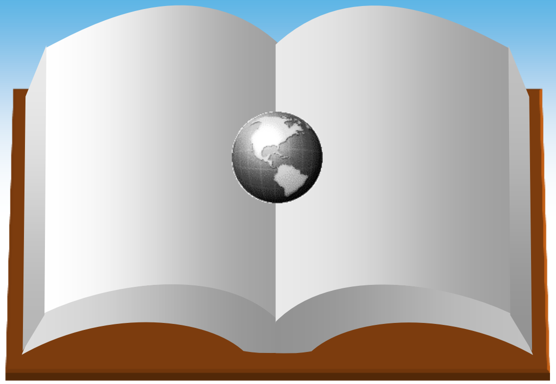

Performance, Biosafety and Microbial Community Structure during Dry Co-digestion of Food Waste and Pig Manure

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Gillian E. Gardiner [c], Conor Dennehy [a].

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Agriculture and Food Development Authority

Waterford Institute of Technology
Institiúid Teicneolaíochta Phort Láirge

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1. Background
2. Experiment performance
3. Pathogen elimination
4. DNA sequencing

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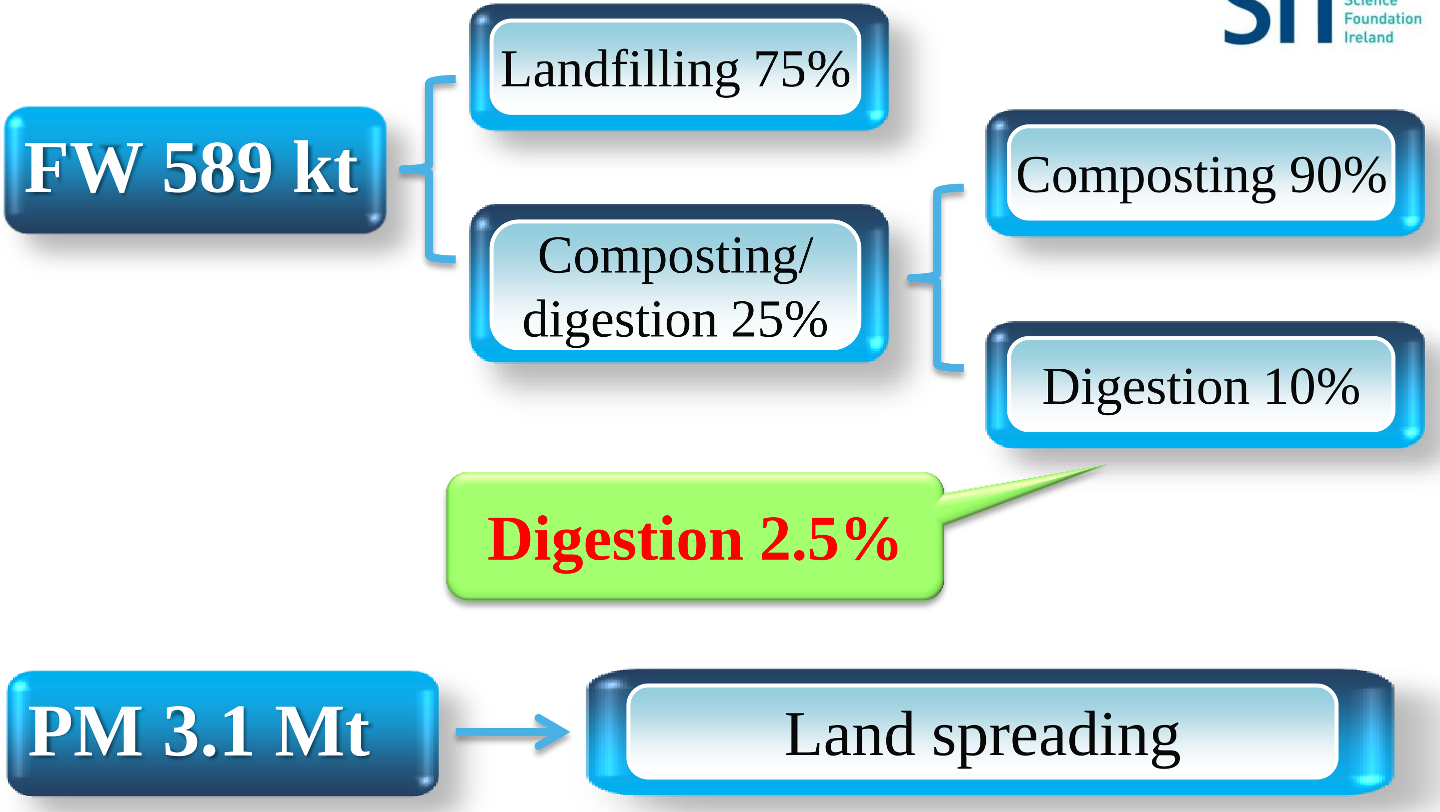
Introduction



