

Più-BIOGAS App: Le biotecnologie al servizio del biogas per ottimizzare la gestione degli impianti

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Più-Biogas App: obiettivi di progetto

Il progetto prevede il sviluppo di:

- un sistema rapido ed innovativo per lo studio delle **dinamiche di popolazione microbica**
- **un algoritmo per correlare i risultati** dei monitoraggi delle popolazioni microbiche
- **tecniche di “bio-arricchimento”** finalizzate all’ottenimento di inoculanti batterici
- un **software/app**

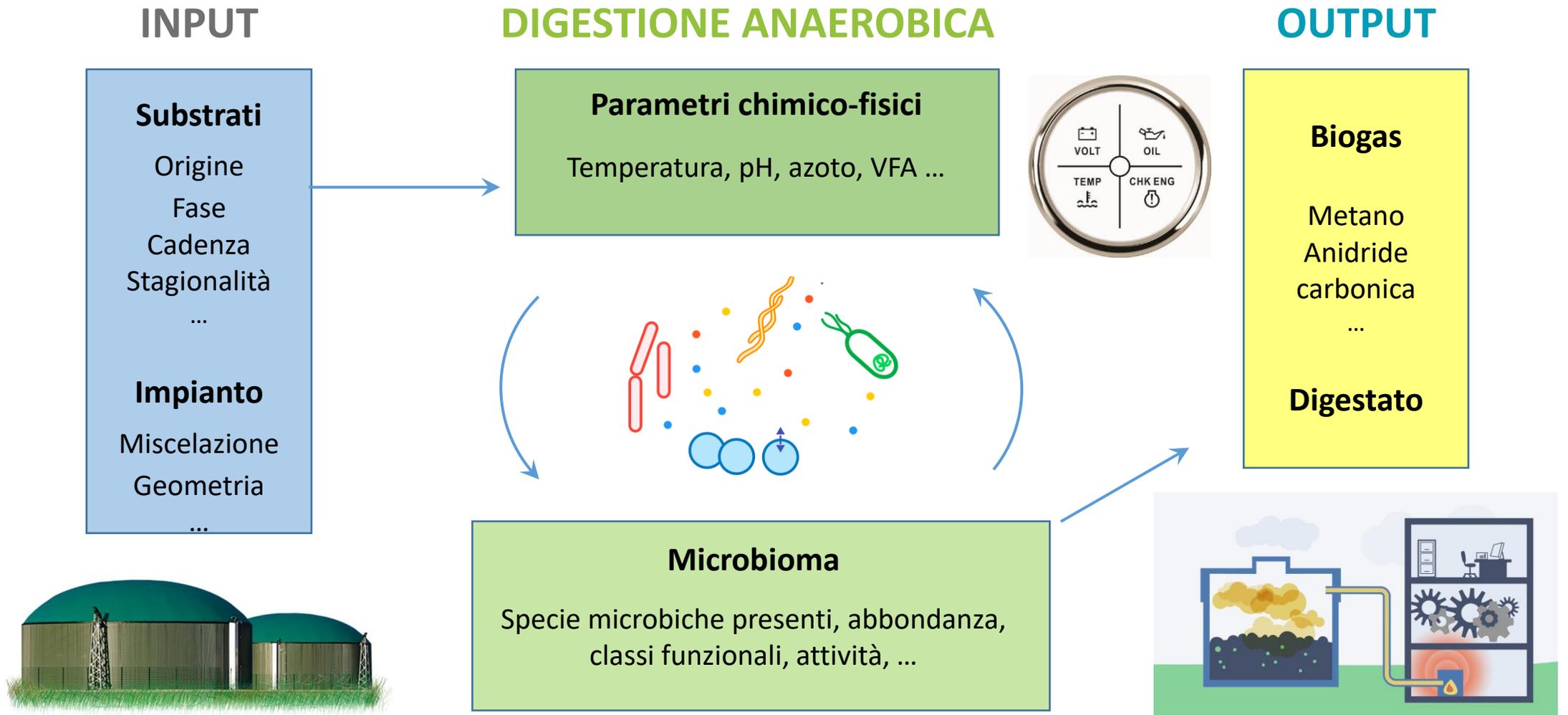


Agostini Sara
Biotechnologa



Guido Zampieri
Bioinformatico

Analisi biologica del processo

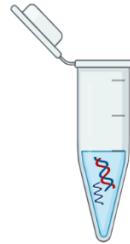


Dall'impianto al "meta-genoma"

