

# 10. Discussion on specialized databases/tools

Guillaume GAUTREAU, 29/09/2022

# Outline of the presentation

- Databases of Carbohydrate Active enzymes
- Antimicrobial resistance genes
- Virulence genes
- Plasmid databases
- Mobile Genetics Elements: IS / Integron / ICE
- CRISPR/CAS
- Phage genomes

# CAZy / dbCAN2

- Old database (1998) created by the B. Henrissat
- A massive resource on enzymes working on carbohydrate molecules
- All kind of enzymes:
  - Glycoside Hydrolases (GHs) : hydrolysis and/or rearrangement of glycosidic bonds (see CAZypedia definition)
  - GlycosylTransferases (GTs) : formation of glycosidic bonds (see definition)
  - Polysaccharide Lyases (PLs) : non-hydrolytic cleavage of glycosidic bonds
  - Carbohydrate Esterases (CEs) : hydrolysis of carbohydrate esters
  - Auxiliary Activities (AAs) : redox enzymes that act in conjunction with CAZymes.
- Enzymes are classified in families according to their structural and functional features
- To characterize your genes according to this resource:
  - work with the CAZy team
  - work with a data similar to CAZy: dbCAN2

# Antimicrobial resistance genes

- Drug inactivation or modification toward an enzyme:
  - example :  $\beta$ -lactamases.
- Alteration of antibiotic target:
  - penicillin-resistant bacteria.
- Alteration of metabolic pathway:
  - sulfonamide-resistant bacteria
- Drug permeability or active efflux (pumping out) of the drugs
  - resistances to some macrolides
  - fluoroquinolone resistance
- And other mechanisms

# Antimicrobial resistance genes: plenty of resources

- Abricate
- amrfinderplus
- ariba
- **rgi (CARD)**
  - <https://card.mcmaster.ca/analyze/rgi>
- **resfinder**
  - <https://cge.cbs.dtu.dk/services/ResFinder/>
- srax
- deeparg
- kmerresistance
- srst2
- staramr
- csstar
- amrplusplus
- resfams
- groot
- tbprofiler
- mykrobe
- pointfinder
- ⇒ all of these results can be combined using hAMRonization:
  - <https://github.com/pha4ge/hAMRonization>

# VirulenceFinder

- Database of virulence factors:
  - Toxin, enterotoxins (shiga...)
  - Superantigens
  - Some secretion systems
  - and many others: <https://cge.food.dtu.dk/services/data.php>
- <https://cge.cbs.dtu.dk/services/VirulenceFinder/>
- For Salmonella only : SPIFinder

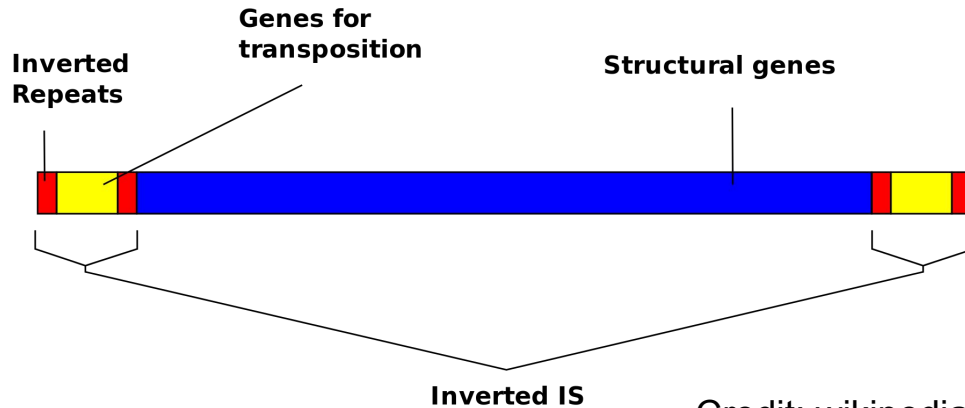
# Plasmid databases

- PlasmidFinder: <https://cge.cbs.dtu.dk/services/PlasmidFinder/>
- PlaScope
- PLSDB: <https://ccb-microbe.cs.uni-saarland.de/plsdb>

# ISFinder

- IS: Insertion Sequences (IS):
  - A short DNA sequence that acts as a simple transposable element
  - Carry some accessory genes such as antibiotic resistance genes
- <https://isfinder.biotoul.fr/>

