

Supplementary Table 1. Publicly available *Xc* genome sequences.

Strain	Alternate Name(s)	Pathovar	Geographic Origin	Host Origin	% GC	Genome Size	Coding Sequences	Plasmids (bp)	Sequencing Method	Genbank Chromosome	Genbank Plasmid	Reference
17	N/A	campestris	Taiwan	Unknown	65.1	4,994,430	4086	None	GAllx Illumina platform	CP011946	N/A	(Liu et al. 2015)
3811	N/A	campestris	United States	<i>Brassica oleracea</i>	65.1	5,072,566	4167	39,063	Illumina MiSeq, Pacific Biosciences	CP025750.1	N/A	(Kong et al. 2019)
8004	NCPPB1145	campestris	Sussex, UK	<i>Brassica oleracea</i> var. <i>botrytis</i>	64.94	5,148,708	4273	None	ABI3700 and MegaBACE DNA autosequencer	CP000050	N/A	(Qian et al. 2005)
CFBP 5817	658pCS1	campestris	Chile	<i>Brassica oleracea</i> var. <i>botrytis</i>	65.1	4,965,622	4057	32,000	HiSeq 2000 Illumina	CM002673.1	CM002674.1	(Bolot et al. 2015)
756c	N/A	raphani	East Asia	<i>Brassica oleracea</i> var. <i>capitata</i>	65.3	4,941,214	4020	None	Dideoxy sequencing on AB3730xl sequencer	CP002789.1	N/A	(Bogdanove et al. 2011)
ATCC 33913	NCPPB 528 [ICMP 13, LMG 568, PDDCC 13]	campestris	United Kingdom	<i>Brassica oleracea</i> var. <i>gemmifera</i>	65.1	5,076,188	4179	None	Not Reported	AE008922.1	N/A	(da Silva et al. 2002)
B100	ATCC 29497, DSM 60151, DSM1526,	campestris	Italy	<i>Brassica oleracea</i> var. <i>botrytis</i> ("Igloo")	65	5,079,002	4471	None	MegaBACE capillary sequencer	AM920689.1	N/A	(Vorhölter et al. 2008)
bra1	N/A	campestris	Aranguez, Trinidad and Tobago	<i>Brassica oleracea</i> var. <i>italica</i>	65.1	5,144,932	4,214	None	Illumina MiSeq	N/A	N/A	(Belhau et al. 2017)
BRE17	N/A	nonpathogenic	France	<i>Arabidopsis thaliana</i>	65.4	5,049,594	4057	None	Illumina HiSeq	N/A	N/A	(Wang et al. 2018)
CFBP 1606R	N/A	incanae	France	<i>Matthiola incana</i>	65.2	4,967,188	4,105	None	HiSeq2000 Illumina	CM002635.1	N/A	(Roux et al. 2015)
CFBP 1869	LMG 8035	campestris	Ivory Coast	<i>Brassica oleracea</i> var. <i>botrytis</i>	65.1	5,008,832	4114	None	HiSeq 2000 Illumina	CM002546.1	CM002545.1	(Bolot et al. 2015)
CFBP 2527R	NCPPB 937, ATCC 13462, ICMP 574, LMG 7490	incanae	USA	<i>Matthiola incana</i>	65.1	4,925,675	4077	None	HiSeq2000 Illumina	CM002636.1	N/A	(Roux et al. 2015)
CFBP 5828r	LMG 547, ATCC 13460, ICMP 438, ICPB XB2, LMG 547, NCPPB 983	raphani	USA	<i>Raphanus sativus</i>	65.4	4,912,085	4,003	None	HiSeq2000 Illumina	CM002637	N/A	(Roux et al. 2015)
CFBP7 700	N/A	nonpathogenic	Unknown	<i>Phaseolus vulgaris</i>	65.3	5,044,897	4163	None	Illumina HiSeq	N/A	N/A	(Meline et al. 2019)
CFPB5 825r	LMG 7505, ICMP 1640	nonpathogenic	USA	<i>Barbarea vulgaris</i>	65.1	5,053,608	4,116	None	HiSeq2000 Illumina	CM002638	N/A	(Roux et al. 2015)
CN03	CFBP8239, LN949, CFBP-Labo 13230	campestris	Dalian, China	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	65.05	5,035,984	4219	75,753	Pacific Biosciences	CP017308	CP017309	(Denancé et al. 2018)
CN11	N/A	campestris	Nanyang, China	<i>Brassica oleracea</i> var. <i>capitata</i>	65	5,053,930	4,157	None	Pacific Biosciences	N/A	N/A	N/A
CN12	CFBP8246, LN958	campestris	Wuhan, China	<i>Brassica napus</i> subsp. <i>oleifera</i>	65.1	5,115,137	4187	None	Pacific Biosciences	CP017310	N/A	(Denancé et al. 2018)
CN14	CFPB8247, MA38	campestris	Guilin, China	<i>Brassica juncea</i> var. <i>foliosa</i>	65.1	5,033,560	4163	48,995	Pacific Biosciences, Illumina HiSeq	CP017317	CP017318	(Bolot et al. 2013b; Denancé et al. 2018)
CN15	BP8248, LN960	campestris	Guilin, China	<i>Brassica rapa</i> subsp. <i>chinensis</i>	65.04	5,030,187	4193	61,451	Pacific Biosciences, Illumina HiSeq	CP017323	CP017325	(Bolot et al. 2013b; Denancé et al. 2018)