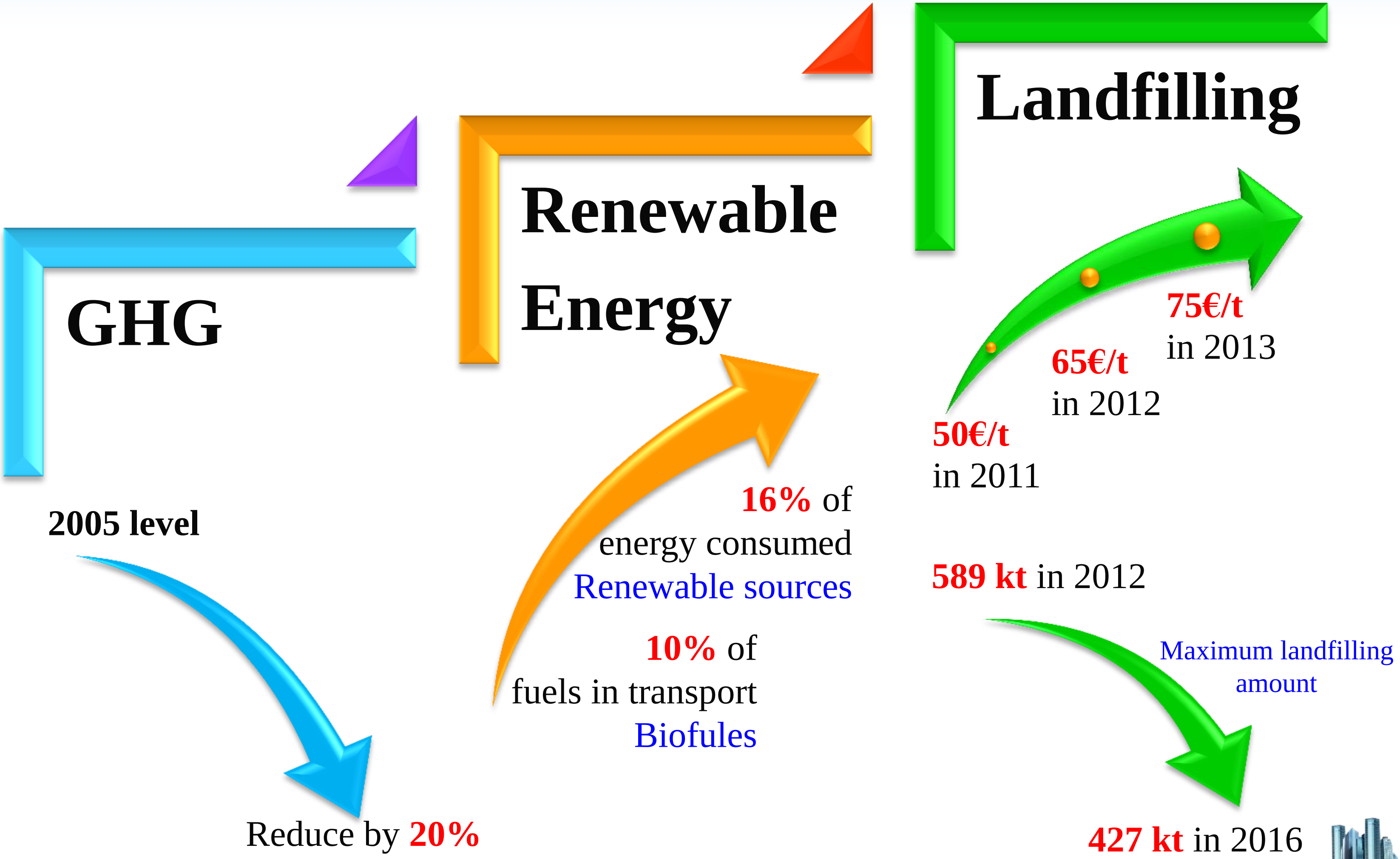
FW 589 kt

- Landfilling 75%
- Composting/ digestion 25%
  - Composting 90%
  - Digestion 10%

Digestion 2.5%

PM 3.1 Mt → Land spreading

Regulations



GHG

2005 level

Reduce by **20%**

Renewable Energy

16% of
energy consumed
Renewable sources

10% of
fuels in transport
Biofules

Landfilling

50€/t
in 2011

65€/t
in 2012

75€/t
in 2013

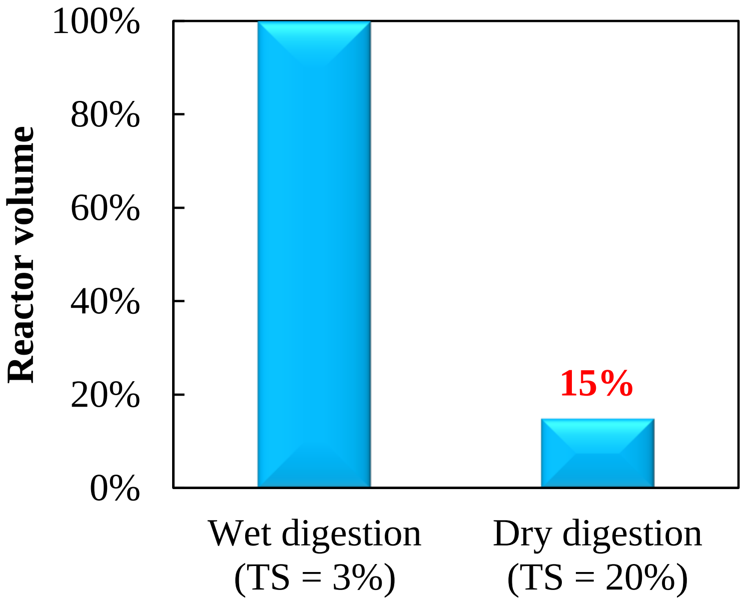
589 kt in 2012

Maximum landfilling amount

427 kt in 2016

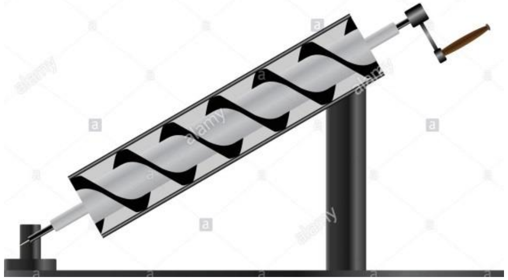
Dry Co-Digestion

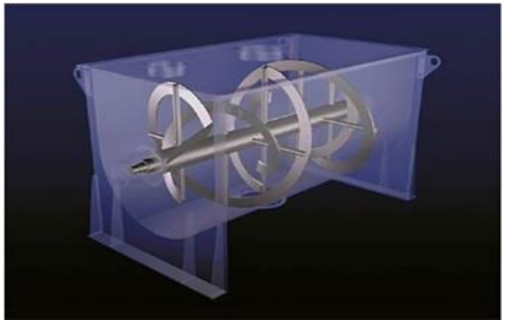
Advantages



- Small volume → Capital investment
- Low energy for heating → Operation cost
- High organic concentration → Biosafety

