

Supplementary Materials

Comparable Bioavailability and Disposition of Pefloxacin in Patients with Cystic Fibrosis and Healthy Volunteers Assessed via Population Pharmacokinetics

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Table 1. Estimates from the original dataset compared to the median and 95% confidence intervals from nonparametric bootstrapping (200 replicates) for the final population PK model.

PK Parameters	Symbol	Unit	Population Mean		Between Subjects Variability (CV)	
			Original Dataset	Median (95% CI) (2.5 th to 97.5 th percentile)	Original Dataset	Median (95% CI) (2.5 th to 97.5 th percentile)
<i>Pefloxacin</i>						
Oral bioavailability	F _{BIO}	-	1.00 ^a	1.01 (0.909–1.11) ^a	0.146 ^a	0.140 (0.0548–0.210) ^a
			1.03 ^b	1.03 (0.934–1.10) ^b	0.127 ^b	0.119 (0.0478–0.160) ^b
Absorption lag-time	T _{lag}	min	13.3	13.4 (12.8–14.1)	0.0712	0.0631 (0.0261–0.0867)
Absorption half-life	T _{abs}	min	19.8 ^a	20.2 (9.65–45.1) ^a	1.10 ^a	1.01 (0.627–1.35) ^a
			11.2 ^b	11.3 (6.20–18.1) ^b	0.983 ^b	0.969 (0.518–1.34) ^b
Reabsorption half-life from intestine	T _{reabs}	min	65.4 ^a	65.5 (41.0–89.7) ^a	0.334 ^a	0.0720 (0.00768–0.600) ^a
			20.8 ^b	20.0 (6.37–41.8) ^b	0.804 ^b	0.747 (0.0965–1.27) ^b
Volume of distribution for central comp.	V ₁	L	40.8	39.8 (22.2–58.6)	0.435	0.417 (0.0313–0.632)
Volume of distribution for peripheral comp.	V ₂	L	65.4	66.6 (50.2–76.7)	0.131	0.0619 (0.00851–0.309)
Non-renal clearance	CL _{NR}	L/h	8.56	8.59 (7.44–9.77)	0.238	0.224 (0.125–0.310)
Renal clearance	CL _R	L/h	0.705	0.710 (0.662–0.753)	0.168	0.166 (0.0111–0.265)
Distribution clearance	CL _D	L/h	406	414 (164–1,199)	1.19	1.18 (0.693–2.05)
Disease factor for nonrenal clearance	F _{CYF, NR}	-	0.861	0.850 (0.694–1.07)	0.05	fixed
Disease factor for renal clearance	F _{CYF, R}	-	1.53	1.53 (1.21–1.78) ^c	0.05	fixed
Disease factor for volume of distribution	F _{CYF, VSS}	-	0.916	0.931 (0.739–1.15)	0.05	fixed
Maximum rate of exsorption	CL _{gut}	L/h	66.0	66.0 (fixed)	0	fixed
Plasma conc. associated with half-maximal V _{MEX}	K _{mEX}	mg/L	1.44	1.50 (0.711–2.50)	0.1	fixed
<i>Norfloxacin</i>						
Formation fraction	f _{mNOR}	-	0.201 ^a	0.198 (0.168–0.239) ^a	-	-
			0.174 ^b	0.172 (0.162–0.185) ^b	-	-
<i>Pefloxacin-N-oxide</i>						
Formation fraction	f _{mNOX}	-	0.244 ^a	0.247 (0.220–0.271) ^a	-	-
			0.178 ^b	0.180 (0.167–0.190) ^b	-	-

^a Parameter estimates for patients with CF.

^b Parameter estimates for healthy volunteers. When only one line of parameter estimates is reported, the same estimate was used in patients with CF and healthy volunteers.

^c Significantly different from 1.0 ($p < 0.05$; two-sided test) based on 200 bootstrap replicates.