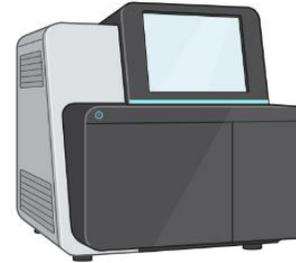
Prelievo di digestante



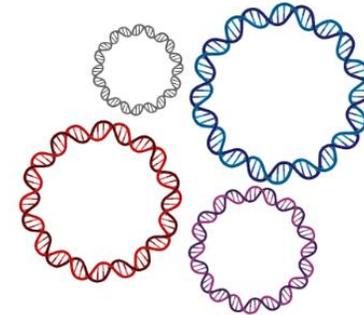
Estrazione di DNA



Sequenziamento



Ricostruzione dei genomi

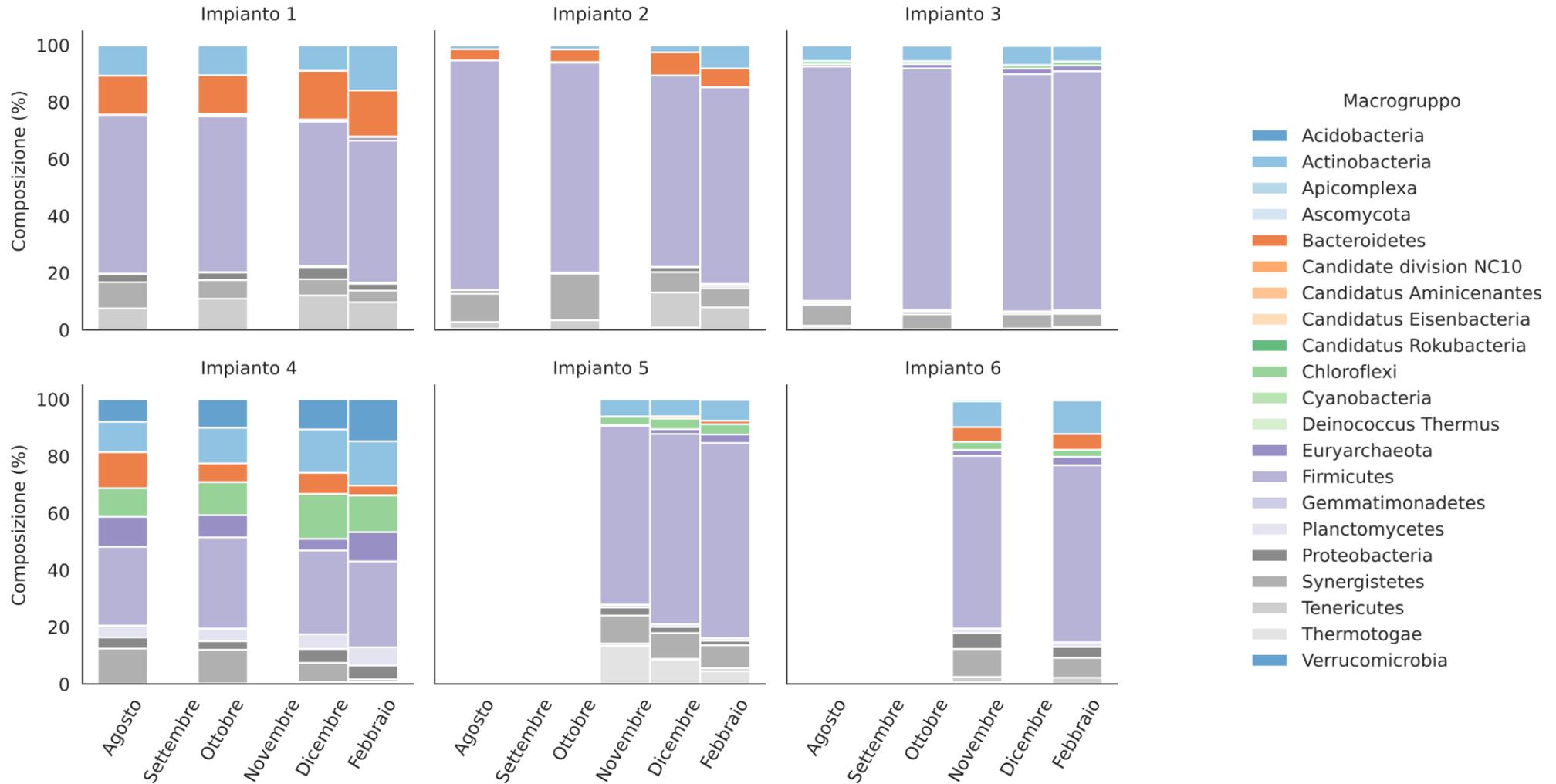


Monitorati sei impianti
nell'arco di un anno e
mezzo (di cui sette mesi
già analizzati)

Ottenute oltre
520'000 sequenze

Individuati 529 genomi,
di cui il 42% con