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CN16	CFBP8249, LN961	campestris	Guilin, China	<i>Brassica rapa</i> subsp. <i>pekinensis</i>	65.01	5,023,147	4208	2,125	Pacific Biosciences, Illumina HiSeq	CP017389	CP017401	(Bolot et al. 2013a; Denancé et al. 2018)
CN17	CFBP8252, LN962	campestris	Nanning, China	<i>Brassica rapa</i> subsp. <i>chinensis</i>	65.1	5,122,268	4129	None	Pacific Biosciences	CP017307	N/A	(Denancé et al. 2018)
CN18	CFBP8250, LN963	campestris	China	<i>Brassica juncea</i> var. <i>foliosa</i>	65	5,133,109	4284	69,402	Pacific Biosciences	CP017319	CP017322	Denancé, 2018 #26}
E1	N/A	nonpathogenic	Taiwan	<i>Brassica oleracea</i>	65.4	5,001,440	4,120	None	Illumina HiSeq	N/A	N/A	(Lee et al. 2020)
ICMP 21080	N/A	campestris	Southbridge, New Zealand	<i>Brassica oleracea</i> WK882	64.6	4,927,810	4371	None	Illumina HiSeq2000	CP012145	N/A	(Desai et al. 2015)
ICMP 4013	N/A	campestris	Auckland, New Zealand	<i>Brassica oleracea</i> var. <i>capitata</i>	64.55	4,972,211	4428	None	Illumina HiSeq2000	CP012146	N/A	(Desai et al. 2015)
JX	CCTCC M2012178	campestris	Shanghai, China	Unknown	65	5,023,003	4323	None	Illumina GA system	N/A	N/A	(Tao et al. 2012)
LMCP 11	N/A	nonpathogenic	Michigan, USA	<i>Arabidopsis thaliana</i>	65.3	5,063,130	4179	None	Illumina HiSeq	N/A	N/A	(Wang et al. 2018)
LMCP 73	N/A	nonpathogenic	Midwest, USA	<i>Arabidopsis thaliana</i>	65.5	4,898,430	3931	None	Illumina HiSeq	N/A	N/A	(Wang et al. 2018)
LMG8031	N/A	campestris	France	<i>Brassica oleracea</i>	65.1	5,017,935	4085	None	Illumina Miseq	N/A	N/A	(Schmid et al. 2016)
MAFF 106181	N/A	raphani	Aomori, Japan	<i>Raphanus sativus</i> var. <i>longipinnatus</i>	65.3	4,942,039	4041	None	Illumina Hiseq, Pacific Biosciences RSII	CP058243	N/A	(Fujikawa and Inoue 2020)
MAFF 106712	N/A	campestris	Ibaraki, Japan	<i>Brassica rapa</i> subsp. <i>Pekinensis</i>	65.2	5,081,467	4,422	78,747	Pacific Biosciences RS II	AP019682	AP019683	(Takeuchi and Mitsuhashi 2020)
MAFF 301176	N/A	campestris	Hyogo, Japan	<i>Brassica oleracea</i> var. <i>capitata</i>	65.1	5,039,598	4,130	None	Illumina Hiseq, Pacific Biosciences RSII	N/A	N/A	(Fujikawa and Inoue 2020)
MAFF 302021	N/A	campestris	Shiga, Japan	<i>Brassica oleracea</i> var. <i>botrytis</i>	65.1	5,048,651	4421	None	Pacific Biosciences RS II	AP019684	N/A	(Takeuchi and Mitsuhashi 2020)
MEDV A40	N/A	nonpathogenic	Midwest, USA	<i>Arabidopsis thaliana</i>	65.4	5,012,924	4074	None	Illumina HiSeq	N/A	N/A	(Wang et al. 2018)
MEDV P25	N/A	nonpathogenic	Midwest, USA	<i>Arabidopsis thaliana</i>	65.5	4,941,120	3,848	None	Illumina HiSeq	N/A	N/A	(Wang et al. 2018)
NLP121	N/A	nonpathogenic	Midwest, USA	<i>Arabidopsis thaliana</i>	65.4	4,985,793	4038	None	Illumina HiSeq	N/A	N/A	(Wang et al. 2018)
NLP172	N/A	nonpathogenic	Midwest, USA	<i>Arabidopsis thaliana</i>	65.5	4,946,999	3969	None	Illumina HiSeq	N/A	N/A	(Wang et al. 2018)
NRRL B-1459	ATCC 13951, LMG 573, DSM-19000	campestris	Germany	Unknown	65.03	5,077,495	4322	45,729	Illumina MiSeq	N/A	N/A	(Wibberg et al. 2015)
WHRI 10003	N/A	campestris	Germany	<i>Erysimum cheiri</i>	65.2	4,945,175	4077	None	Illumina MiSeq	N/A	N/A	N/A
WHRI 10004	N/A	incanae	Germany	<i>Capsella bursa-pastoris</i>	65.1	5,010,766	4097	None	Illumina Miseq	N/A	N/A	N/A
WHRI 10006	N/A	raphani	Germany	<i>Eruca</i> sp.	65.3	4,884,202	3989	None	Illumina MiSeq	N/A	N/A	(Wang et al. 2018)
WHRI 8473	N/A	incanae	UK	<i>Erysimum cheiri</i>	65.2	4,992,473	4064	None	Illumina Miseq	N/A	N/A	N/A
WHRI 8481	N/A	unknown	UK	<i>Iberis</i> sp.	65.3	4,966,217	4188	None	Illumina MiSeq	N/A	N/A	N/A

