

Part1 :

In BIGSdb Bordetella Alleles & profiles database:

Considering locus *fim3*, compare alleles 1 and 2 (i.e *fim3*-1 and *fim3*-2) using locus explorer;
What Bp-agST correspond to the following profiles :

ptxP	ptxA (BP3783)	ptxB (BP3784)	ptxC	ptxD (BP3785)	ptxE (BP3786)	fhaB-2400_5550	fim2 (BP1119)	fim3 (BP1568)
3	1	1	4	1	4	1	1	1
ptxP	ptxA (BP3783)	ptxB (BP3784)	ptxC	ptxD (BP3785)	ptxE (BP3786)	fhaB-2400_5550	fim2 (BP1119)	fim3 (BP1568)
3	1	1	4	1	4	1	1	2

Part2: Genome comparator

In BIGSdb Bordetella Isolates database:

Considering all isolates from the [public project 25](#),

Visualize the percentage of isolates per country in a pie chart (Field breakdown option)

Visualize the number of isolates resistant to macrolide per country (Two field breakdown option)

Using genome comparator, compare isolates FR5015 and FR5016, is it the same strain?

Using genome comparator, compare isolates FR5015 and FR4964, is it the same strain?

Part 3: GrapeTree :

In BIGSdb Bordetella Isolates database:

Considering all isolates from the public project [project 25](#)

Perform a first GrapeTree analysis based on Bp-vaccine-Antigen scheme

Color isolates per country, label BpAg-ST, indicate branch length

Visualize metadata

Perform a second GrapeTree based on cgMLST_pertussis

Color isolates per BpAg-ST, indicate branch length

Export image

Use Microreact to visualize analysis based on Bp-vaccine antigens and explore Microreact functions