completezza sopra il
90%

Ogni reattore ha il suo “microbioma”



... e di ritorno all'impianto: il processo in numeri

E' possibile spingere oltre il monitoraggio giornaliero per ottimizzare la produzione di biogas?

- Monitoraggio chimico-fisico
- Algoritmi statistici
- Implementazione software

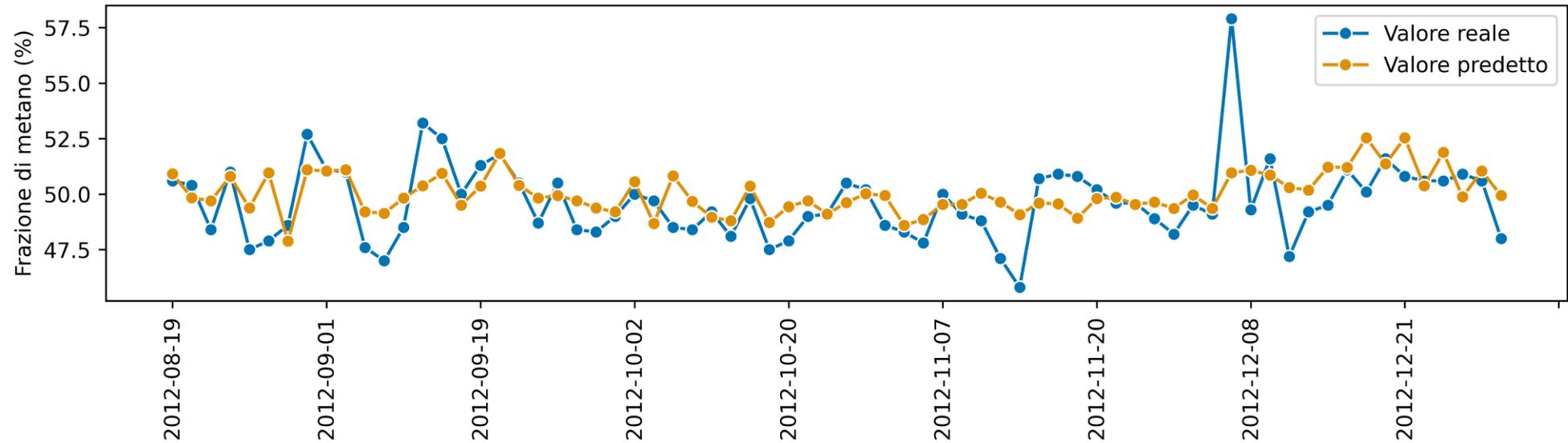
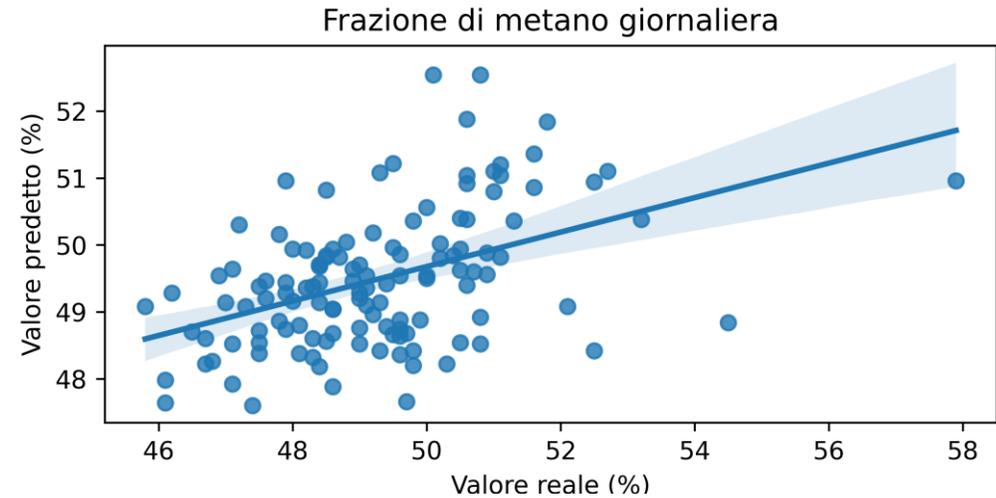


