

# Genomic Analysis of Virulence Factors of *Burkholderia cenocepacia*

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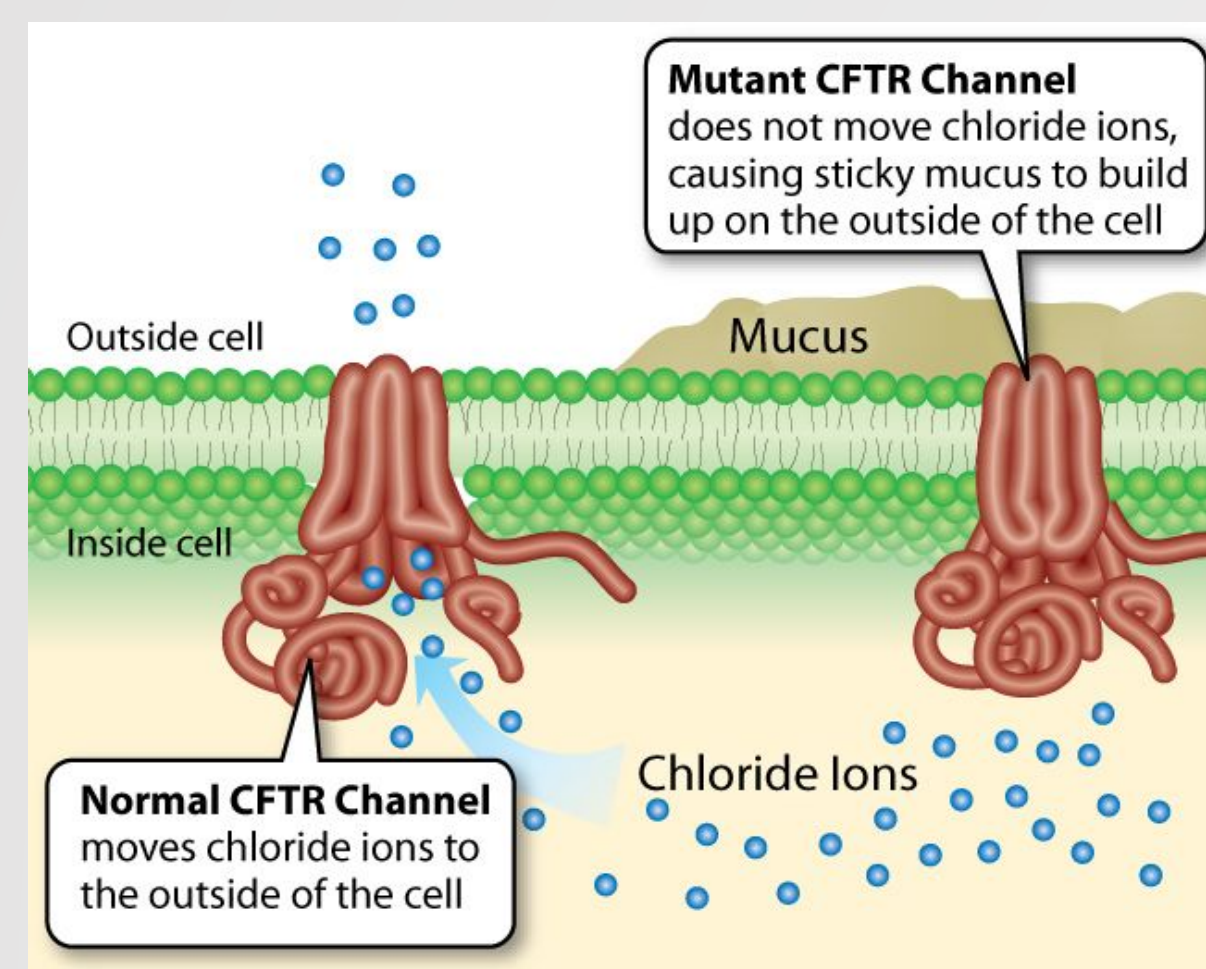
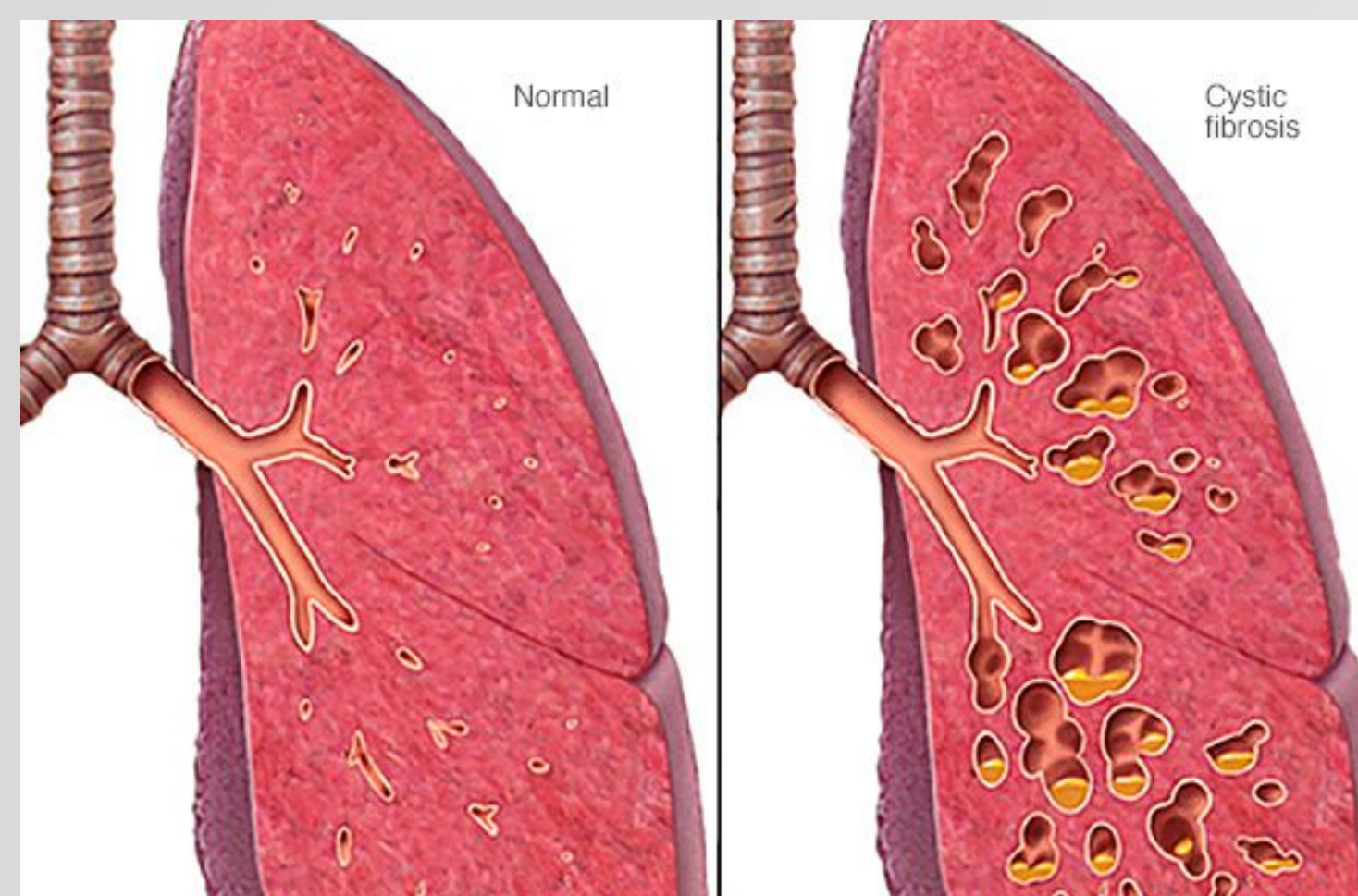


