LIGNIN DEGRADATION BY MICROBIAL CONSORTIA DERIVED FROM TERMITE GUT

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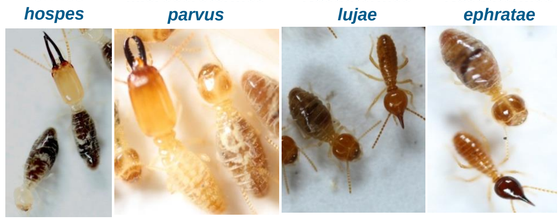
Context

In natural ecosystems, the recycling of lignocellulosic (LC) biomass is performed by microbial communities, or consortia, that are ubiquitous and mostly associated with plant residues. The decay of the strongly recalcitrant lignin fraction of LC involves the action of specific microbial consortia constituted by a large variety of microbial species.
Termite gut microbiomes are ecosystems known for their LC degradation capacity that can be exploited in LC biorefinery. However, little information exists on their LC and lignin degradation capacities.

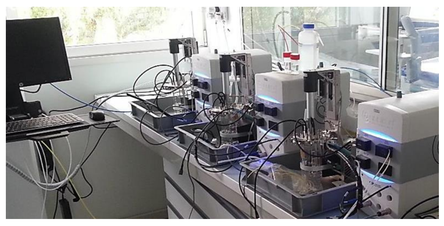
Our aim is to shed light on the lignocellulose and, particularly, the lignin conversion capacity of microbial consortia derived from termite-gut microbiomes. Such communities are implemented in controlled bioreactors using LC and lignin-rich residues as sole carbon source. The multi-omics data obtained from these consortia show important differences in the dynamic of functional species and proteins throughout the lignocellulose deconstruction process.

Methodology

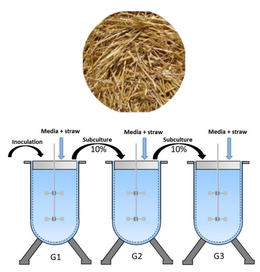
Termes hospes | *Microcerotermes parvus* | *Nasutitermes lujae* | *Nasutitermes ephratae*



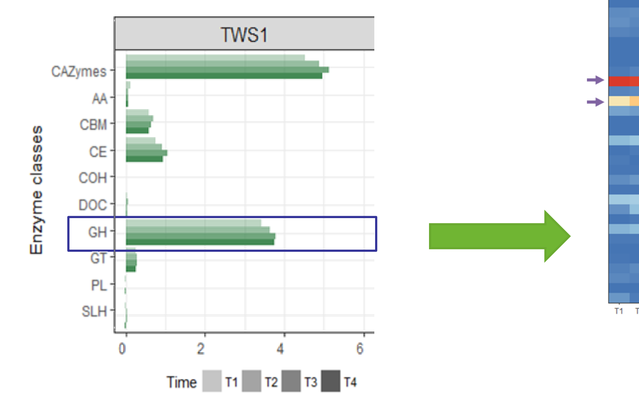
1. Screening of four termite species - duplicate bioreactors
Wheat straw as sole carbon source



2. Enrichment of the most efficient termite-derived lignocellulose degrader on wheat straw



3. Macro-kinetic and Multi-omics characterization of the enriched lignocellulolytic consortium



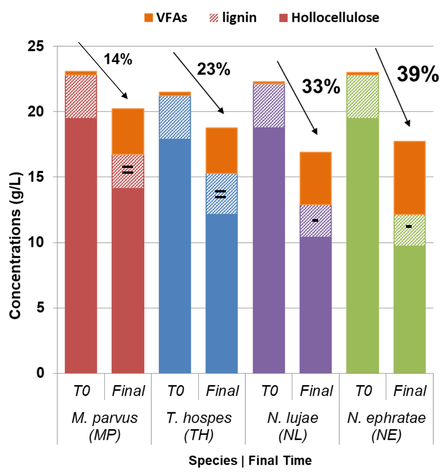
4. Repeat using lignin-reach substrates

- ✓ Exhausted wheat straw/poplar/eucalyptus
- ✓ Technical lignins
- ✓ Monomeric lignin models

