

Gut *plastizyme*: systematic review for searching gut microbiota enzymes to be proposed as plastic-degradation resources

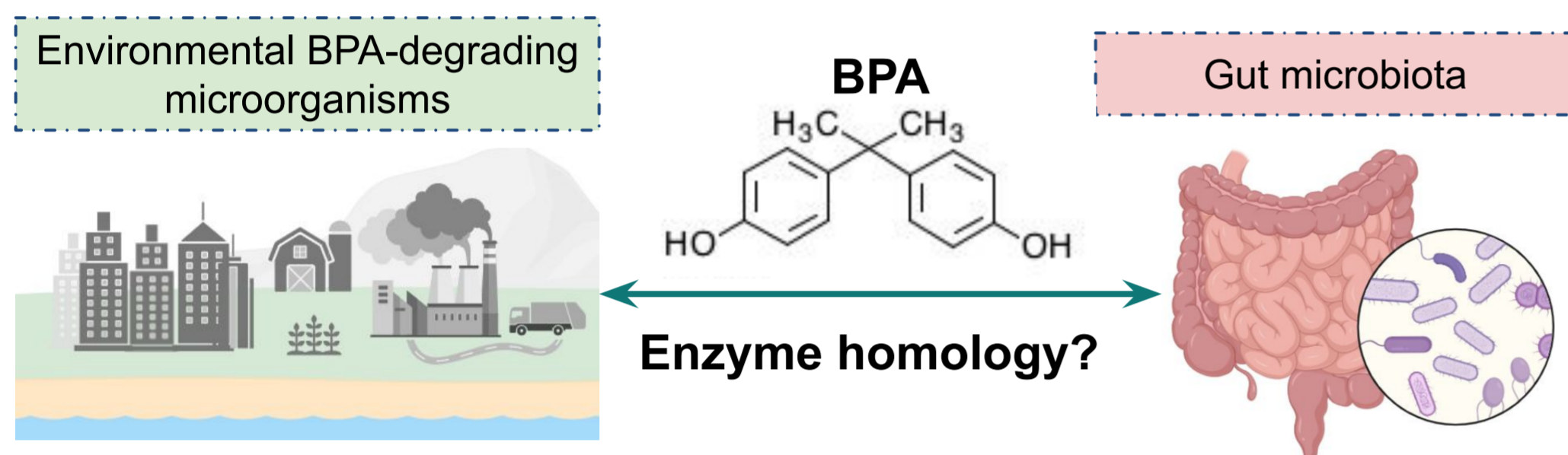
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INTRODUCTION & AIM

Rapid industrialization have led to the widespread occurrence of emerging plasticizers, notably **bisphenol A (BPA)**. While environmental bacterial degradation is well-characterized, the BPA-degrading capacity of the human gut microbiota remains largely unexplored. Therefore, the aim of this systematic review is to bridge the knowledge gap between **environmental *plastizyme*** with metabolic routes and metabolites of BPA described to date within the human gut microbiota. By integrating this knowledge, **we aim to establish a framework for a gut *plastizyme* and identify key enzymes for future validation and potential health interventions.**

