Table S1 - Whole genome resequencing of several clones from each lineage.

A lineage					Day			
genomic location	nt change	overlapping gene(s)	aa change	133	200	314	346	
324022	G->T	sdbA	G157opal			*	*	
375184	C->G	rpoC	L293V	*				
411562	G->A	fur	G84S		*			
1074316	A->G	lpg0981	V46A	*				
1754709-1754710	deletion (-2)	lpg1586	frameshift		*	*	*	
1991160	C->A	fleN	D75Y	*	*	*	*	
2909408	G->C	oivA	S606opal				*	
3041723	deletion (-1)	lphB/pacS	intergenic			*	*	
3273231	deletion (-1)	gidB	frameshift		*		_	

B lineage					Day		
genomic location	nt change	overlapping gene(s)	aa change	133	314	346	
325402	deletion (-1)	sdbA	frameshift	*	*	*	
395104	C->G	rpoA	I46M			*	
930001	T->A	fleQ	H179Q			*	
2577569-2577571	deletion (-3)	uqpQ	K99del		*		
2915886	G->T	sidF	G848ochre		*		
3041723	deletion (-1)	lphB/pacS	intergenic			*	
3084284	T->A	lqsS	N336Y	*	*	*	
3356904	deletion (-1)	argD	frameshift	*	*	*	

C lineage				Day		
genomic location	nt change	overlapping gene(s)	aa change	90	180	180'
897851	G->T	clpA	R646M			*
960031-960032	insertion (TGC)	dapE	A346_T347insA			*
1680473	C->G	lssE (cdgS19)	synonymous		*	
1991063	A->G	fleN	V107A		*	
2910291	C->A	oivA	E313ochre	*	*	*

D lineage					Day		
genomic location	nt change	overlapping gene(s)	aa change	45	90	180	
323591	deletion (-1)	sdbA	frameshift			*	
1990881-1990883	deletion (-3)	fleN	V168del	*			
2026944	G->A	lysC/A	G813R		*	*	
2317543	C->A	dam/lpg2076	intergenic			*	
3262574	G->A	metG	synonymous		*	*	

Illumina reads were aligned by reference assembly to both the published *L. pneumophila* Philadelphia-1 genome and to contigs from the progenitor strain. These alignments were used to identify mutations present in each strain. Each individual mutation was observed in isolates marked with an asterisk. Strain names in italics represent time-points and clones chosen for sequencing in order to explain population behavior identified in Figure 2. Two isolates from day 180 of the C lineage were sequenced, day 180 and day 180'.