BASS  
CONNECTIONS

## Introduction

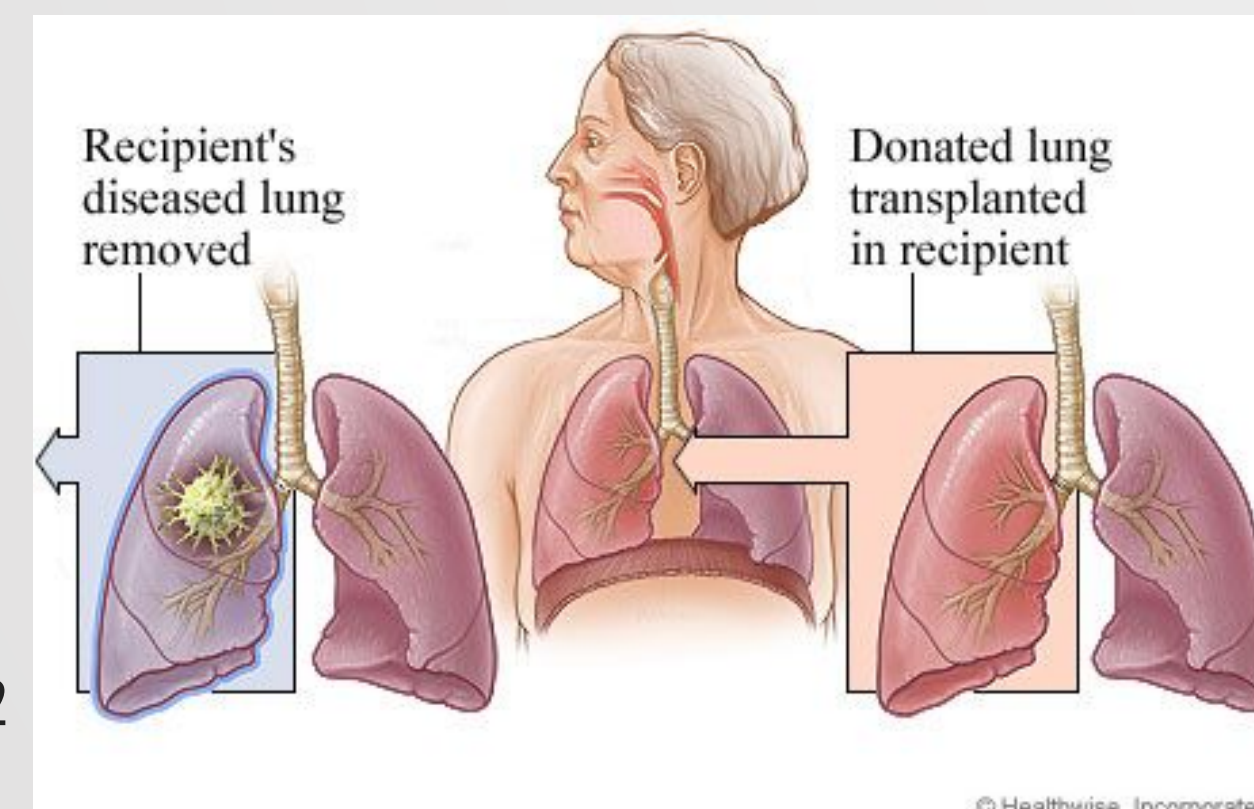
### Cystic Fibrosis (CF)

- Autosomal recessive genetic disorder caused by mutated CFTR gene
- Abnormally thick and sticky mucus clogs the airways, leading to difficulty breathing, respiratory infections, and permanent lung damage
- High risk of frequent onset of opportunistic infections
- Prevalent infectious agents: *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Burkholderia cepacia*



### Lung Transplants: Life-Saving Therapy

- Transplant centers refuse to perform transplants for patients infected by *B. cenocepacia* due to high morbidity rates
  - Post-op immunosuppressants increase risk for infections caused by bacteria occupying airways
- In a study of CF patients who underwent lung transplantation, 75% of *Burkholderia cenocepacia*-infected individuals died within the first year<sup>2</sup>
  - Sepsis due to *B. cenocepacia* is the cause of death in 89% of cases<sup>2</sup>