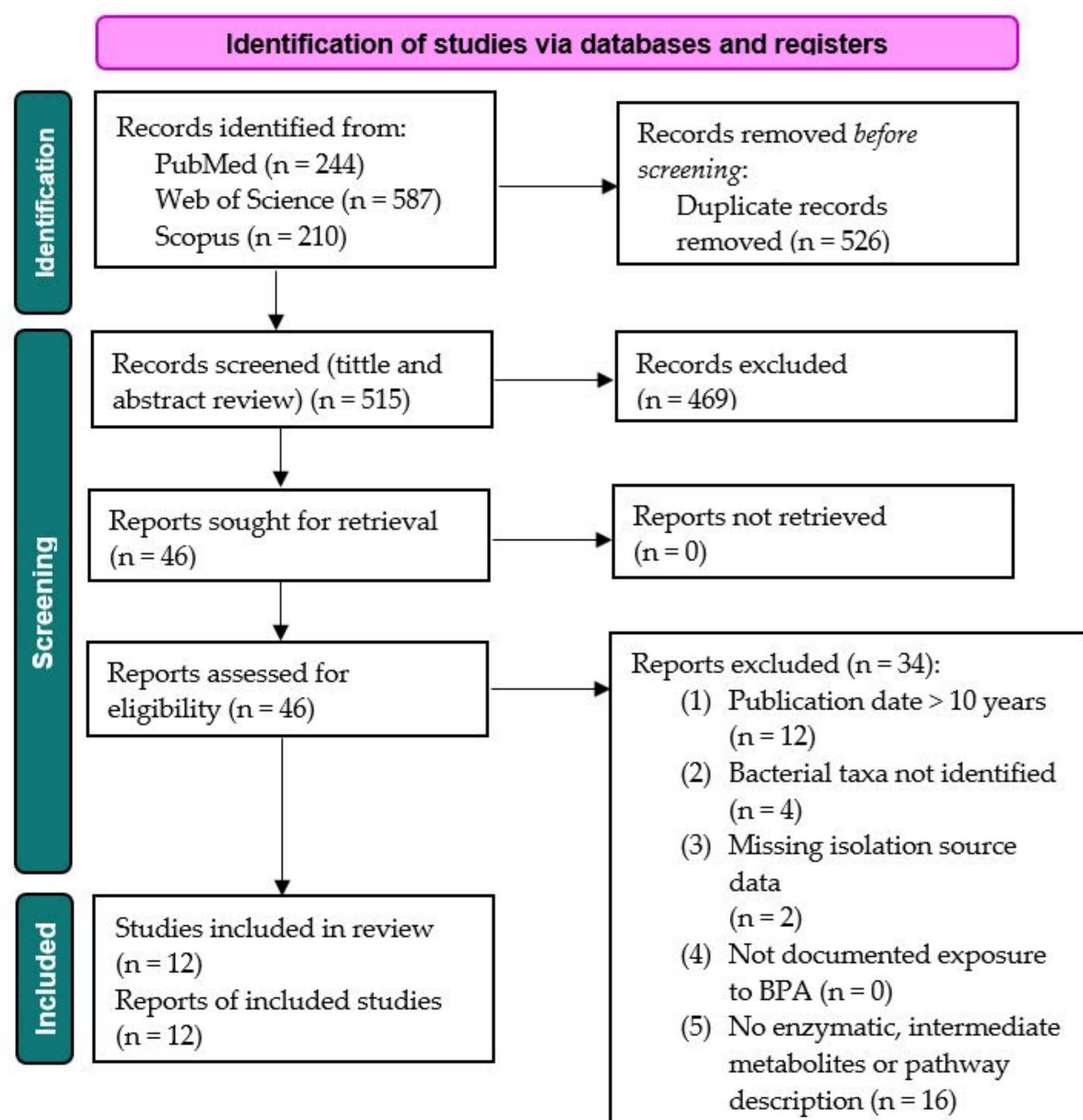


METHODS

The term search strategy was carried out with a combination keywords categorized into three thematic pillars:

- ★ **Target compound:** Bisphenol A (BPA), metabolites.
- ★ **Biological niche:** gut microbiota, environment.
- ★ **Enzymes:** *plastizymes*, degrading enzymes, biodegradation, degradation pathways, (laccase OR “cytochrome P450” OR dioxygenase OR monooxygenase OR hydroxylase).

A PRISMA methodology analysis results in this flow diagram:



RESULTS & DISCUSSION

Diversity of BPA-Degrading Microorganisms

Data from the analysed studies allow to identify 14 taxa capable of metabolize BPA where the most relevant strains featuring characterized pathways are compiled:

Bacillus sp. strains like AM1 (gut) and HV-3 (soil/sludge)	Lactobacillus <i>L. reuteri</i> and <i>L. plantarum</i> (probiotics)	Pseudomonas <i>P. putida</i> and <i>P. palleroniana</i> isolates
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Key functional enzymes

Enzymes	EC	Environment	Gut microbiota
Cyt P450 monooxygenases	1.1.4.14.-	✓	✗
Laccases	1.10.3.-	✓	✓
Dioxygenases	1.13.-	✓	✓
Hydratases	4.2.1.-	✓	✓

Niche adaptation and the efficiency gap

<i>Pseudomonas</i> sp. LM-1	100%
<i>Proteus mirabilis</i> SQ-2	98%
<i>Lactobacillus reuteri</i>	70%
<i>Lactobacillus plantarum</i>	40%

Gut bacteria were less specialized for plasticizers degradation because the physiological exposure concentrations are lower than contaminated industrial wastewater or soil.

BPA Detoxification

The primary xenobiotic intermediate metabolites generated (HQ, HAP, HBA) possess significantly lower estrogenic activity than BPA, validating microbial transformation as an active pathway for partial or complete host detoxification.

Critical limitations

Most verified metabolic routes studied are oxygen dependent. But, human gut is and anaerobic environment.

Over-reliance on simplified *in vitro* models with over-physiological BPA doses, ignoring gut dynamics, bile acid stressors...

CONCLUSION

A theoretical gut *plastizyme* overlap with environmental pathways was confirmed, but underscores that human intestinal BPA biotransformation remains highly unspecialized and restricted by low selective pressure *in vivo*.

FUTURE WORK

To extrapolate these results, a pilot bioinformatic approach will be done with a reconstructed MAGs from gut microbiota from a children cohort to validate the presence of specific gut *BPAzyme*.