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WHRI 8525	N/A	incanae	UK	<i>Erysimum cheiri</i>	65.1	5,019,769	4093	None	Illumina Miseq	N/A	N/A	N/A
WHRI 8527	N/A	incanae	UK	<i>Matthiola incana</i>	65.1	4,956,531	4055	None	Illumina Miseq	N/A	N/A	N/A
WHRI 8960	N/A	incanae	UK	<i>Erysimum cheiri</i>	65.2	4,943,363	4072	None	Illumina Miseq	N/A	N/A	N/A
Xc86	N/A	campestris	North West, South Africa	<i>Zea mays</i> subsp. <i>mays</i>	65.2	4,275,597	3,512	None	Illumina MiSeq	N/A	N/A	(Sanko et al. 2018)
Xca5	N/A	campestris	United States	Unknown	65.2	4,905,337	4592	37,546, 11,218, 2,141	GAllx Illumina platform.	ASM32112v4	N/A	(Bolot et al. 2013a)

References

Bogdanove AJ, Koebnik R, Lu H, Furutani A, Angiuoli SV, Patil PB, Van Sluys M-A, Ryan RP, Meyer DF, Han S-W, Aparna G R, M DA, Phillippy AM, Puiu D, Schatz MC, Shumway M, Sommer DD, Trapnell C, Benahmed F, Dimitrov G, Madupu R, Radune D, Sullivan S, Jha G, Ishihara H, Lee S-W, Pandey A, Sharma V, Sriariyanun M, Szurek B, Vera-Cruz CM, Dorman KS, Ronald PC, Verdier V, Dow JM, Sonti RV, Tsuge S, Brendel VP, Rabinowicz PD, Leach JE, White FF, SL S (2011) Two new complete genome sequences offer insight into host and tissue specificity of plant pathogenic *Xanthomonas* spp. J Bacteriol 193:5450-5464

Bolot S, Cerutti A, Carrère S, Arlat M, Fischer-Le Saux M, Portier P, Poussier S, Jacques M-A, Noël LD (2015) Genome sequences of the race 1 and race 4 *Xanthomonas campestris* pv. *campestris* strains CFBP 1869 and CFBP 5817. Genome Announc 3:e01023-01015

Bolot S, Guy E, Carrere S, Barbe V, Arlat M, Noël LD (2013a) Genome sequence of *Xanthomonas campestris* pv. *campestris* strain Xca5. Genome Announc 1:e00032-00012

Bolot S, Roux B, Carrere S, Jiang B-L, Tang J-L, Arlat M, Noël LD (2013b) Genome sequences of three atypical *Xanthomonas campestris* pv. *campestris* strains, CN14, CN15, and CN16. Genome Announc 1:e00465-00413

da Silva AR, Ferro JA, Reinach F, Farah C, Furlan L, Quaggio R, Monteiro-Vitorello C, Van Sluys M, Almeida N, Alves L (2002) Comparison of the genomes of two *Xanthomonas* pathogens with differing host specificities. Nature 417:459-463

Denancé N, Szurek B, Doyle EL, Lauber E, Fontaine - Bodin L, Carrère S, Guy E, Hajri A, Cerutti A, Boureau T (2018) Two ancestral genes shaped the *Xanthomonas campestris* TAL effector gene repertoire. New Phytol 219:391-407