- Identificazione anticipata di processi inibitori
- Prevenzione di interruzioni

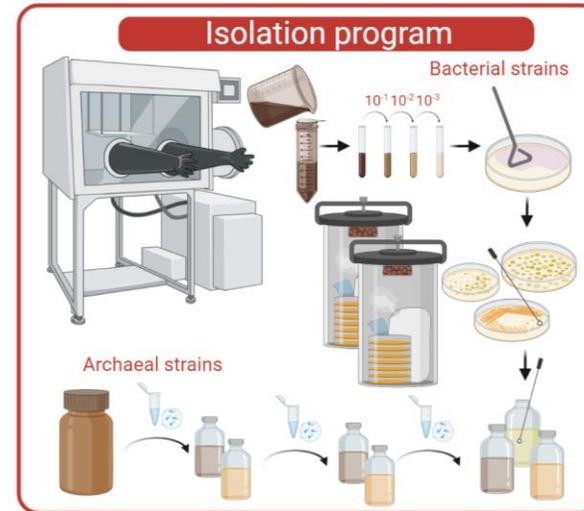
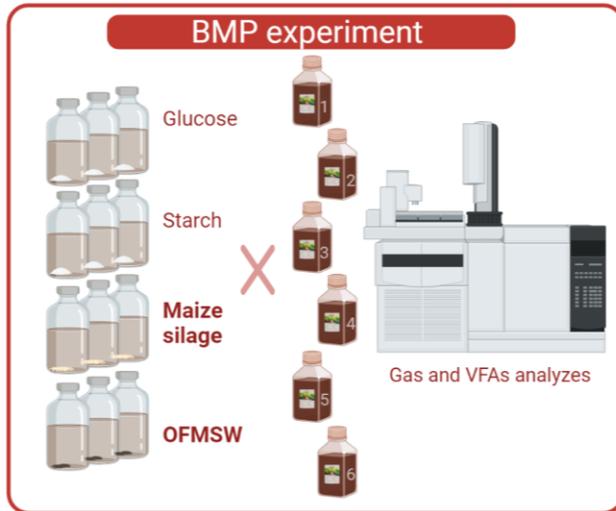
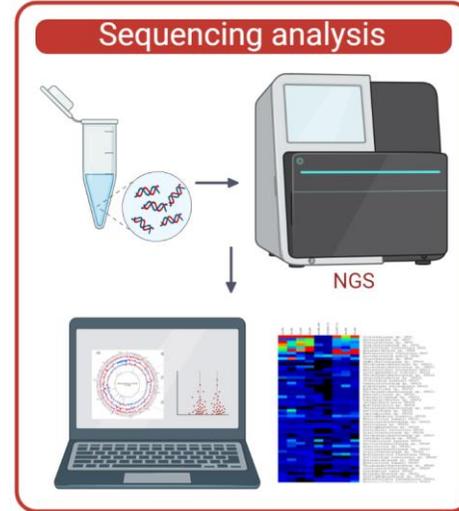
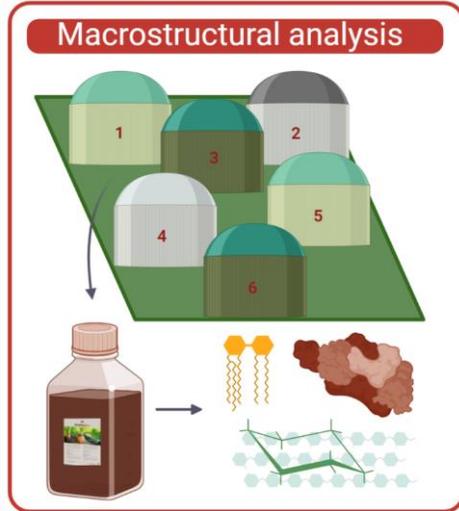
Il processo è prevedibile nel breve termine

