In your country, less common serotypes of *Salmonella* spp. are not routinely sequenced. However, while preparing your yearly surveillance report for 2020, you realise that the number of *S. enterica* identified as belonging to serotype Bovismorbificans by sero-agglutination were particularly high in that year (n=76) and you decide to sequence them all to determine if there were any genomic clusters among them. The genomic data was then submitted to EnteroBase for analysis.

You can find the name of the strains and some metadata in the table Salmonella\_dataset\_GenEpi-BioTrain.xlsx.

With the information available on Enterobase, answer the following questions:

1. Was it possible to confirm the serotype identified by phenotypic methods using the genomic data?
2. Were there outbreaks during the evaluated period? How many? Present how they were identified.
3. Did you identify AMR genes among the studied population? Were they linked to a specific genomic cluster? Describe it.