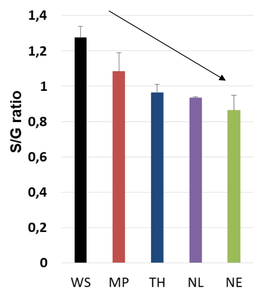
Results

1. Lignocellulose (LC) degradation and VFA production by termite microbiomes

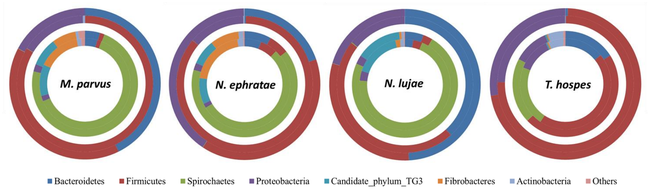
LC degradation



S/G ratio after LC degradation

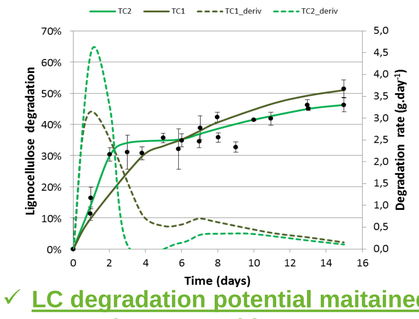


Diversity before (inner circles) and after (outer circles) growing on LC



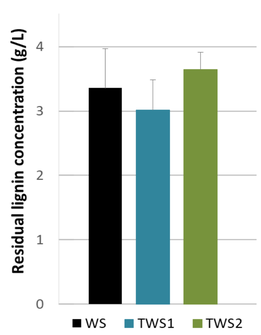
- ✓ High lignocellulose degradation potential
- ✓ Higher lignin degradation potential in NE
- ✓ Strong diversity shift

2. LC degradation by the enriched *N. ephratae* derived-consortium - TWS



- ✓ LC degradation potential maitained in wheat straw bioreactors

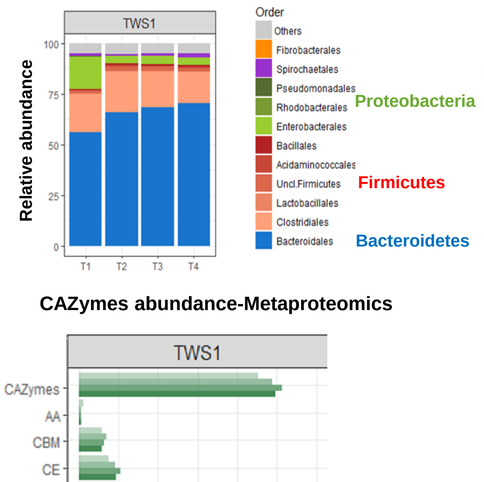
4. Residual lignin after LC degradation by TWS



- ✓ No lignin degradation
- ✓ Lost of potential
- ✓ Enrichment on a suitable substrate

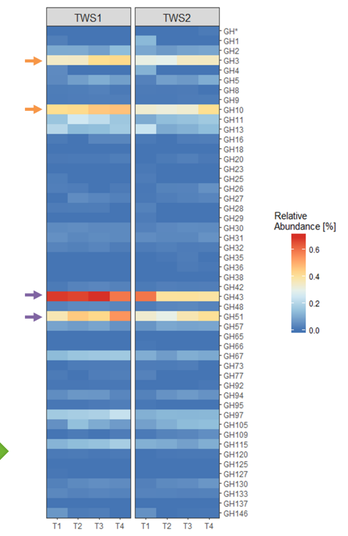
3. Community structure of TWS along LC degradation and CAZymes expression

Community structure-Metaproteomics



CAZymes abundance-Metaproteomics

Glycoside hydrolases (GH) abundance



- ✓ High abundance of Bacteroidetes and Firmicutes related members
- ✓ High expression of CAZymes : GH
- ✓ Most prevalent GHs families: GH3, GH10, GH43, GH51 (>50 % of identified GHs-proteins)

Conclusion and perspectives

A high LC degradation was obtained through screening and enrichment on wheat straw of a termite gut microbiome. The enriched consortium, derived from *Nasutitermes ephratae* showed a high LC degradation potential similar to that measured before enrichment. A multi-omics approach enabled us to better characterize the kinetics of both diversity and lignocellulolytic enzymes expression in this enriched consortium. However, the potential of *N. ephratae* derived-consortium to degrade lignin was lost during enrichment.
It is now planned to highlight this potential through a new round of screening and enrichment on more suitable substrates such as sugar exhausted wheat straw or poplar and technical lignins.

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