

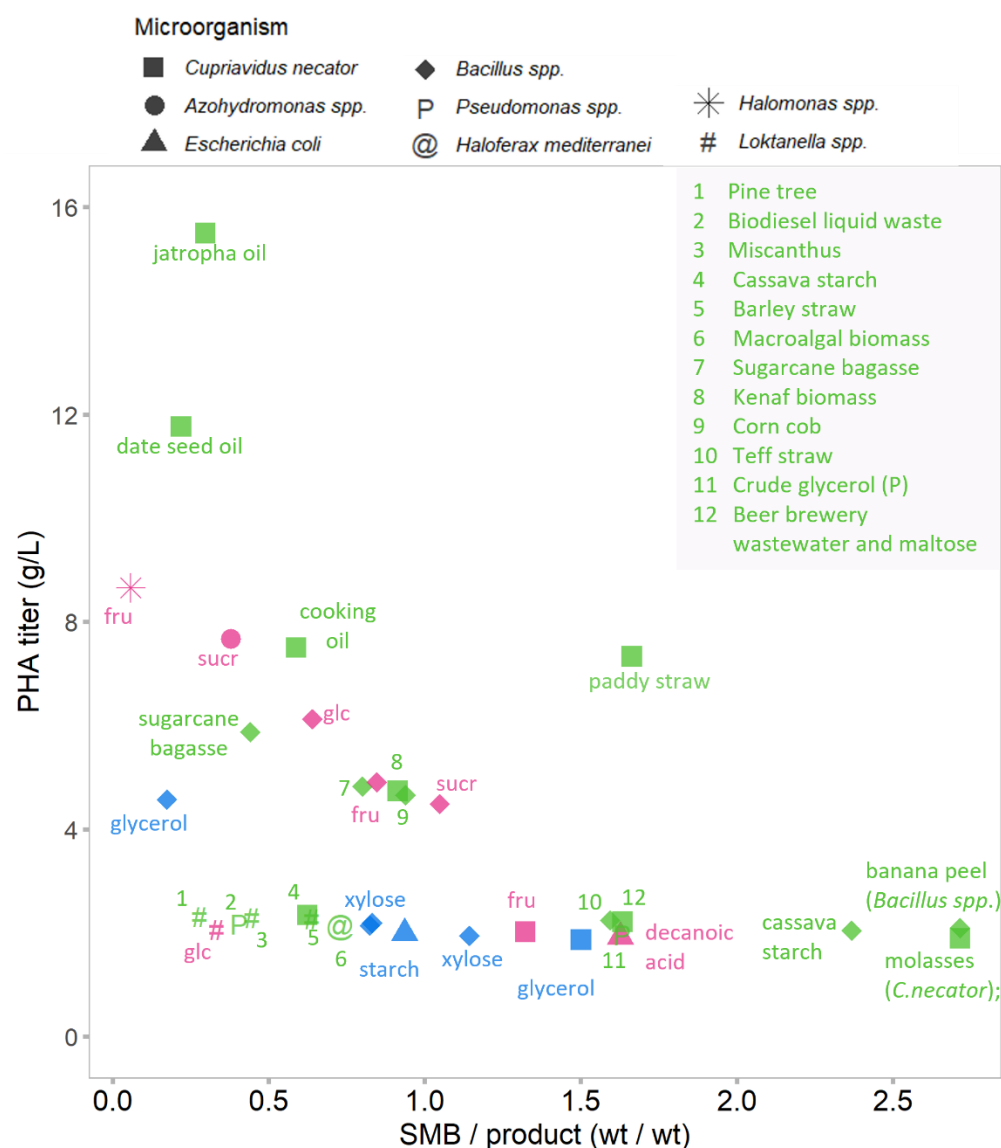
# **Impact of waste as a substrate on biomass formation, and optimisation of spent microbial biomass re-use by sustainable metabolic engineering.**

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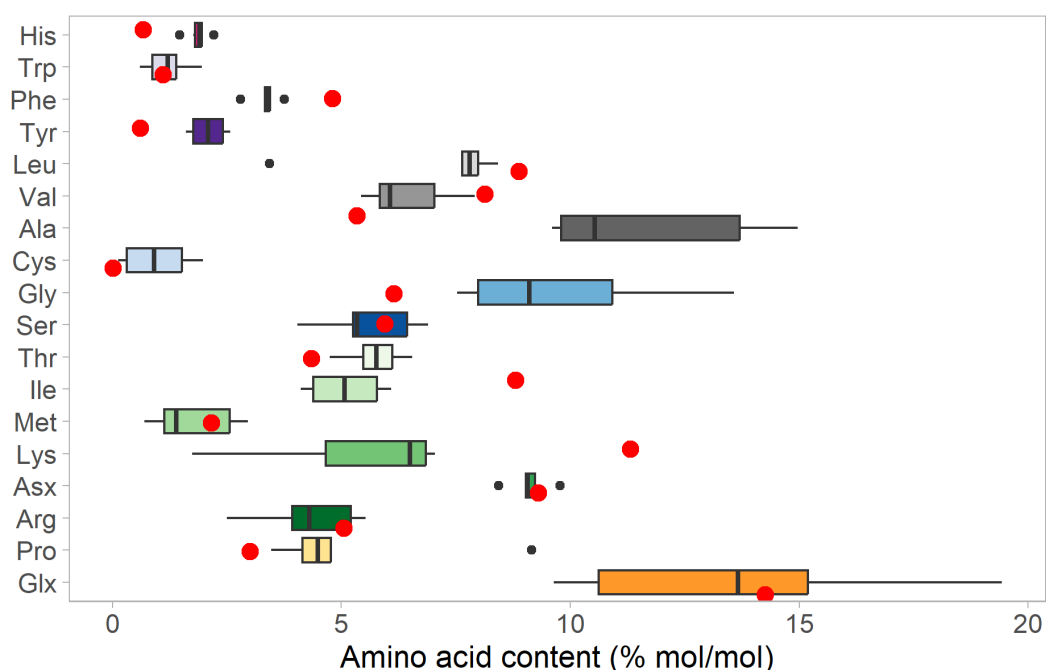
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Supplementary Information



**Figure S1. SMB formation in PHA bioproduction (batch fermentation)** using pure ('lab') substrates (pink) or substrates derived from waste streams ('green') or mimicking main carbon sources from a waste-stream ('blue'). The shape of the points indicates which microorganism was used for PHA production. The carbon substrate is indicated by a label next to the datapoint. glc - glucose, sucr - sucrose, fru - fructose. Note overlap of points 4 and 5 (# - process used *Loktanella* sp.), 10, 11, and 12 (P - used *Pseudomonas* spp.). Further details of the dataset and the sources are shown in supplementary Table S2.



**Figure S2. Variability of amino acid composition selected microorganisms and compared to composition of casamino acids (CasAA), shown as red points[18].** The median value is shown as the bold line in the middle of the box. The left and right bounds of box show the 1<sup>st</sup> and 3<sup>rd</sup> quartiles, respectively, and whiskers indicate  $\pm 1.5 \times$  the interquartile range (IQR). Outliers in the dataset are indicated as individual black dots. Data based on published literature on *E. coli*, *Corynebacterium glutamicum*, *Streptomyces coelicolor*, *Saccharomyces cerevisiae*, *Pichia pastoris* and *Aspergillus niger* as indicated in main article. Due to the experimental limitations some data sources do not distinguish separately Asp and Asn (pooled fraction is named Asx). Similarly, Glx represents pool of Gln and Glu.