

S1 Table. Current assemblies of *Phytophthora infestans*

Strain	Technology	Bases in assembly (Mb)	N50 (kb)	Scaffolds	Predicted genes	Reference
1306	PacBio, Illumina, Bionano optical map, Dovetail (proximity ligation), linkage map	247	970	632	19,981	this study
T30-4	Sanger	190 ^a	44.5	4,921	17,797	[1]
KR_1_A1	Oxford Nanopore, Illumina	201	291	1,510	20,172	[2]
KR_1_A2	Oxford Nanopore, Illumina	231	152	3,344	23,771	[2]
RC1-10	PacBio	203	120	2,902	n.d. ^b	[3]

^aTotal predicted size of 229 Mb.

^bNot determined.

References

1. Haas BJ, Kamoun S, Zody MC, Jiang RH, Handsaker RE, Cano LM, et al. Genome sequence and analysis of the Irish potato famine pathogen *Phytophthora infestans*. *Nature*. 2009;461(7262):393-8.
2. Lee Y, Cho KS, Seo JH, Sohn KH, Prokchorchik M. Improved genome sequence and gene annotation resource for the potato late blight pathogen *Phytophthora infestans*. *Mol Plant Microbe In*. 2020;33(8):1025-8.
3. Ayala-Usma DA, Cardenas M, Guyot R, De Mares MC, Bernal A, Munoz AR, et al. A whole genome duplication drives the genome evolution of *Phytophthora betacei*, a closely related species to *Phytophthora infestans*. *BMC Genomics*. 2021;22(1):795.