Input: matrici introdotte

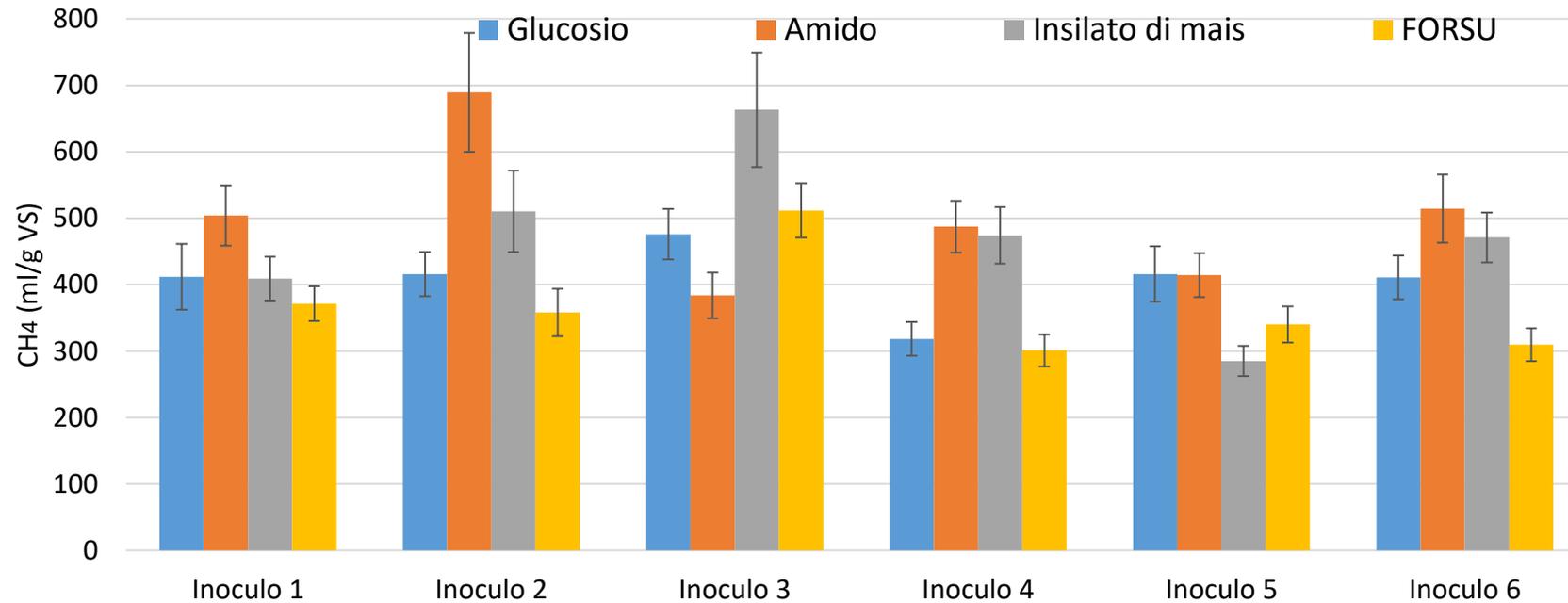
Output: frazione di metano nei giorni successivi



