**Supplementary Data**

Table S1. Accession numbers for genomes sequenced.

|  |  |
| --- | --- |
| Isolate | Accession No. |
| 903 | [NTAE00000000](http://www.ncbi.nlm.nih.gov/nuccore/NTAE00000000) |
| 856 | [NTAD00000000](http://www.ncbi.nlm.nih.gov/nuccore/NTAD00000000) |
| 1098 | [NTAC00000000](http://www.ncbi.nlm.nih.gov/nuccore/NTAC00000000) |
| 982 | [NTAB00000000](http://www.ncbi.nlm.nih.gov/nuccore/NTAB00000000) |
| 1090 | [NTAA00000000](http://www.ncbi.nlm.nih.gov/nuccore/NTAA00000000) |
| 994 | [NSZZ00000000](http://www.ncbi.nlm.nih.gov/nuccore/NSZZ00000000) |
| 886\_1 | [NSZY00000000](http://www.ncbi.nlm.nih.gov/nuccore/NSZY00000000) |

**Table S2.** Counts of overall variable sites, SNPs and Indels between each polymyxin resistant isolate genome compared with PA01 and PA14 respectively, by short read mapping and variant calling. Ts = transition and Tv = Transversion.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Strain | SNP count | Indel count | Total count | Ts | Tv | Ts/Tv |
| vs PAO1 reference genome | | | | | | |
| 903 | 56361 | 887 | 57248 | 43128 | 13233 | 3.26 |
| 856 | 125303 | 1884 | 127187 | 92796 | 32507 | 2.85 |
| 1098 | 57288 | 927 | 58215 | 43734 | 13554 | 3.23 |
| 982 | 29399 | 498 | 29897 | 21979 | 7420 | 2.96 |
| 1090 | 28373 | 538 | 28911 | 21404 | 6969 | 3.07 |
| 994 | 28454 | 507 | 28961 | 21415 | 7039 | 3.04 |
| 886\_1 | 29138 | 532 | 29670 | 22016 | 7122 | 3.09 |
| vs PA14 reference genome | | | | | | |
| 903 | 35750 | 613 | 36363 | 27611 | 8139 | 3.39 |
| 856 | 130312 | 1985 | 132297 | 96630 | 33682 | 2.87 |
| 1098 | 42853 | 768 | 43621 | 32050 | 10803 | 2.97 |
| 982 | 59452 | 953 | 60405 | 45147 | 14305 | 3.16 |
| 1090 | 61403 | 1050 | 62453 | 46431 | 14972 | 3.1 |
| 994 | 60900 | 1004 | 61904 | 46129 | 14771 | 3.12 |
| 886\_1 | 59378 | 950 | 60328 | 45211 | 14167 | 3.19 |

**Table S3.** All amino acid changes identified in the 7 genome sequenced veterinary *P. aeruginosa* isolates through whole genome sequencing.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | 856 | 886 | 903 | 994 | 982 | 1090 | 1098 |
| *pyrC* | D16G  T184S  Q247R  N297S  S355A  R368S  V402I  G423STOP | D16G  Q383E | D16G | D16G | D16G | D16G  G130S  R363H | D16G  G423STOP |
| *pyrB* | P272S |  |  |  |  |  |  |
| *phoQ* | D90E  E267Q  V369L |  |  |  |  |  |  |
| *pdxB* | Q369L | A307V  T337N  Q365R | V109K  H183Y  P192T | A105V  L310M  A361T | E191G  D324A  Q365R | R179H  R247H | V109K  H183Y  P192T |
| *parR* | T135A  L153R |  | L153R  S170N | P128S  L153R  S170N | L153R  S170N |  | L153R  S170N |
| *mpl* | S221T  I226S  Q347R  A404P  E451STOP | V358I | V297M  A415V | V297M |  |  |  |
| *rmlD* | V98I |  |  |  |  |  |  |
| *ampR* | E114A  G283E  M228R  R291STOP | E114A  E172V  A208T | E114A  G283E  M228R |  |  |  | E114A  I251V  G283E  M228R |
| *tpiA* | S47G  T78I |  |  |  |  |  |  |
| *pmrA* | L71R | L71R |  | L71R |  | L71R | L71R |
| *wapR* | A83T  T85A  W114R  295STOP | T85A | R58H  R78K  T85A | T85A | R78K  T85A |  | R58H  R78K  T85A |
| *Ssg* | S35G |  |  |  |  |  | A109V |
| *aroB* | L54F  Q58E  V85A  E89G  A200E | V85A  A200E | V85A  A200E | V85A  A200E  S235L  I297T | V85A  A200E | V85A  A200E  I297T | V85A  A200E |
| *amgS* | Q100R |  | I260V |  |  | I260V | I260V |
| *galU* |  |  |  |  | N338S |  |  |
| *pyrD* |  |  |  |  |  |  |  |
| *sucC* |  |  |  |  |  |  |  |
| *lptC* |  |  |  |  |  |  |  |
| *arnA* | T42I  L50F  H199R  V250I  T297A  C312S  S313G  V564I | C312S  S313G  S509N  I551V | H59Y  F80Y  C312S  S313G | C312S  S313G  I551V | C312S  S313G | C312S  S313G | F80Y  C312S  S313G |
| *arnB* | G120S  T143A  V153I  I231V  K286E  V302A  S321T  H332R  R363G  E376D | A316V  V302A | K286E  V302A  E376D | V302A  A316V | V302A  A316V | V302A | V302A  K286E  E376D |
| *arnC* | P23A  E35G  A265S  T316A |  |  |  |  |  |  |
| *arnD* | E25D  F58L  V123T  G208S  A284D |  | F58L |  |  |  |  |
| *arnE* | A32T  D33S  T26A  L56V  A84V  F87L  S114N |  |  |  |  |  | R28H |
| *arnF* | A129T  P137L |  |  |  | V14M | T106I |  |
| *arnT* | C7W  L93F  L163F  A267S  P290A  L337Q  D440G  T443A  H447Y  R502Q  I509V | R502Q  I509V | C7W  H151Y  L337Q  I509V  T16S  E386D | R502Q | A267S  R448H  R502Q  I509V | V266I  A282S | C7W  A214V  T443A  I509V |
| *colS* | Q60K  V425I |  |  |  |  |  |  |
| *cprR* | V27A  I59V  E183D |  |  |  |  |  |  |
| *cprS* | V22I  A78E  D89G  V159I  V165I  T170A  E386D |  |  |  |  |  | T16S |
| *parS* | E90K  A115E  V304I  H398R | H398R | H398R  R243H | H398R | H398R | H398R | H398R |
| *pmrB* |  |  |  |  |  |  |  |
| *colR* |  |  |  |  |  |  |  |

**Figure S1.tif**

**Figure S1**. Ciprofloxacin resistance in the veterinary *P. aeruginosa* isolates.

**Figure S2.tif**

**Figure S2**. Heat map of resistance genes present in 7 veterinary *P. aeruginosa* isolates identified through whole genome sequencing. (White: no sequence matching the protein; dark blue: perfect match found (>90% sequence ID); light blue: partial match found).