## Bacterial composite transposon

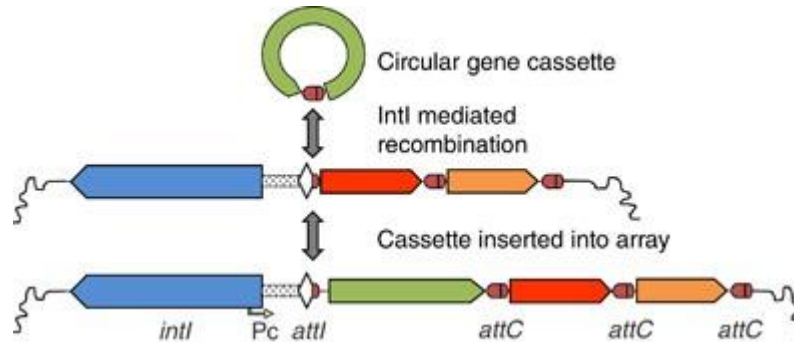


Credit: wikipedia



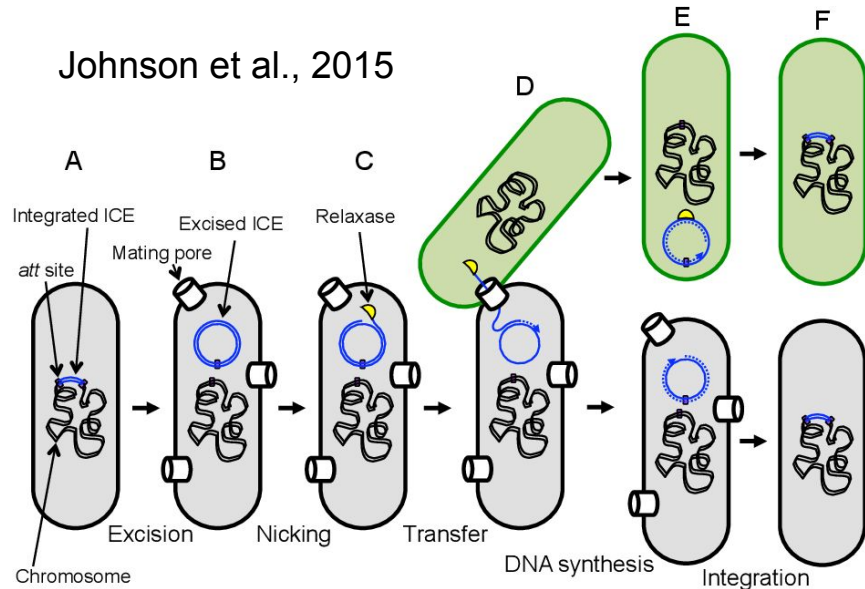
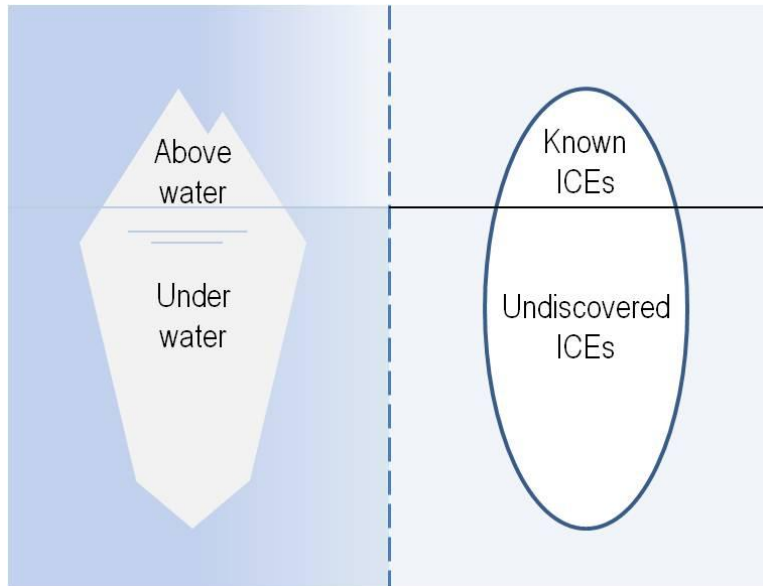
# IntegronFinder