Bio-arricchimento: approccio sperimentale



Screening dei digestanti



Letame di pollina,
liquame suino e
insilato di mais

Letame di
pollina, patate,
cipolle e
insilato di mais

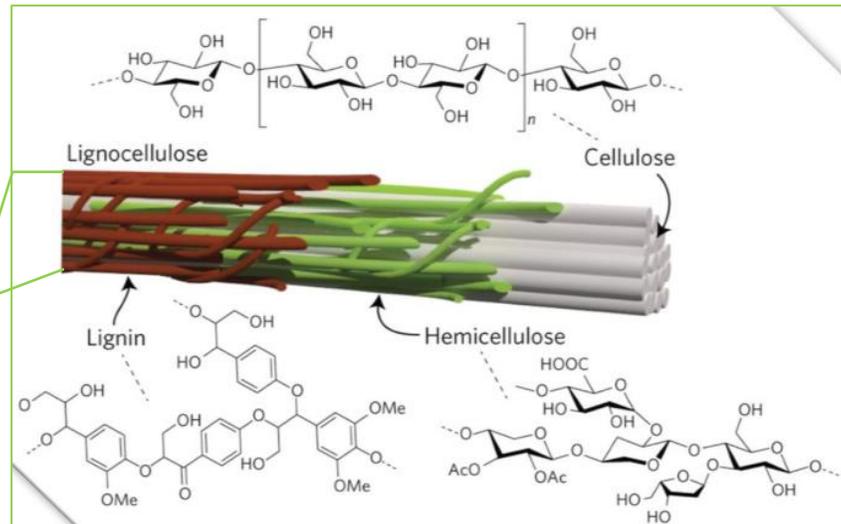
Letame di
pollina, letame
bovino, farina di
mais, sorgo,
scarti di patate,
insilato di mais

Insilato di mais e
insilato di orzo

Sansa di oliva e
crusca di
frumento

Insilato di mais e
letame bovino

Effetto enzimatico su digestante lignocellulosico



Bianco



Enzima A 20%



Enzima B 20%



Enzima C 20%



Enzima A 100%



Enzima B 100%



Enzima C 100%



Enzima A 500%

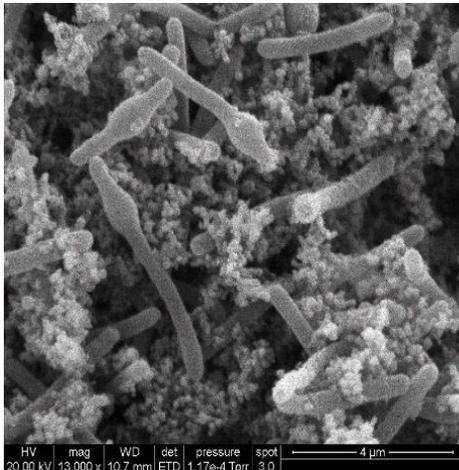
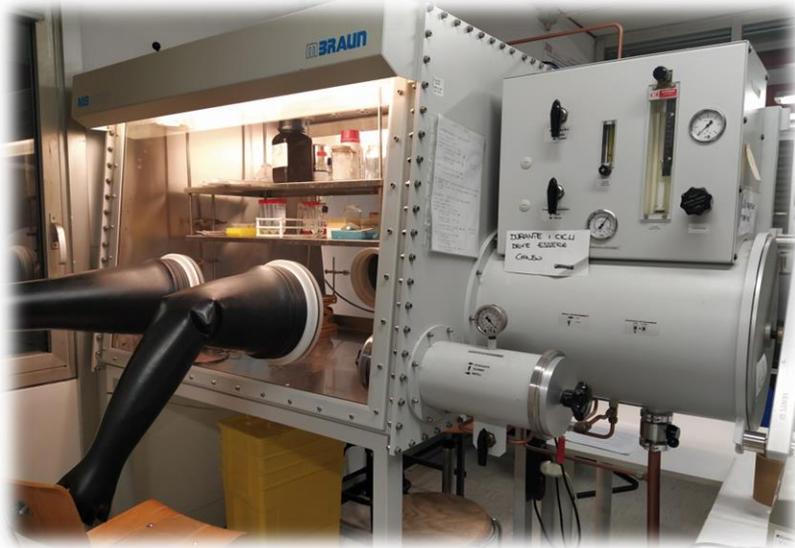