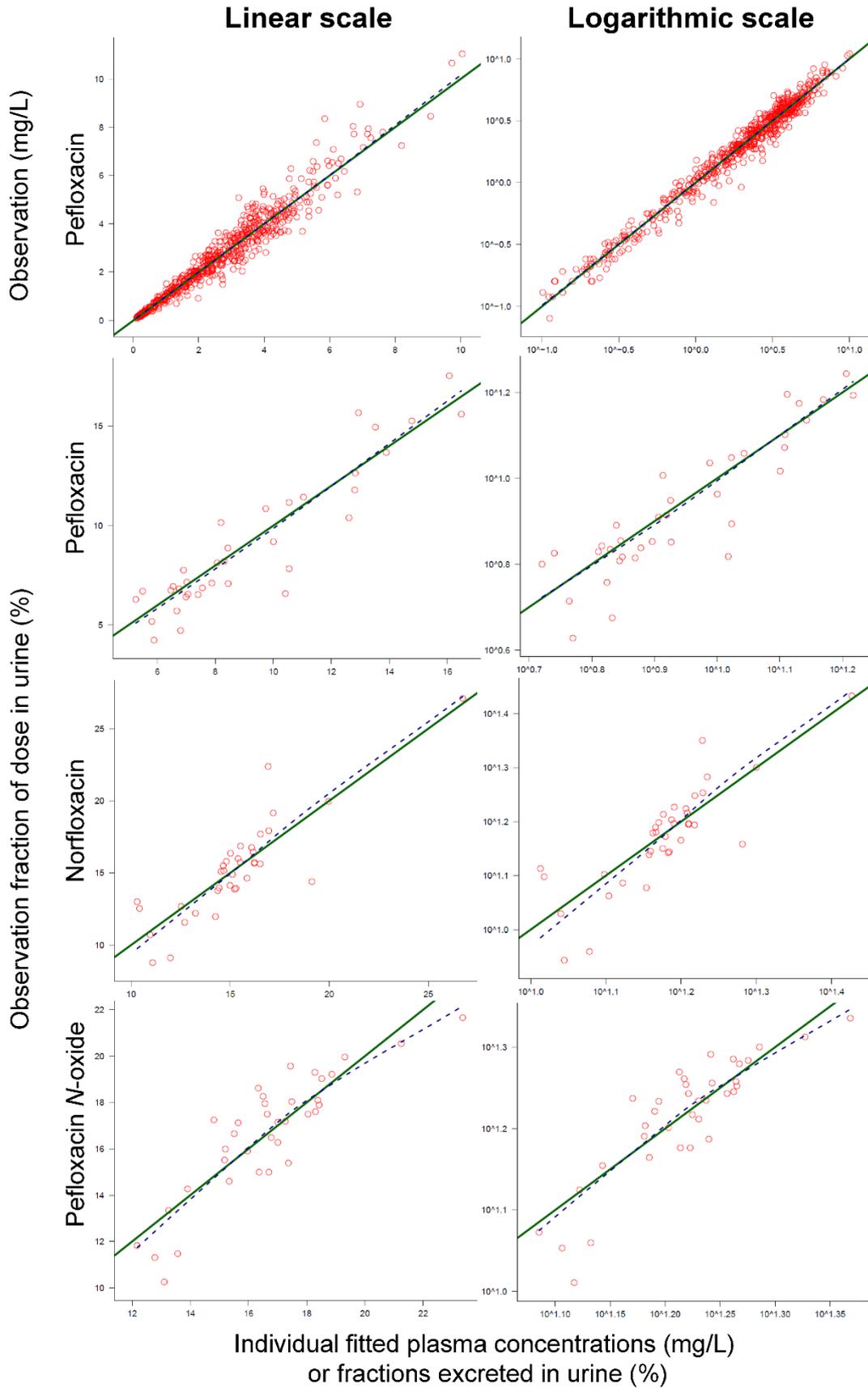


Figure S1. Observed vs. individual fitted plasma concentrations (top) and fractions of dose excreted in urine (rows 2 to 4) on linear (left side) and logarithmic scale (right side). The green line represents the line of identity and the dashed blue line a LOESS smoother.

