



Ascertaining the Genomic Composition of *Pasteurella multocida* Isolates in testing for presence of Antimicrobial Resistance and Antiviral Defense Systems

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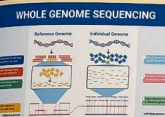


Background



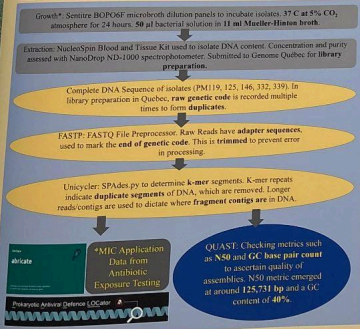
Pasteurella multocida is a class of Gram-Negative AMR bacteria, primarily targeting cattle lungs, causing pneumonia, and developing into **Brucella Respiratory Disease (BRD)**.
P. multocida is zoonotic. In humans, it causes abscesses in soft tissue. In severe cases, pneumonia, meningitis, and sepsis can develop.
With *P. multocida* a common yet understudied class of zoonotic AMR bacteria, measures need to be taken to ascertain the antiviral defense systems and AMR capability present in the bacteria to develop methods of treatment.

Research Questions and Aims

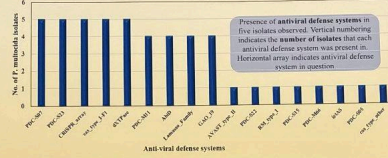


Using bioinformatic processing, this project aims to analyze AMR and antiviral defense in *P. multocida* isolates (PM119, PM125, PM146, PM332, PM339) with Whole-Genome Sequencing (WGS) to determine:
> What AMR genes are present in each isolate?
> What antiviral defense systems are present in each isolate?

Methodology



Antiviral Defense Systems Results

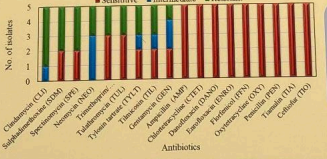


Presence of antiviral defense systems in five isolates observed. Vertical numbering indicates the number of isolates that each antiviral defense system was present in. Horizontal array indicates antiviral defense system in question.

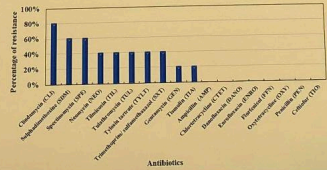
Antimicrobial Genes (AMR) Results

Number of resistance genes found in *P. multocida* isolates. Minimum zero to maximum 4 genes were identified within a single bacterial isolate with '+' indicating presence and '-' indicating absence of a gene.

<i>P. multocida</i> isolates	tet(b) 3	aadA14_1	aph(3)'-Ib	2_aph(3)'-Ia	3_aph(6)-Ib-1	No. of resistance genes present	Percentage positivity
119	+	-	-	-	-	2/5	40%
125	+	-	-	-	-	0/5	0%
146	-	+	+	+	+	4/5	80%
332	-	-	-	-	-	0/5	0%
339	-	+	+	+	+	4/5	80%



AMR resistance pattern in *P. multocida* isolates. Colour of bar chart represent the no. of sensitive (red), intermediate (yellow) and resistant (green) isolates against a particular antibiotic.



Percentage of resistance against a particular antibiotic found in *P. multocida* isolates. Maximum resistance was observed against clindamycin. Most of the isolates were susceptible to antibiotics tested.

Conclusions

- The analysis of antiviral defense systems and antimicrobial resistance in the 5 isolates concluded that:
 - AMR genes *aad* and *aph* class were detected, giving resistance towards aminoglycoside class antibiotics, such as Gentamicin, Neomycin, and Streptomycin, found in three isolates (PM119, PM146, and PM339).
 - AMR gene *tet* (b) 3 was also detected in PM119. However, given sensitivity was noted from all 5 isolates towards tetracyclines, this at most indicates developing resistance towards tetracyclines.
 - Isolates on average possessed resistance towards Aminoglycosides, Macrolides, and Lincosamides antibiotics.
 - Four isolates possessed Lamisnu family, PDC 5-Series system, and CRISPR-Cas type antiviral defense systems. The making of individual antiviral defense systems was near identical across four strains (PM119, PM146, PM332, and PM339).
 - PM125 contained when other distinct antiviral defense systems in comparison to the other four strains. It also lacks four abortive infection and metabolic influence antiviral defense systems found in the 4 other strains.

Future Development

- As stated previously, *P. multocida* is a relatively understudied species of zoonotic bacteria that poses AMR. By studying the presence of antiviral defense systems and AMR resistance on such bacteria, we can determine:
 - Antibiotics that each isolate possess enhanced resistance towards (Resistant, Figure 2), and antibiotics each isolate is weak to defend against (Sensitive, Figure 2).
 - Trends in AMR and MDR signatures across different isolates and species of bacteria.
 - Antiviral defense systems present in individual species, pinpointing which viruses and external chemical influences that each isolate of bacteria is or is not affected by.
 - Trends in antiviral defenses across isolates and species of bacteria.
 - Phylogenetic trees which can be formed to establish evolutionary trends from bacteria isolates to other isolates, as well as from species to species.

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