Disadvantages





- Transport
- Mixing

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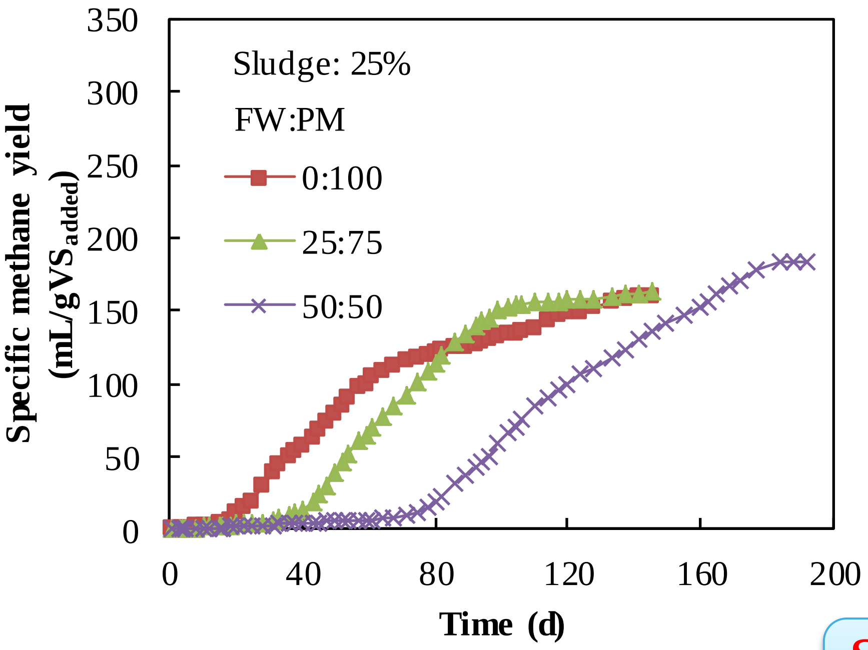
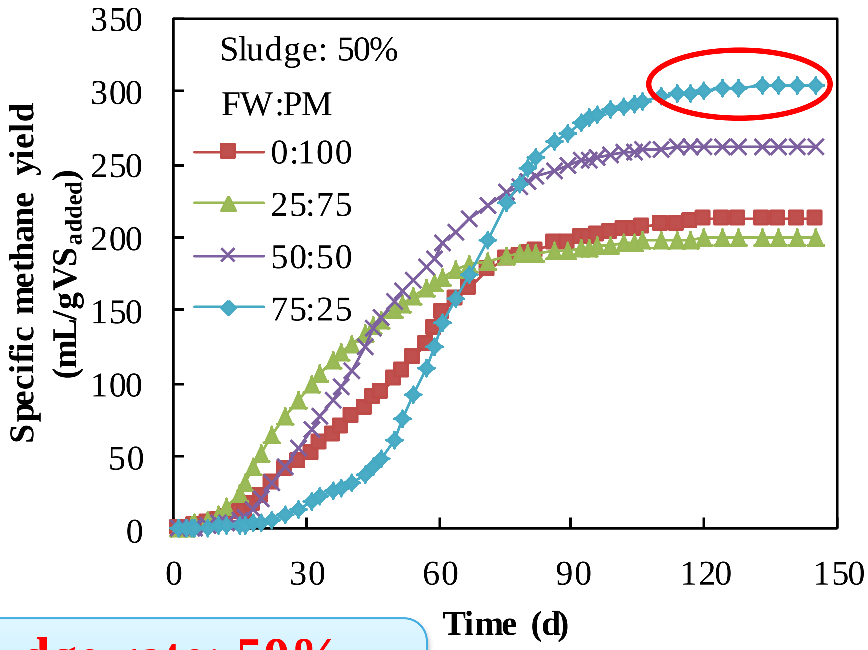
Experiment 1

- TS : 20%
- T : 37 ℃

Inoculum	Inoculum rate (%, VS base)	FW : PM (VS base)
Dewatered anaerobic sludge	25%	0 : 100
		25 : 75
		50 : 50
		75 : 25
		100 : 0
Dewatered anaerobic sludge	50%	0 : 100
		25 : 75
		50 : 50
		75 : 25
		100 : 0