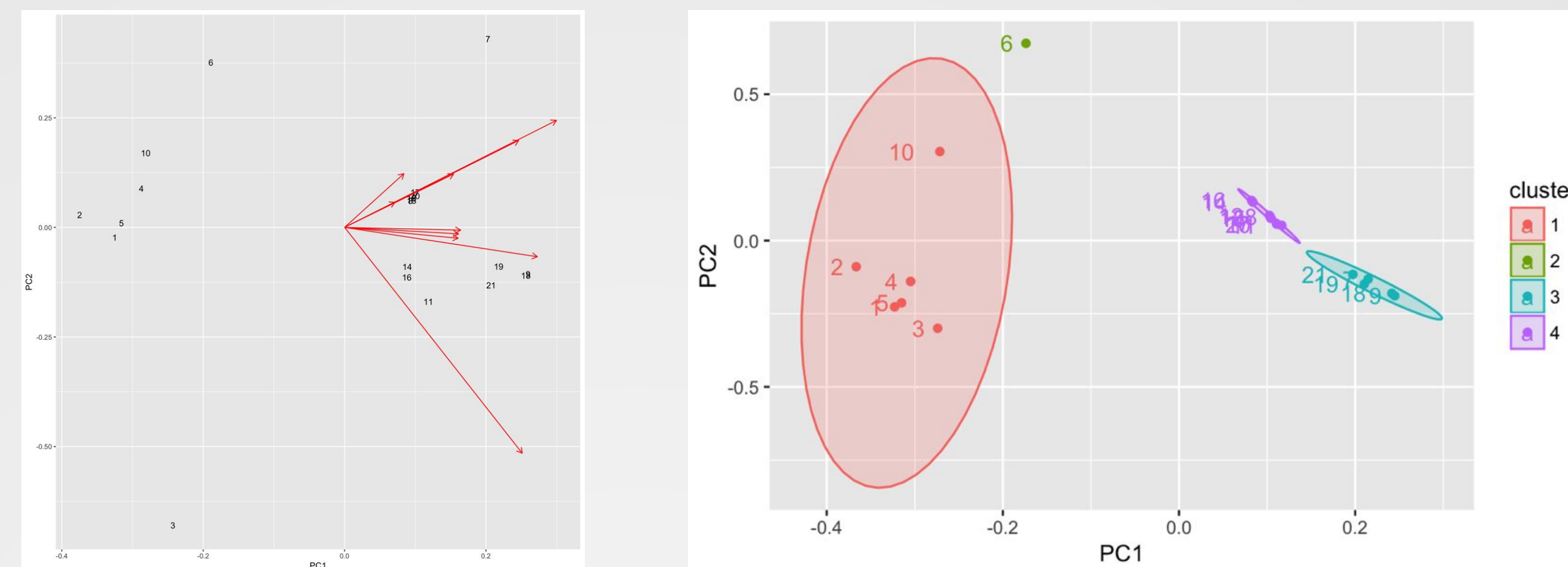


## Methods

- 21 samples of *B. cenocepacia* collected and sequenced from CF patients who underwent lung transplantation (Duke University Hospital)
- Literature review to develop a targeted list of putative virulence genes
- Custom BLAST to analyze sequences for presence of targeted genes
- PCA and K-means clustering analysis on BLAST results from targeted genes for each sample and identification of subsequent clusters

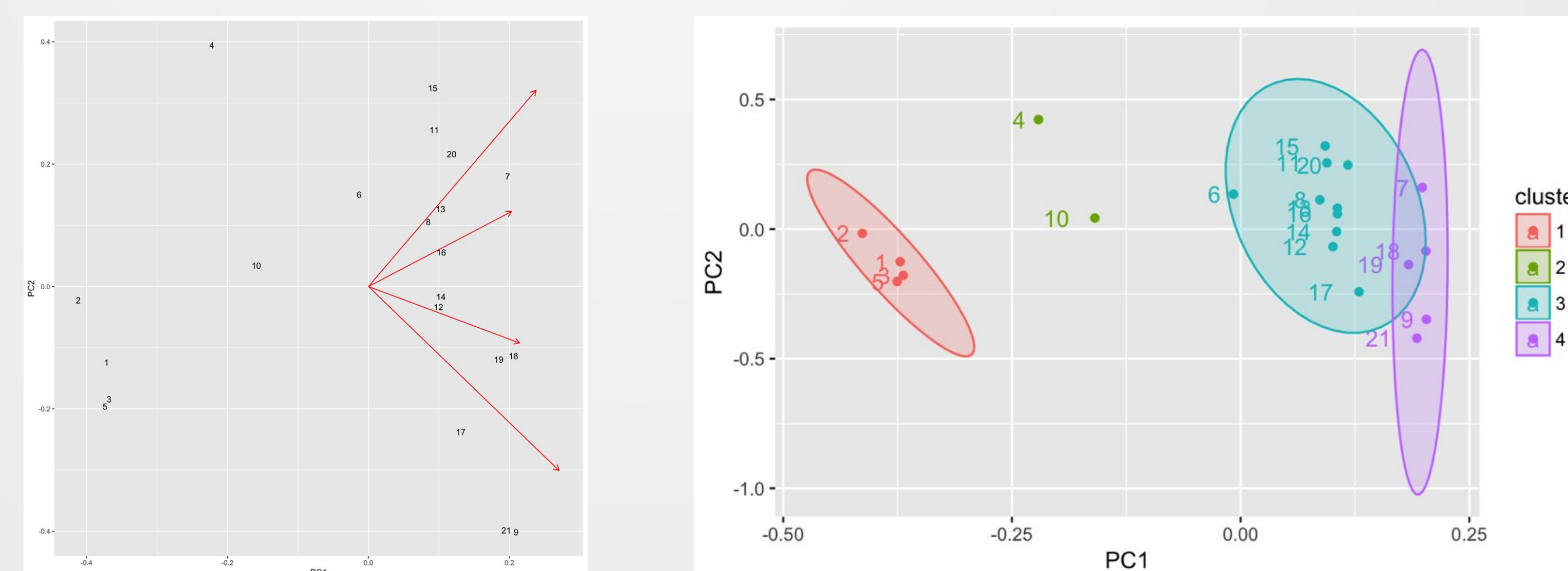
## Efflux Pump Gene

- Efflux pumps are a common mechanism for multidrug antibiotic resistance
- RND Channels 3, 4, 9, and 10 and their regulators were analyzed



