**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* | D16GT184SQ247RN297SS355AR368SV402IG423STOP | D16GQ383E | D16G | D16G | D16G | D16GG130SR363H | D16GG423STOP |
| *pyrB* | P272S |  |  |  |  |  |  |
| *phoQ* | D90EE267QV369L |  |  |  |  |  |  |
| *pdxB* | Q369L | A307VT337NQ365R | V109KH183YP192T | A105VL310MA361T | E191GD324AQ365R | R179HR247H | V109KH183YP192T |
| *parR* | T135AL153R |  | L153RS170N | P128SL153RS170N | L153RS170N |  | L153RS170N |
| *mpl* | S221TI226SQ347RA404PE451STOP | V358I | V297MA415V | V297M |  |  |  |
| *rmlD* | V98I |  |  |  |  |  |  |
| *ampR* | E114AG283EM228RR291STOP | E114AE172VA208T | E114AG283EM228R |  |  |  | E114AI251VG283EM228R |
| *tpiA* | S47GT78I |  |  |  |  |  |  |
| *pmrA* | L71R | L71R |  | L71R |  | L71R | L71R |
| *wapR* | A83TT85AW114R295STOP | T85A | R58HR78KT85A | T85A | R78KT85A |  | R58HR78KT85A |
| *Ssg* | S35G |  |  |  |  |  | A109V |
| *aroB* | L54FQ58EV85AE89GA200E | V85AA200E | V85AA200E | V85AA200ES235LI297T | V85AA200E | V85AA200EI297T | V85AA200E |
| *amgS* | Q100R |  | I260V |  |  | I260V | I260V |
| *galU* |  |  |  |  | N338S |  |  |
| *pyrD* |  |  |  |  |  |  |  |
| *sucC* |  |  |  |  |  |  |  |
| *lptC* |  |  |  |  |  |  |  |
| *arnA* | T42IL50FH199RV250IT297AC312SS313GV564I | C312SS313GS509NI551V | H59YF80YC312SS313G | C312SS313GI551V | C312SS313G | C312SS313G | F80YC312SS313G |
| *arnB* | G120ST143AV153II231VK286EV302AS321TH332RR363GE376D | A316VV302A | K286EV302AE376D | V302AA316V | V302AA316V | V302A | V302AK286EE376D |
| *arnC* | P23AE35GA265ST316A |  |  |  |  |  |  |
| *arnD* | E25DF58LV123TG208SA284D |  | F58L |  |  |  |  |
| *arnE* | A32TD33ST26AL56VA84VF87LS114N |  |  |  |  |  | R28H |
| *arnF* | A129TP137L |  |  |  | V14M | T106I |  |
| *arnT* | C7WL93FL163FA267SP290AL337QD440GT443AH447YR502QI509V | R502QI509V | C7WH151YL337QI509VT16SE386D | R502Q | A267SR448HR502QI509V | V266IA282S | C7WA214VT443AI509V |
| *colS* | Q60KV425I |  |  |  |  |  |  |
| *cprR* | V27AI59VE183D |  |  |  |  |  |  |
| *cprS* | V22IA78ED89GV159IV165IT170AE386D |  |  |  |  |  | T16S |
| *parS* | E90KA115EV304IH398R | H398R | H398RR243H | H398R | H398R | H398R | H398R |
| *pmrB* |  |  |  |  |  |  |  |
| *colR* |  |  |  |  |  |  |  |

****

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

****

**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).