

Table S-1: Goodness of fit test based on the residual sum of squares (RSS). The P-value corresponds the null hypothesis that, for given estimated parameters $\frac{RSS}{\sigma^2} \sim \chi_{df}^2$.

	Bintje	BP3 Möwe	Désirée	Bintje	BP6 Möwe	Désirée
Lesion model						
RSS	3678152	4451584	2672717	1283997	1363795	2206778
$df = n - 2$	125	97	102	137	102	123
P-value	0.46	0.45	0.45	0.48	0.48	0.44
Sporulation model						
RSS	3.985e+12	3.001e+12	1.257e+12	1.384e+12	2.530076e+12	6.063e+11
$df = n - 3$	124	96	101	136	101	122
P-value	0.43	0.41	0.41	0.48	0.41	0.39