Model 3
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial (logit)
Formula: IMGa ~ IMGb + abDCT(yes-no) + (1 | herd)

Data: data

AIC	BIC	logLik	deviance	df.resid
2461.8	2486.4	-1226.8	2453.8	3458

Scaled residuals:

Min	1Q	Median	3Q	Max
-0.6647	-0.3637	-0.3141	-0.2849	3.6921

Random effects:

Groups	Name	Variance	SD
herd	(Intercept)	0.1875	0.433

Number of observations: 3462, groups: herd, 251

Fixed effects:

	Estimate	SE	z value	Pr(>|z|)	
(Intercept)	-2.2356	0.0930	-24.046	< 2e-16	***
IMGb	0.7464	0.1165	6.406	1.5e-07	***
abDCT(yes-no)1	-0.1911	0.1167	-1.637	0.102	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model 3a
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial (logit)
Formula: IMGa ~ IMGb + abDCT(group) + (1 | herd)

Data: data

AIC	BIC	logLik	deviance	df.resid
2466.3	2509.3	-1226.1	2452.3	3455

Scaled residuals:

Min	1Q	Median	3Q	Max
-0.6657	-0.3633	-0.3167	-0.2818	3.8172

Random effects:

Groups	Name	Variance	SD
herd	(Intercept)	0.1845	0.4296

Number of observations: 3462, groups: herd, 251

Fixed effects:

	Estimate	SE	z value	Pr(>|z|)
(Intercept)	-2.23492	0.09277	-24.092	< 2e-16 ***
IMGb	0.75440	0.11686	6.456	1.08e-10 ***
penicillins	0.02607	0.21177	0.123	0.9020
cloxacillin	-0.25684	0.13130	-1956	0.0504 .
cephalosporins	-0.19180	0.34995	-0.548	0.5836
rifaximin	-0.09794	0.56104	-0.175	0.8614

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1