Methane





Sludge rate: 50%
FW/PM: 50:50

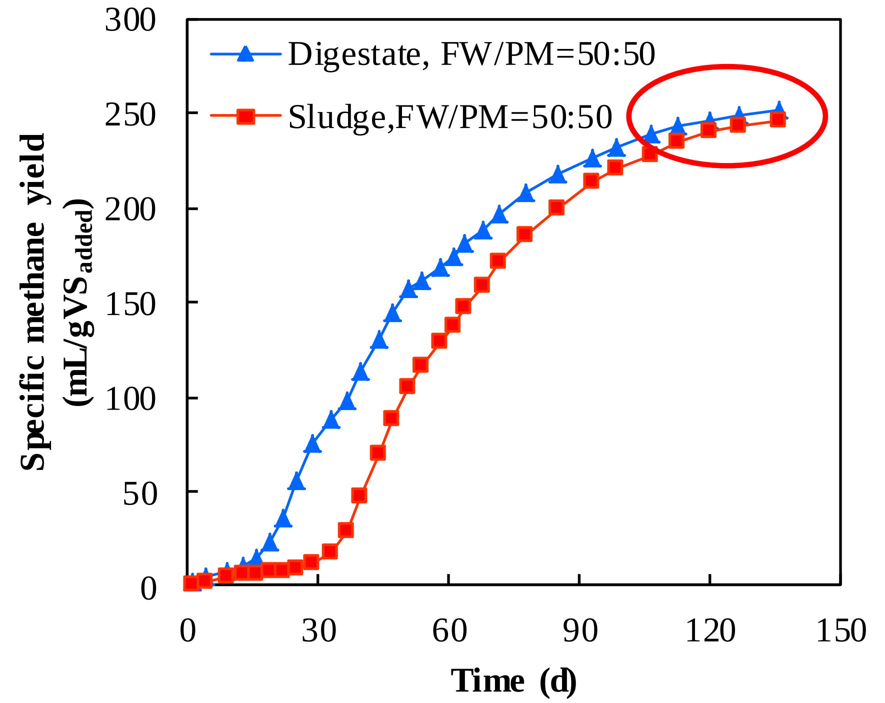
Sludge	25%					50%				
FW : PM	0:100	25:75	50:50	75:25	100:0	0:100	25:75	50:50	75:25	100:0
SMY (mL/gVS$_{add}$)	161	163	184	-	-	213	200	263	304	-
Lag phase (d)	18	36	72	-	-	17	9	18	39	-

Experiment 2

- TS content: 20%
- T: 37 °C

Inoculum	Inoculum rate (%, VS base)	FW : PM (VS base)
Digestate	50%	50:50
Dewatered anaerobic sludge	50%	50:50

Methane

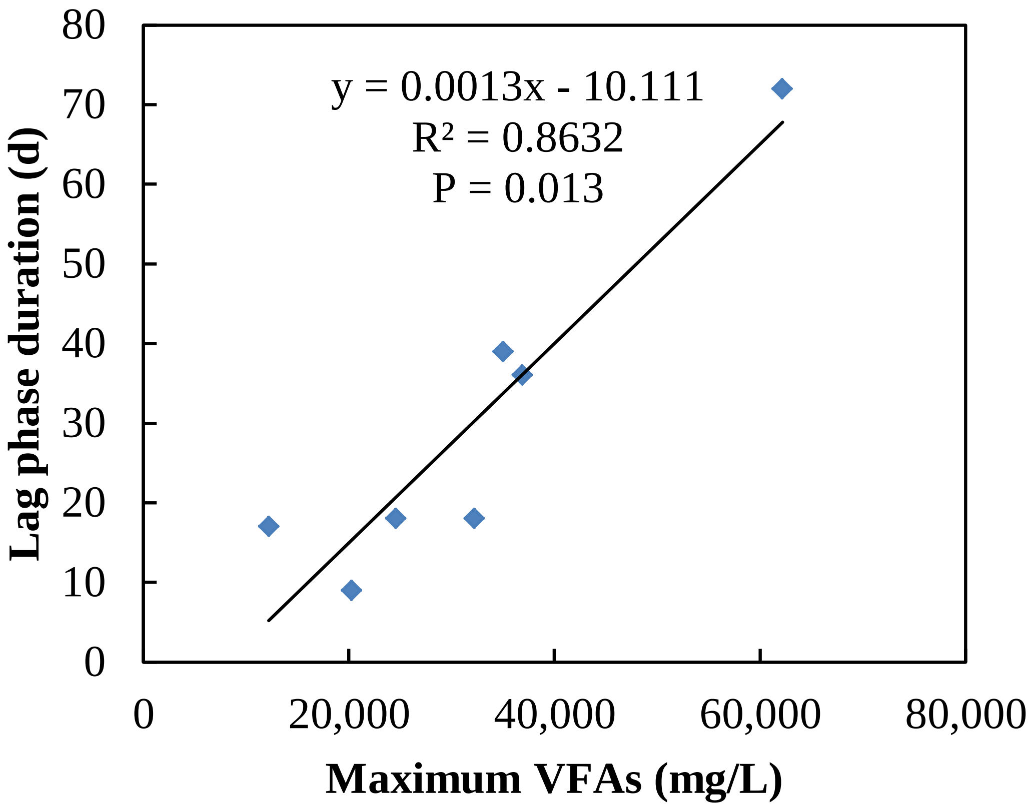


Digestate rate: 50%

FW/PM: 50:50

Inoculum	**Digestate**	**Sludge**
FW/PM	**50:50**	**50:50**
SMY (mL/g VS$_{add}$)	252±7	246±2
Lag phase (d)	13±1	28±1