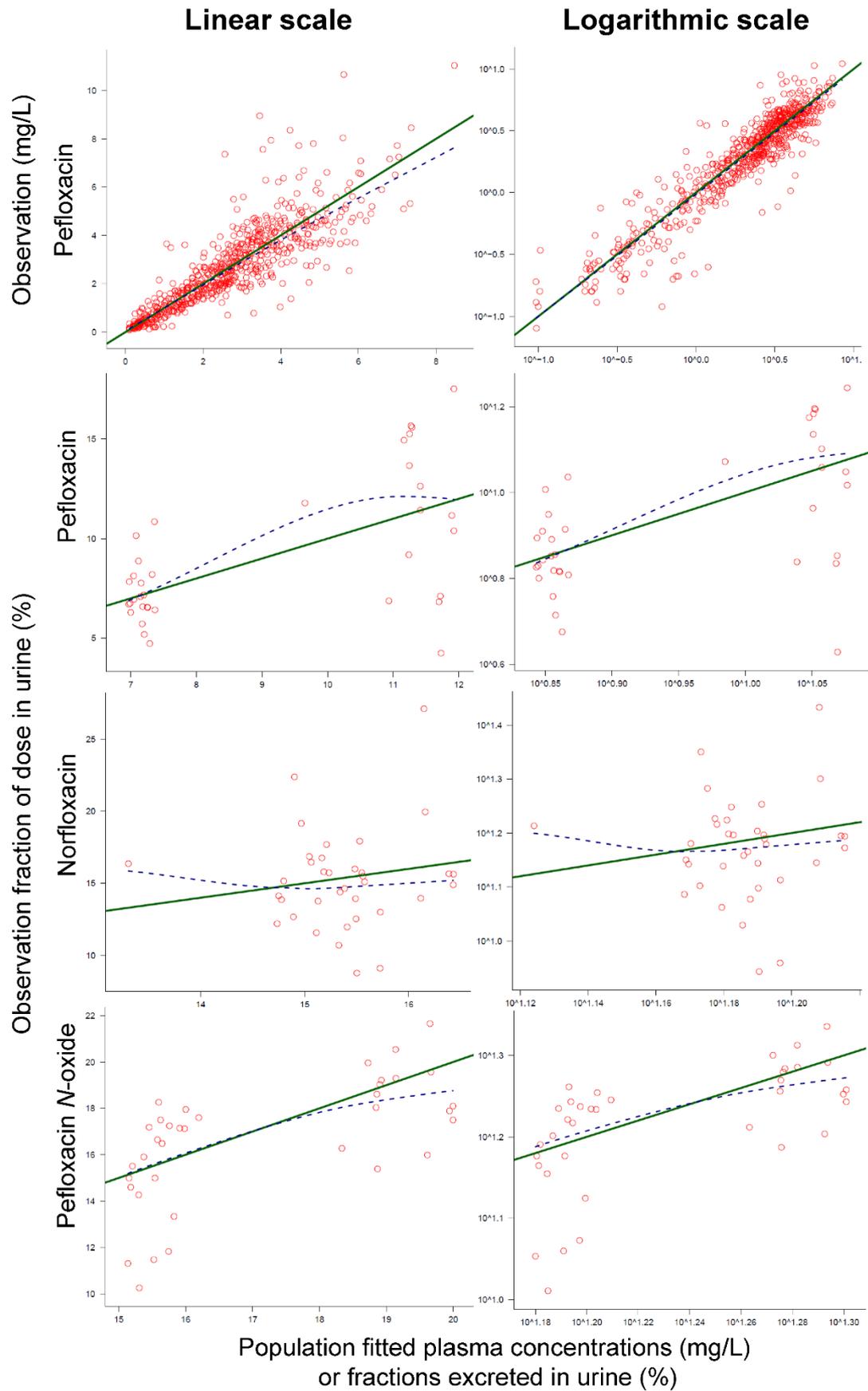


Figure S2. Observed vs. population fitted plasma concentrations (top) and fractions of dose excreted in urine (rows 2 to 4) on linear (left side) and logarithmic scale (right side). The green line represents the line of identity and the dashed blue line a LOESS smoother.