- Integrons are an assembly of several genetic elements that include an integrase (IntI) and a succession of gene cassettes flanked by recombination attachment sites (att)
- IntegronFinder is a program that detects integrons in DNA sequences
- [https://github.com/gem-pasteur/Integron\\_Finder](https://github.com/gem-pasteur/Integron_Finder)



# Integrative and Conjugative Elements

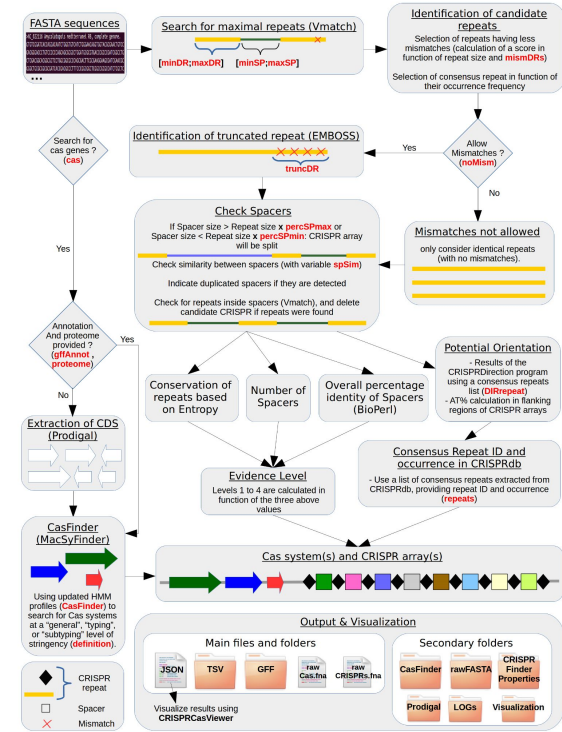
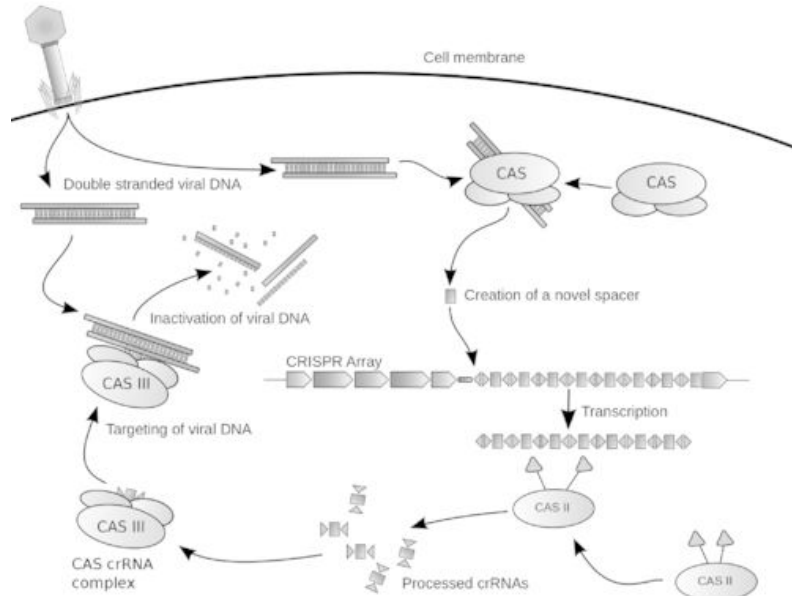
- ICEberg 2.0: an updated database of Integrative and Conjugative Elements
- <https://bioinfo-mml.sjtu.edu.cn/ICEberg2/index.php>



# Different kinds of non coding genes : CRISPR

<https://github.com/dcouvin/CRISPRCasFinder>

<https://crisprcas.i2bc.paris-saclay.fr/CrisprCasFinder/Index>



# Phage genome databases

- Detection of prophage in genome PHASTER: <https://phaster.ca/>
- Phagonaute: <https://genome.jouy.inra.fr/phagonaute/>
- Phage homologous families Phrog: <https://phrogs.lmge.uca.fr/>

# Discussion

*If it is the case, what specialized resources do you want to share with us ?*

# Proposed database: Enterobase

<https://enterobase.warwick.ac.uk/species/index/senterica>