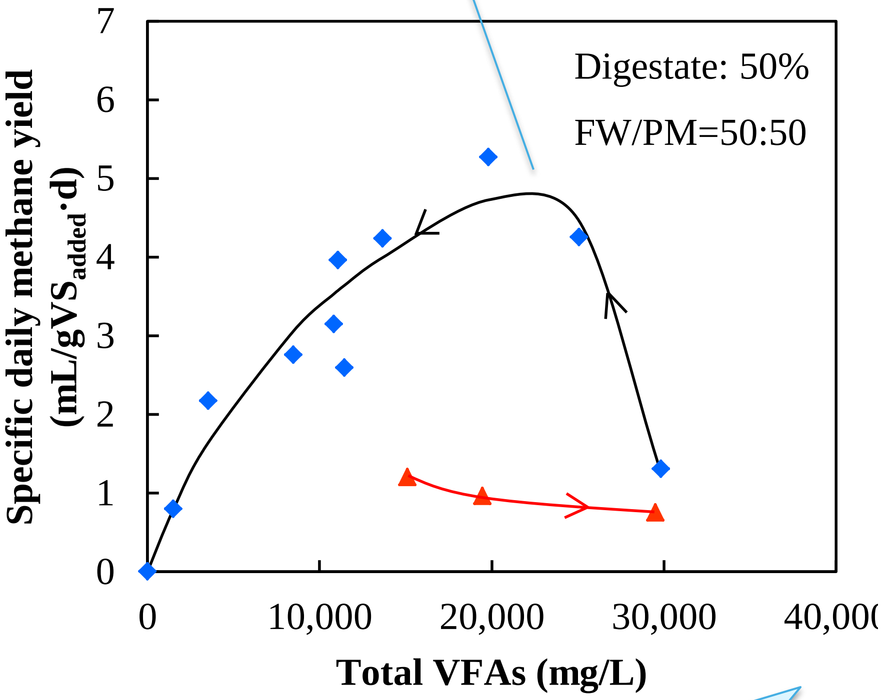
Max VFA – Lag phase



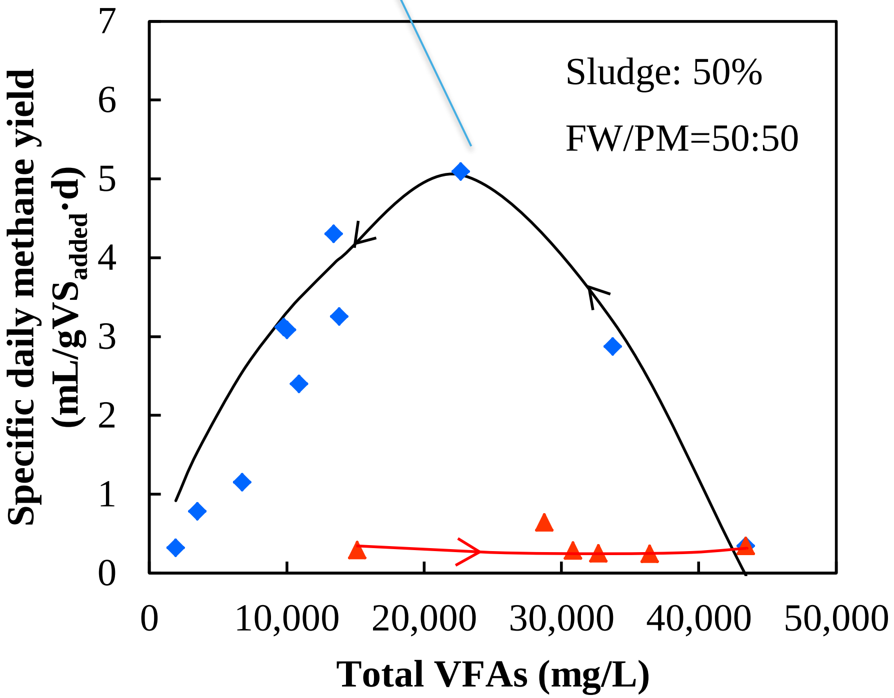
- **VFAs** are main inhibition factors for methane production

VFA - SDMY

20.0 g/L



21.0 g/L



- VFAs should be controlled **< 20 g/L**.

Experiment conclusion

- Preferable conditions: **Digestate 50%, FW/PM=50:50**.
- **VFAs** are main inhibition factors for methane production.
    - VFAs **< 20 g/L**.

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Enteric indicator bacteria

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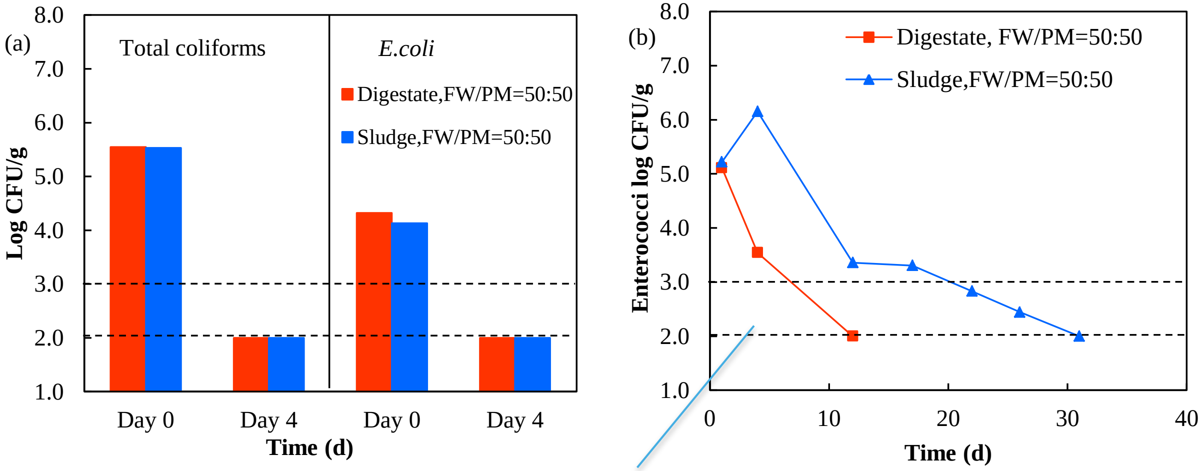
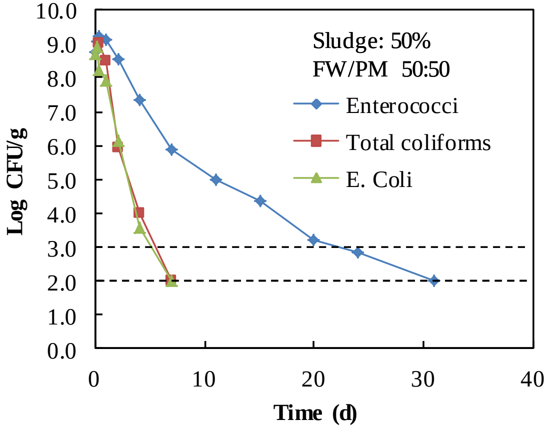
Batch 1



