG fouling deposit distribution along the PHE allowed us to put forward several important fouling mechanims: i) there is a decrease in the deposited mass when the aggregation process prevails, well before that CU decreases, ii) very little U species into the bulk fluid is required (e.g., $\alpha = 0.012$, α giving the ratio between the concentration of the partially unfolded and native BLG under the conditions used) for BLG to be deposited onto the plates of the heat exchanger, iii) the dry deposit mass distribution depends pretty much on a single parameter, the ratio denoted R. The analysis of the database of the experimental runs clearly shows that the mass of dry deposit on each pass of the PHE is fairly well correlated with R ($p<0.05$) and that this parameter alone is able to predict the location of the fouling deposit. It is observed that the amount of deposited BLG decreases when the ratio R is beyond 1. Results suggest that the precursor species of fouling is the unfolded BLG (or BLG in the molten globule state). This investigation also indicates that aggregates are not the cause of a proteinaceous fouling.