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Abstract title

Metabolism of heterocyclic aromatic amines (HAA) by *Lactobacillus reuteri* DSM 20016

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Heterocyclic aromatic amines (HAA) are mainly formed during the heating of protein rich food, especially meat and fish. Although the concentration in food is low (ppb range), HAA could be relevant for human health because of their ubiquitous occurrence and highly mutagenic and/or carcinogenic potential.[1] In contrast to the detailed studied human xenobiotic metabolism[2], only limited information is available regarding the transformation of HAA by the human microbiota. We addressed this point and investigated the metabolism of selected HAA (IQ, MeIQ, MeIQx, AαC, Trp-P-1, Harman and Norharman) in the presence of *Lactobacillus reuteri* DSM 20016, a natural inhabitant of the human gastrointestinal tract[3], which is known to metabolise PhIP.[4] Batch incubations were performed anaerobically in modified MRS medium supplemented with 200 mM glycerol and in presence of two different glucose concentrations (10 mM or 111 mM) at 37 °C for up to 72 h. The stability of HAA was measured by HPLC-DAD-UV or -FLD and -MS/MS.

We observed a significant degradation for AαC and MeIQx (each up to 100 %), IQ (81 %) and MeIQ (66 %), respectively. The extent of degree was strongly dependent on the initial glycerol/glucose ratio. In batch cultures with less glucose no (AαC, MeIQx) or significantly less degradation (IQ, MeIQ) was observed. Different microbial metabolites were detected for MeIQx (two) and AαC (up to eleven). Based on mass spectrometric data we assume that at least some of these metabolites are chemical reaction products between the HAA and microbial glycerol metabolites, e.g. 3-hydroxypropionaldehyde, as is described for PhIP.[4] Therefore first structures were postulated. Further studies will focus on the chemical characterisation and bioactivity (bioavailability, toxicity) of these unknown microbially derived HAA metabolites with the aim to contribute to a complete risk assessment of HAA for human health.

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