Batch 2



- Limit of detection (LOD): **100 CFU/g**
- Limit of regulations (UK PAS 100; Irish industry standard; ABP Regulations)
  - ***E. coli* ≤ 1,000 CFU/g, *Enterococaceae* ≤ 1000 CFU/g**

Batch	T_c* (d)	*E. coli*	Total coliforms	Enterococci
1	Initial concentration (CFU/g)	10^4-10^5	10^5-10^6	10^5-10^6
	Digestate	4	4	12
	Sludge	4	4	31
2	Initial concentration (CFU/g)	6.20×10^8	1.56×10^9	6.10×10^8
	Sludge	7	7	31

* Tc: Time required to reduced to the limit of detection (LOD).

Enteric indicator bacteria

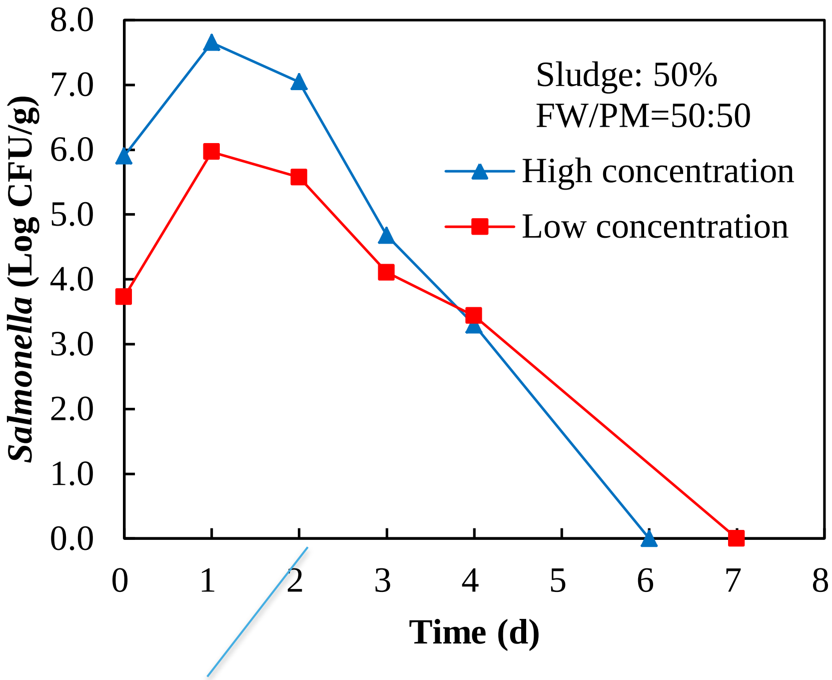
Multiple linear regression analysis (stepwise): Sludge 50% FW/PM=50:50

Dependent variable	Constant	Coefficient						R^2
		Digestion time (d)	pH	Total VFAs (mg/L)	Free VFAs (mg/L)	TAN (mg/L)	FA (mg/L)	
Enterococci	12.886	-0.165***						0.929
Total coliforms	9.422				-0.184**			0.975
E. coli	8.994				-0.174**			0.961

*P < 0.05; **P < 0.01; ***P < 0.001

- **Digestion time** was main inhibition factor for enterococci.
- **Free VFAs** were main inactivation factor for total coliforms and *E. coli*.

Enteric indicator bacteria



- Limit of regulations (UK PAS 100; Irish industry standard; ABP Regulations)
  - ***Salmonella*: 0 CFU/g in digestate**

Initial concentration	***Salmonella***	**T (d)**
High concentration (CFU/g)	8.15×10^5	6
Low concentration (CFU/g)	5.88×10^3	7

Pathogen conclusion

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- Dry co-digestion can eliminate pathogens **(*E. coli*, total coliforms, enterococci and *Salmonella*)** effectively.
    - **Digestion time** was main inhibition factor for enterococci.
    - **Free VFAs** were main inactivation factor for total coliforms and *E. coli*.

