

## Changes in soil bacteria community associated with an introduction of an antagonist of potato disease

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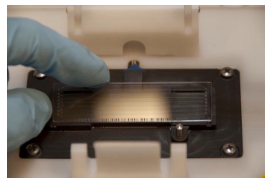


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**Luke**  
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## Next generation sequencing in microbial ecology

- **MiSeq-sequencing (FIMM)**
  - 10 milj. seqs/run
  - 20 000 – 200 000 seqs/sample in published research articles
  - Allows for a repeatable view of the whole microbial community
    - Including the minor groups
  - In our case, 206 000 seqs/sample from same plots on two consecutive years



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The bacterial community in field soil after addition of an antagonist bacterium against potato common scab

Plot	Year of treatment				
	2009	2010	2011	2012*	2013*
C					
A1				■	
A3	■	■	■		
A4	■	■	■	■	

3

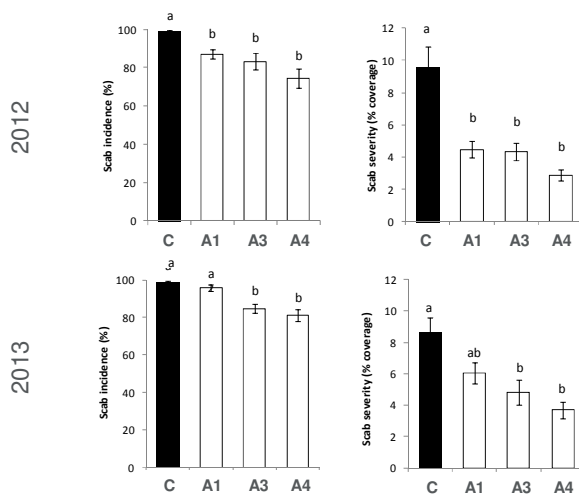
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Incidence and severity of common scab on potato tubers post treatment



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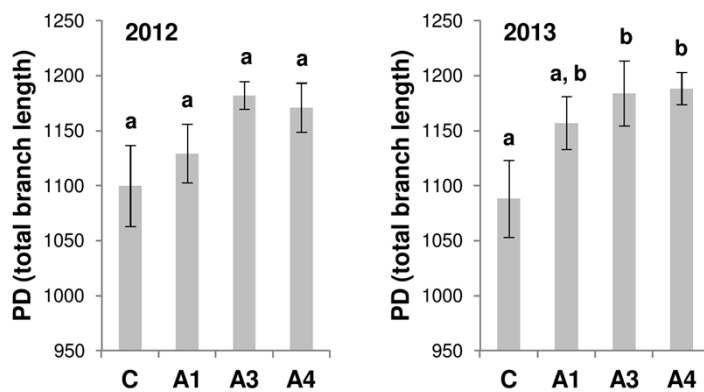
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### Bacterial diversity post treatment ( $\alpha$ )



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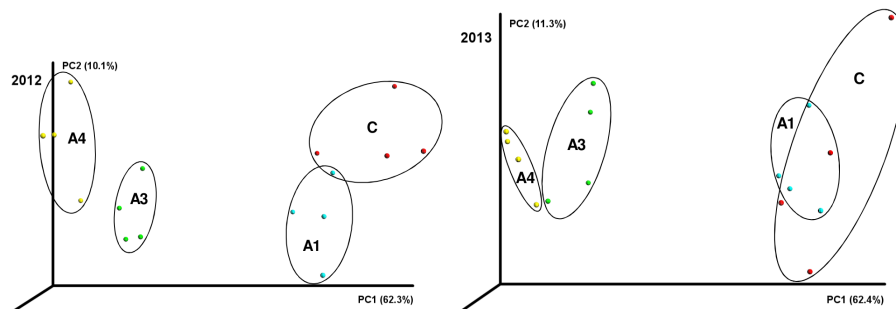
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### Bacterial communities post treatment ( $\beta$ )



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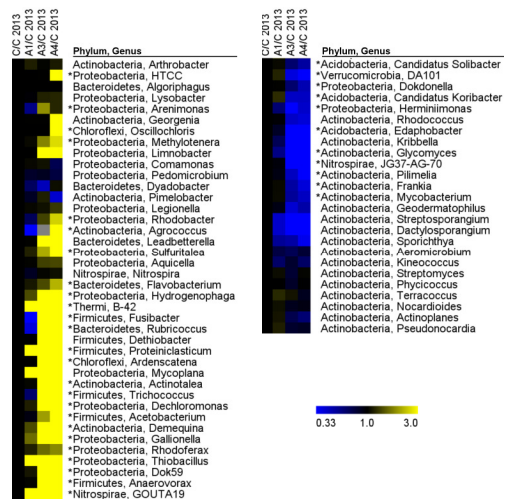
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## Looking at the changes at taxonomic level



- Adds the function of the bacterial group to considerations
- Slow growers ↓
- Fast growers ↑
- *E.g.* 5 genera up that use S, SO<sub>3</sub><sup>2-</sup> and/or SO<sub>4</sub><sup>2-</sup>