- Desai D, Li J-H, de Jong EvZ, Braun R, Pitman A, Visnovsky S, Hampton J, Christey M (2015) Draft genome sequences of two New Zealand *Xanthomonas campestris* pv. *campestris* isolates, ICMP 4013 and ICMP 21080. *Genome Announc* 3:e01247-01215
- Fujikawa T, Inoue Y (2020) Genome sequences of two pathogens of cruciferous crops, *Xanthomonas campestris* pv. *raphani* MAFF 106181 and *X. campestris* pv. *campestris* MAFF 301176. *Microbiol Resour Announc* 9:e00887-00820
- Kong C, Horta de Passo V, Fang Z, Yang L, Zhuang M, Zhang Y, Wang Y, Vicente JG, Lv HJMP-MI (2019) Complete genome sequence of strain WHRI 3811 race 1 of *Xanthomonas campestris* pv. *campestris*, the causal agent of black rot of cruciferous vegetables. *Mol Plant Microbe Interact* 32:1571-73
- Lee Y-A, Yang P-Y, Huang S-C (2020) Characterization, phylogeny, and genome analyses of nonpathogenic *Xanthomonas campestris* strains isolated from *Brassica* seeds. *Phytopathology* 110:981-988
- Liu Y-C, Wang S-C, Yu Y-J, Fung K-M, Yang M-T, Tseng Y-H, Tsai S-F, Sun HS, Lyu P-C, Chou S-H (2015) Complete genome sequence of *Xanthomonas campestris* pv. *campestris* strain 17 from Taiwan. *Genome Announc* 3:e01466-01415
- Meline V, Delage W, Brin C, Li - Marchetti C, Sochard D, Arlat M, Rousseau C, Darrasse A, Briand M, Lebreton G (2019) Role of the acquisition of a type 3 secretion system in the emergence of novel pathogenic strains of *Xanthomonas*. *Mol Plant Pathol* 20:33-50
- Qian W, Jia Y, Ren S-X, He Y-Q, Feng J-X, Lu L-F, Sun Q, Ying G, Tang D-J, Tang H (2005) Comparative and functional genomic analyses of the pathogenicity of phytopathogen *Xanthomonas campestris* pv. *campestris*. *Genome Res* 15:757-767
- Roux B, Bolot S, Guy E, Denancé N, Lautier M, Jardinaud M-F, Fischer-Le Saux M, Portier P, Jacques M-A, Gagnevin L, Pruvost O, Lauber E, Arlat M, Carrère S, Koebnik R, Noël L (2015) Genomics and transcriptomics of *Xanthomonas campestris* species challenge the concept of core type III effectome. *BMC Genomics* 16:975
- Sanko TJ, Kraemer AS, Niemann N, Gupta AK, Flett BC, Mienie C, Bezuidenhout CC (2018) Draft genome assemblages of 10 *Xanthomonas vasicola* pv. *zeae* strains, pathogens causing leaf streak disease of maize in South Africa. *Genome Announc* 6:e00532-00518
- Schmid J, Huptas C, Wenning M (2016) Draft genome sequence of the xanthan producer *Xanthomonas campestris* LMG 8031. *Genome Announc* 4:e01069-01016

Takeuchi K, Mitsuhashi I (2020) Complete genome sequences of two strains of *Xanthomonas campestris* pv. *campestris* isolated in Japan. Microbiol Resour Announc 9:e01239-01219

Tao F, Wang X, Ma C, Yang C, Tang H, Gai Z, Xu P (2012) Genome sequence of *Xanthomonas campestris* JX, an industrially productive strain for Xanthan gum. J Bacteriol 194:4755-4756

Vorhölter F-J, Schneiker S, Goesmann A, Krause L, Bekel T, Kaiser O, Linke B, Patschkowski T, Rückert C, Schmid J, Sidhu V, Sieber V, Tauch A, Watt S, Weisshaar B, Becker A, Niehaus K, Pühler A (2008) The genome of *Xanthomonas campestris* pv. *campestris* B100 and its use for the reconstruction of metabolic pathways involved in xanthan biosynthesis. J. Biotechnol 134:33-45

Wang M, Roux F, Bartoli C, Huard-Chauveau C, Meyer C, Lee H, Roby D, McPeck MS, Bergelson J (2018) Two-way mixed-effects methods for joint association analysis using both host and pathogen genomes. Proc National Acad Sci USA 115:E5440-E5449

Wibberg D, Alkhateeb RS, Winkler A, Albersmeier A, Schatschneider S, Albaum S, Niehaus K, Hublik G, Pühler A, Vorhölter F-J (2015) Draft genome of the xanthan producer *Xanthomonas campestris* NRRL B-1459 (ATCC 13951). J Biotechnol 204:45-46