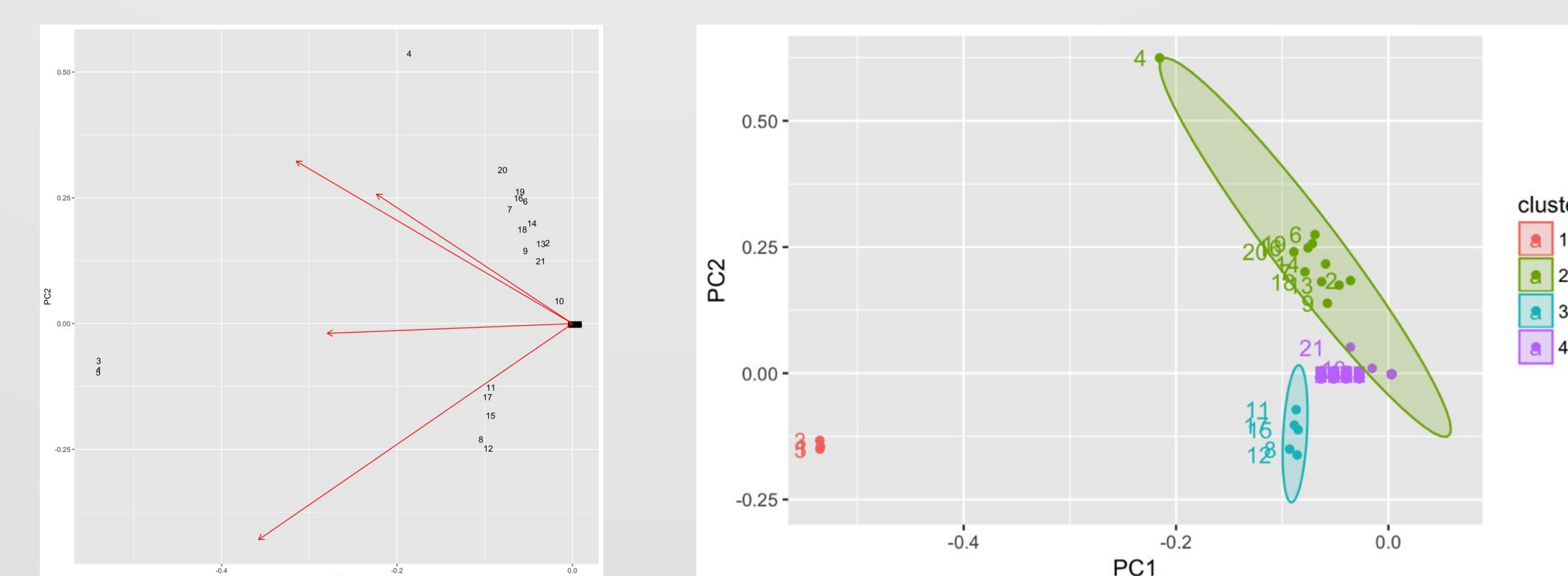
## Quinolone Resistance Gene

- Quinolone antibiotics treat nosocomial infections by preventing DNA ligation using 2 DNA repair proteins: gyrase and topoisomerase IV
- Mutations in the gyrase and topoisomerase genes are thought to inhibit quinolones interaction, promoting multidrug resistance



## Psl Gene Family

- Encodes exopolysaccharide responsible for bacterial biofilm formation
- Biofilms allow development and proliferation of bacteria in thick mucus layers in lungs



## Limitations

- Samples lacked correlating clinical data, obscuring the relationships of PCA clusters to specific clinical outcomes
- Clinical DNA samples could not be relocated for further sequencing analysis

## Conclusion

- The data is inconclusive until clinical data is obtained.
- There are promising results in the consistent clustering of sample
- Between Efflux pumps and Quinolone Resistance samples: 1,2,3, 4, 5, 10 and 6 clustered together

## Future Directions

- Obtain clinical data to determine relationships between PCA clusters and specific clinical outcomes.
- Conduct multidrug resistant assays on all clinical samples
- Run PCR to confirm the presence of selected genes in patient samples
- Sequencing of PCR amplified virulence genes from patient samples to analyze for mutations
- Query raw sample reads against *B. cenocepacia* to investigate the presence of genes at low read count

## References

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