Enzima B 500%



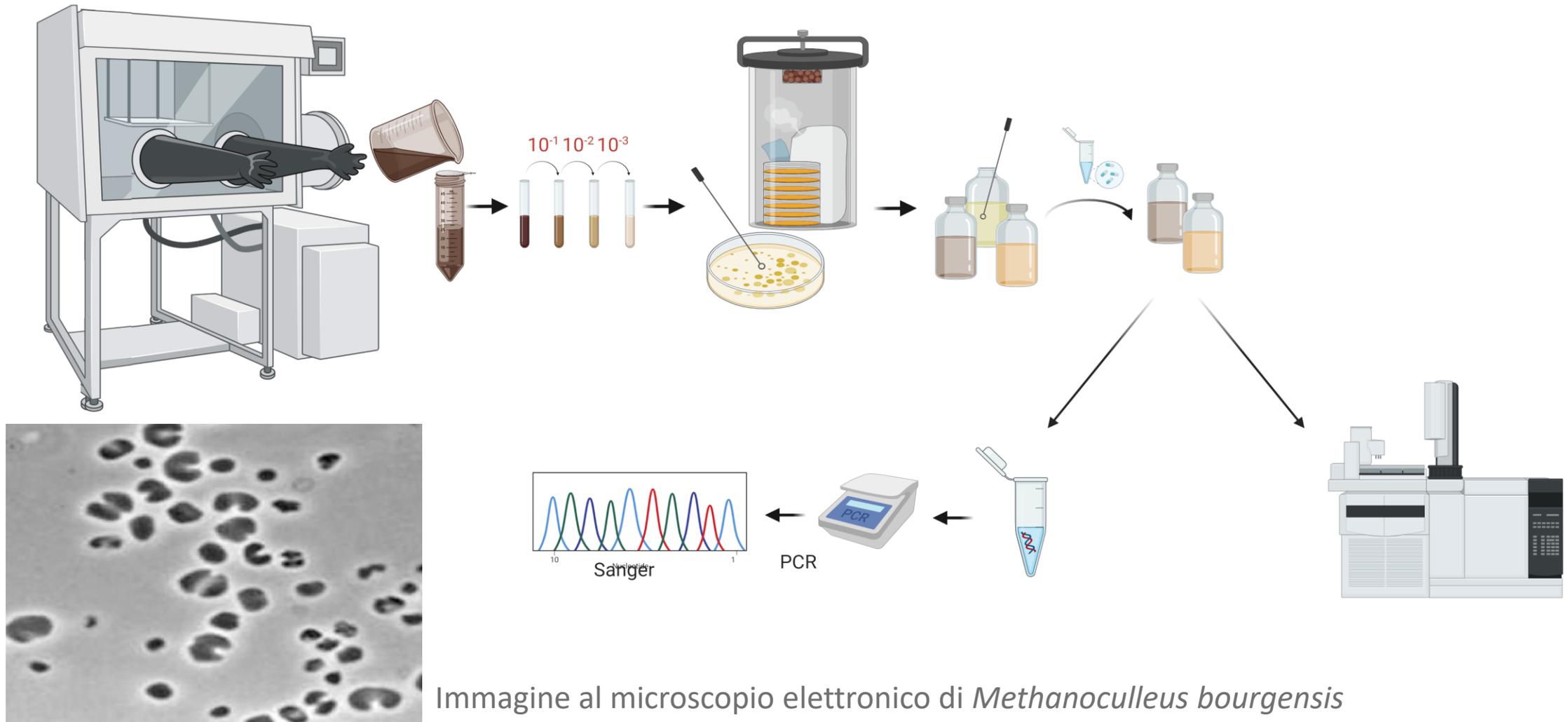
Enzima C 500%

Isolamento di specie batteriche



| Specie | Identità di sequenza | Famiglia |
|-----------------------------------|----------------------|---------------------|
| <i>Asaccharospora irregularis</i> | 99,02% | Alicyclobacillaceae |
| <i>Tissierella praeacuta</i> | 97,60% | Clostridiaceae |
| <i>Xanthomonas oryzae</i> | 96,73% | Bacillaceae |
| <i>Clostridium sartagoforme</i> | 99% | Tissierellaceae |
| <i>Clostridium cochlearium</i> | 99% | Clostridiaceae |
| <i>Enterococcus faecium</i> | 98,64% | Oscillospiraceae |
| <i>Schnuerera ultunensis</i> | 97,00% | Tissierellaceae |
| <i>Pseudomonas boreopolis</i> | 96,51% | Xanthomonadaceae |
| <i>Caldibacillus hisashii</i> | 99,26% | Bacillaceae |
| <i>Brevibacillus agri</i> | 99,56% | Paenibacillaceae |