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1 |$PROJECT THIS WILL BE A TERRIFIC PROJECT
2
3 $DIFFEQ_DIF
4
5 GUT      = X(1)
6 DC1     = X(2)/V1_COV
7 DC2     = X(3)/V2_COV
8 URI     = X(4) ; Amount of pefloxacin      in urine
9 URINO   = X(5) ; Amount of norfloxacin    in urine
10 URIDE  = X(6) ; Amount of pefloxacin-N-oxide in urine
11 GUTEHC = X(7)
12
13 TPD = MOD(T,72)
14
15 IF (TPD.GT.TLAGH) THEN
16     KAT = KA
17 ELSE
18     KAT = 0
19 ENDIF
20
21 CLMM = CLgut_COV*KM / (KM+DC1)
22
23 XP(1) = - KAT*GUT
24 XP(2) = R(1) + KAT*GUT - CLR_COV*DC1 - CLNR_COV*DC1 - CLMM*DC1 - CLD_COV*DC1 + CLD_COV*DC2 + KAEHC*GUTEHC
25 XP(3) = CLD_COV*DC1 - CLD_COV*DC2
26
27 XP(4) = CLR_COV*DC1
28 XP(5) = FM_NOR*CLNR_COV*DC1
29 XP(6) = FM_NOX*CLNR_COV*DC1
30
31 XP(7) = CLMM*DC1 - KAEHC*GUTEHC
32
33 $OUTPUT_GLB
34
35 IF (GRP.EQ.1) THEN
36 ; Patients with Cystic Fibrosis
37 FBIO      = FBIO_CF
38 KA        = LOG(2)/(TABS_CF/60)
39 KAEHC     = LOG(2)/(TAEHC_CF/60)
40
41 FCYF_CLR  = FCLR
42 FCYF_CLNR = FCLNR
43 FCYF_CLEX = FCLEX
44 FCYF_VSS  = FVSS
45
46 TFM_NOR   = TFM_NORCF
47 DFM_NOX   = DFM_NOXCF
48 ELSE
49 ; Healthy volunteers
50 FBIO      = FBIO_HV
51 KA        = LOG(2)/(TABS_HV/60)
52 KAEHC     = LOG(2)/(TAEHC_HV/60)
53
54 FCYF_CLR  = 1
55 FCYF_CLNR = 1
56 FCYF_CLEX = 1
57 FCYF_VSS  = 1
58
59 TFM_NOR   = TFM_NORHV
60 DFM_NOX   = DFM_NOXHV
61 ENDIF
62

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Figure S3. code for the final model in SADAPT-TRAN format.

```

63 BOLUSF(1) = FBIO
64
65 FM_NOR      = 1/(1+EXP(-TFM_NOR))
66
67 TFM_NORNOX = DFM_NOX + TFM_NOR
68 FM_NORNOX  = 1/(1+EXP(-TFM_NORNOX))
69
70 FM_NOX2     = FM_NORNOX - FM_NOR
71 FM_NOX      = MAX(0,FM_NOX2) ; to improve robustness of code
72
73 TLAGH= TLAG/60
74
75 FWTCL = (FFM/53)**0.75
76 FWTV  = (FFM/53)
77
78 ; Elimination clearances
79 CLR_COV      = FCYF_CLR  * FWTCL * CLR
80 CLNR_COV     = FCYF_CLNR * FWTCL * CLNR
81 CLgut_COV    = FCYF_CLEX * FWTCL * CLgut
82 CLD_COV      =          FWTCL * CLD
83 V1_COV       = FCYF_VSS  * FWTV  * V1
84 V2_COV       = FCYF_VSS  * FWTV  * V2
85
86 $OUTPUT_ICs
87
88 $OUTPUT_EQN
89
90 IF (X(1).LT.0) X(1) = 0
91 IF (X(2).LT.0) X(2) = 0
92 IF (X(3).LT.0) X(3) = 0
93 IF (X(4).LT.0) X(4) = 0
94 IF (X(5).LT.0) X(5) = 0
95 IF (X(6).LT.0) X(6) = 0
96 IF (X(7).LT.0) X(7) = 0
97
98 C1  = X(2)/V1_COV ; Serum concentrations of pefloxacin (mg/L)
99
100 Y(1) = C1
101
102 Y(2) = 100*X(4)/400 ; fraction of dose excreted in urine as unchanged pefloxacin
103 Y(3) = 100*X(5)/400 ; fraction of dose excreted in urine as norfloxacin
104 Y(4) = 100*X(6)/400 ; fraction of dose excreted in urine as pefloxacin-N-oxide
105
106 ; Empty the bucket for the cumulative amount excreted into urine (=reset event)
107 IF (EVID.EQ.5) THEN
108     X(1) = 0
109     X(2) = 0
110     X(3) = 0
111     X(4) = 0
112     X(5) = 0
113     X(6) = 0
114     X(7) = 0
115 ENDIF
116
117 $VARMOD_EQN
118
119 V(1) = ( SDin + SDs1*Y(1) ) * ( SDin + SDs1*Y(1) )
120
121 V(2) = UPin * UPin
122 V(3) = URin * URin
123 V(4) = UXin * UXin
124
125 $POPMOD_EQN
126

```

Figure S3. code for the final model in SADAPT-TRAN format (continued).