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Phylum level

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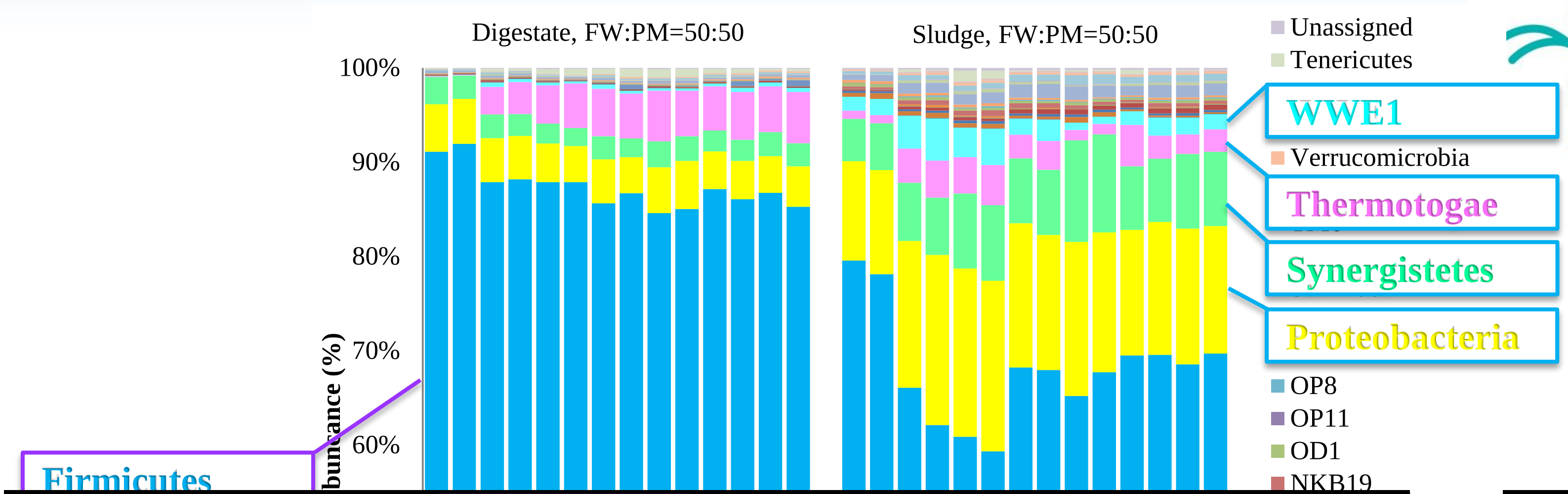
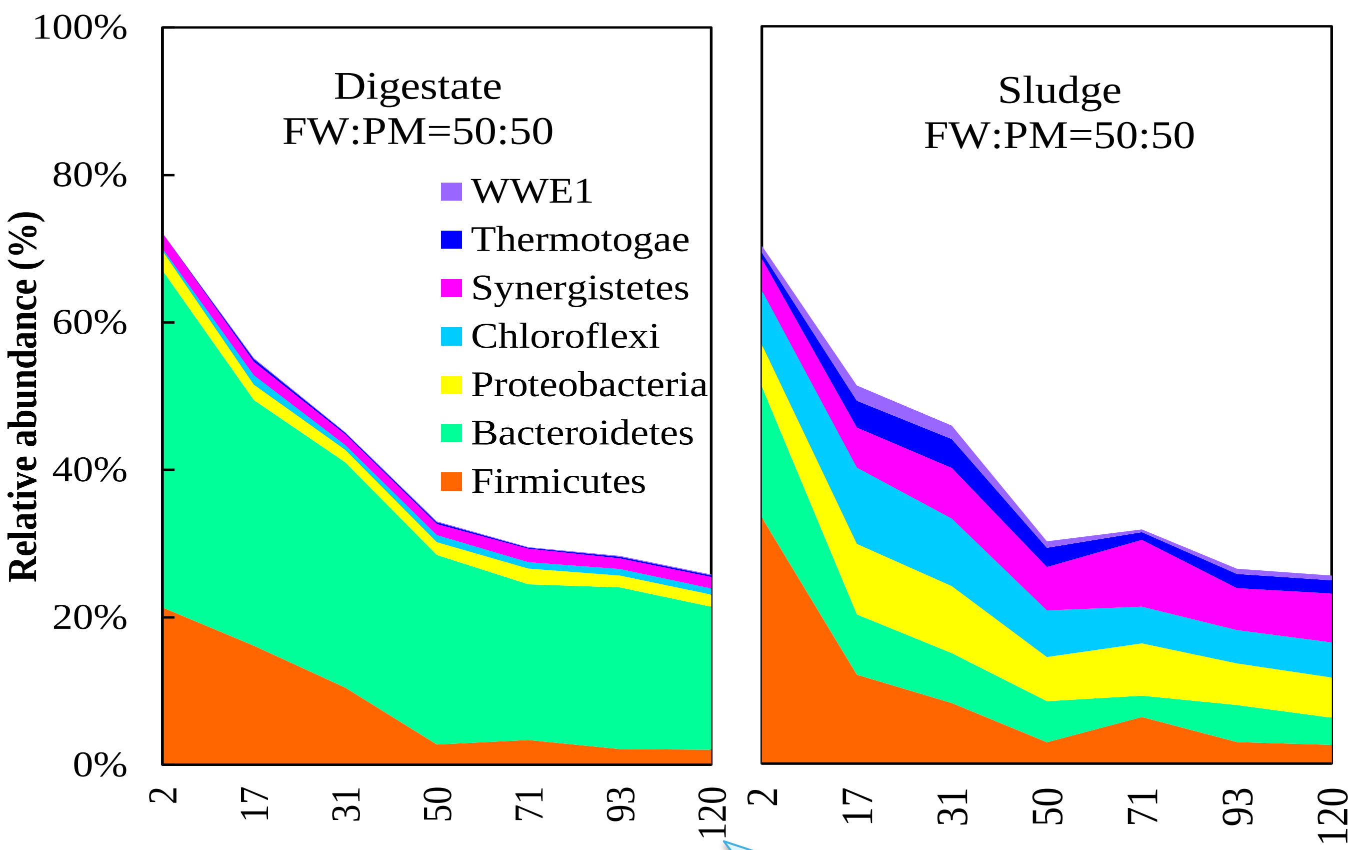


RA (%)	Digestate	Sludge	P value
Euryarchaeota	5.0 ± 2.2	4.0 ± 1.8	
Actinobacteria	2.5 ± 0.3	6.3 ± 1.2	***
Bacteroidetes	28.9 ± 8.8	10.9 ± 5.0	***
Chloroflexi	1.1 ± 0.3	7.5 ± 2.3	***
Firmicutes	49.9 ± 4.7	39.4 ± 7.4	***
Proteobacteria	4.4 ± 0.5	14.8 ± 2.3	***
Synergistetes	2.4 ± 0.3	7.0 ± 1.5	***
Thermotogae	4.2 ± 1.5	2.6 ± 1.3	***
WWE1	0.3 ± 0.1	2.2 ± 1.1	***