Genomica e biotecnologie per l'isolamento di Archaea



Partecipazione a convegni internazionali



DAFNAE SIMB – 44TH SYMPOSIUM ON BIOMATERIALS, FUELS AND CHEMICALS 800-2022 UNIVERSITY DEGLI STUDI DI PADOVA
New Orleans (Louisiana) – May 1-4, 2022

Exploring full-scale biogas inoculants to boost biogas production from different organic waste streams

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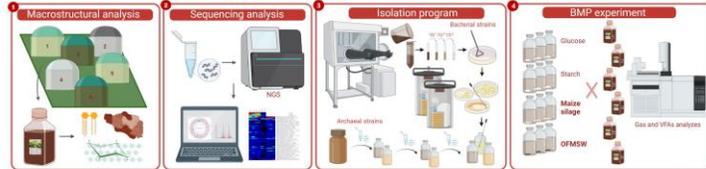
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Background

Agricultural and livestock waste has been efficiently exploited for the production of biogas and biomethane through anaerobic digestion (AD). Several parameters, such as inoculum, substrate loading and temperature need to be finely tuned and optimized to increase biomethane yield, thus further improving the overall process efficiency. Moreover, the knowledge of the microbiological structure and of the relationships between the microbes in the reactor allows for the optimization of the process through bioaugmentation programs with cultures enriched with archaea and/or hydrolytic bacteria.

Aim

This study aimed to develop efficient AD inoculants to be used for the conversion of several organic waste streams into biogas. Next generation sequencing (NGS) approaches were developed to assist the ongoing isolation programs.



1 Digestate from six full-scale biogas plants was collected and inocula were maintained at 37°C. Digestates macrostructural analyses were performed. 2 DNA sequencing was performed by the Illumina NovaSeq platform. Microbial taxonomic assignment (Campanaro et al., 2018) were useful to study their community compositions and 3 support the isolation program of both bacterial and archaeal strains. 4 Digestates were then exploited as inocula for BMP (Biomechanical Potential) of different organic substrates such as maize silage and organic fraction of municipal solid waste (OFMSW). Glucose and raw corn starch were used as benchmark with an organic loading (OL) of 2 g VS/L. Biogas measurements were performed every two days and volatile fatty acids (VFA) concentrations were periodically monitored.

Results

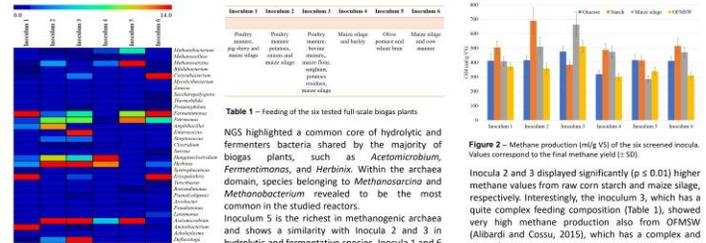


Figure 1 – Abundance of microorganisms in the selected biogas plants, grouped by genus. Figure 2 – Methane production (mL/g VS) of the six screened inocula. Values correspond to the final methane yield (± SD). Inocula 2 and 3 displayed significantly ($p \leq 0.01$) higher methane values from raw corn starch and maize silage, respectively. Interestingly, the inoculum 3, which has a quite complex feeding composition (Table 1), showed very high methane production also from OFMSW (Alibardi and Cossu, 2015), which has a complex and diversified compositional structure. Inoculum 2 easily degraded starch most probably because of being adapted to starchy feedstocks (ie potato residue, Table 1) and its microbial composition (e.g. Acetomicrobium, genus known for the abundance of amylolytic strains).

Conclusions

NGS approach can be a promising tool to monitor microbial populations involved in the AD of different organic feedstocks and was pivotal to support the ongoing isolation of the most efficient fermentative bacterial and archaeal strains. The screening of a wide range of digestates with different feeding regimes proved to be a promising strategy to boost biogas yields even from OFMSW.

References

Alibardi L., Cossu R. (2015). Composition variability of the organic fraction of municipal solid waste and effects on biogas and methane production potentials. Waste management, 36, 347-355.
Campanaro et al. (2018). Metagenomics driven reveals the functional roles of core abundant microorganisms in ten full-scale biogas plants. Water research, 140, 122-134.

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www.wastetobioproducts.com

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