Scale
1
0.05
0.01
0.001
0.0001

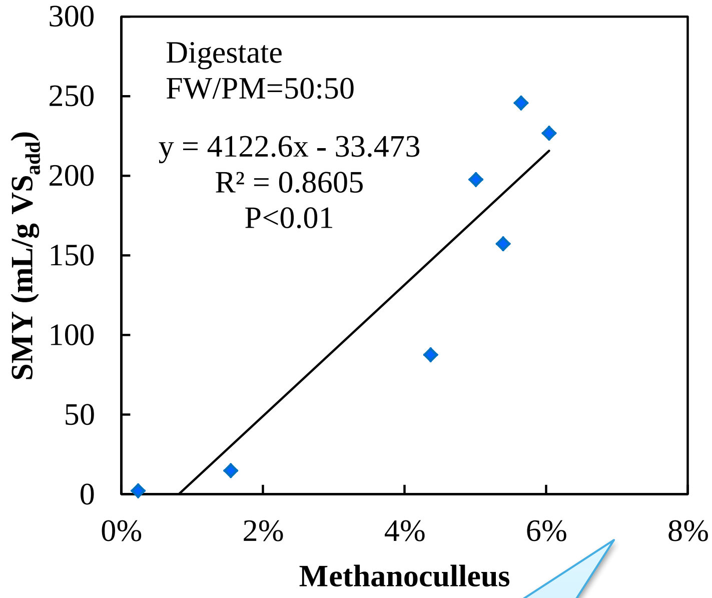
* $P<0.05$
** $P<0.01$
*** $P<0.001$

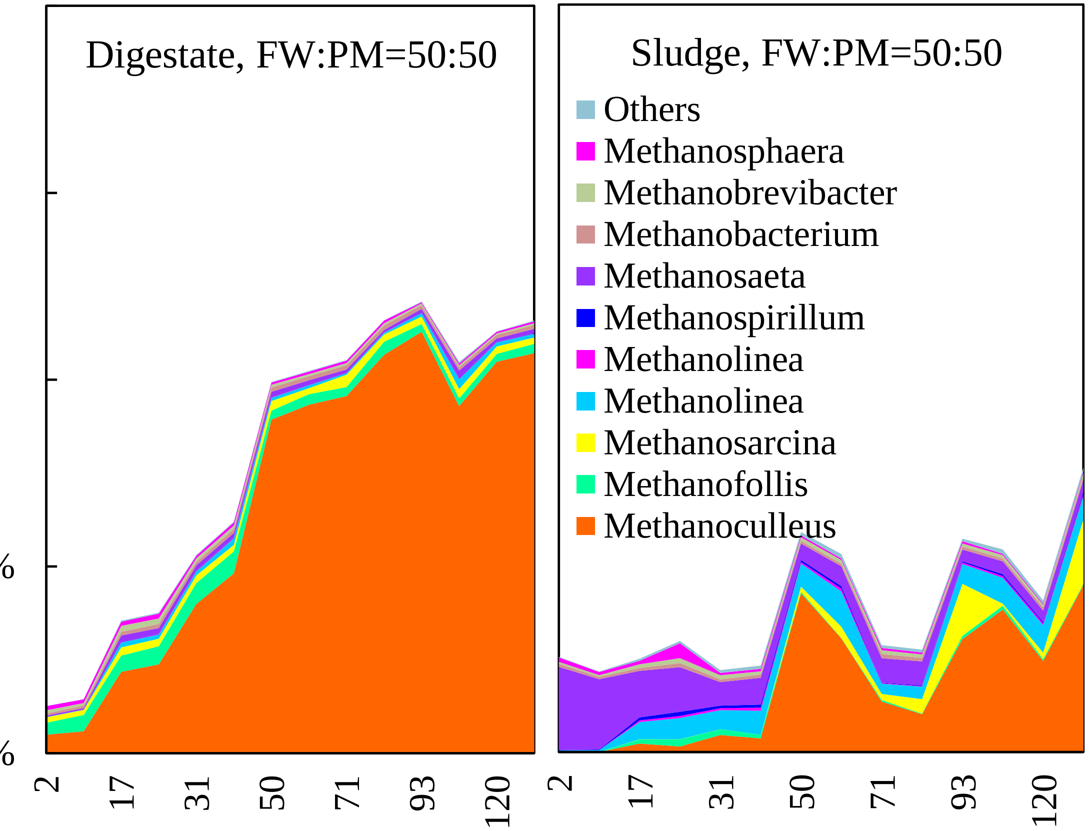
Hydrolysis & Fermentation



- Digestate: ***Bacteroidetes, Firmicutes***
- Sludge: various bacteria.

Methanogen





- ***Methanoculleus*** is main contributor for SMY.
- **Hydrogenotrophic** pathway dominated.

DNA conclusion

- Microbial community structures are significantly different in digestate and sludge inoculum systems.
- Hydrolysis and fermentation:
  - Digestate: ***Bacteroidetes* and *Firmicutes***
  - Sludge: various bacteria
- Methanogenesis:
  - ***Methanoculleus*** dominate
  - **Hydrogenotrophic** pathway dominated.

Conclusion

- Preferable conditions: **Digestate 50%, FW/PM=50:50**.
- VFAs **< 20g/L** to prevent inhibition.
- Dry co-digestion of FW and PM can **eliminate pathogens effectively**.
- ***Methanoculleus*** dominated.

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THANKS!