

Genome Resource of Barley Bacterial Blight and Leaf Streak Pathogen *Xanthomonas translucens* pv. *translucens* strain UPB886

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Abstract

Xanthomonas translucens pv. *translucens* causes bacterial leaf streak and bacterial blight diseases of barley. This pathogen limits barley production globally but remains understudied, with limited genomic resources. To better understand the biology of this *X. translucens* subgroup, we sequenced the complete genome of the *X. translucens* pv. *translucens* strain UPB886.

Genome Announcement

The plant-pathogenic bacterial species *Xanthomonas translucens* cause diseases of cereals, grasses, and even some dicots (Facelli et al. 2009; Jones et al. 1916). The pathovar *translucens* within *X. translucens* is most often associated with barley infection. *X. translucens* pv. *translucens* is not a wheat pathogen but has been previously isolated from wheat leaves (Bragard et al. 1997; Curland et al. 2018). *X. translucens* pv. *translucens* has been reported on all continents and is genetically diverse, comprising three subgroups (A, B, and C) based on phylogeny of concatenated housekeeping genes (Curland et al. 2018). Here, we describe the complete genome sequence of the *X. translucens* pv. *translucens* group C strain UPB886 for a better comparative understanding of *X. translucens* host adaptation and biology.

X. translucens pv. *translucens* UPB886 was isolated from barley in Iran in 1990 (Alizadeh et al. 1995). We validated that strain UPB886 has pathogenic virulence on barley but not on spring wheat (pathogenicity test not shown). DNA was extracted by a standard phenol/chloroform method (Booher et al. 2015). Strain UPB886 genomic DNA was sequenced using long-read, single-molecule real-time sequencing and assembled using HGAP v4 (PacBio, Menlo Park, CA, U.S.A.). Functional annotation of the two assembled contigs was done using Prokka v1.13.3, and secreted proteins were predicted based on SignalP algorithm as part of Prokka analysis (Petersen et al. 2011; Seemann 2014). Whole-genome comparison based on average nucleotide identity confirmed that this strain belonged to the *X. translucens* pv. *translucens* subgroup C and had a high degree of synteny with other *X. translucens* genomes (Table 1) (data not shown) (Curland et al. 2018; Rodriguez-R and Konstantinidis 2016).

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Keywords

bacteria, barley, genome, TALE, *Xanthomonas translucens*

The *X. translucens* pv. *translucens* UPB886 genome encoded typical virulence factors found in *Xanthomonas* spp. The genome has 15 genes encoding extracellular plant cell-wall-degrading enzymes, 7 genes involving in copper resistance cluster, and 21 genes related to the type II secretion system. Type III secretion is critical for *X. translucens* pv. *translucens* pathogenesis (Pesce et al. 2017), and the strain UPB886 genome encoded 41 conserved type III-secreted proteins including transcriptional activator-like effectors (TALEs). The strain UPB886 genome had five TALEs (Table 2); three were shared with other *X. translucens* and assigned to classes TalCV, TalDD, and TalCT. The remaining two TALEs were unique to strain UPB886 and belong to classes TalAJ and TalEU (Falahi Charkhabi et al. 2017; Grau et al. 2016; Peng et al. 2016). *X. translucens* pv. *translucens* UPB886 provides a genomic resource to advance *X. translucens* research. This resource will allow further genetic diversity

Table 1. Complete genomes summary of *Xanthomonas translucens* pvs. *undulosa* and *translucens*

Strain ^a	Isolation source		Genome analysis			Annotation			
	Year	Country	Genome size (bp)	Contigs	GC content (%)	CDS ^b	TALEs ^c	Total secreted proteins	ANI ^d
<i>X. translucens</i> pv. <i>translucens</i>									
UPB886	1990	Iran	4,674,364	2	67.9	3,889	5	547	100
SAMN11831831									
DSM18974	1933	United States	4,715,357	1	67.7	3,957	8	563	99
NZ_LT604072.1									
<i>X. translucens</i> pv. <i>undulosa</i>									
XT4699	1999	United States	4,561,137	1	68.1	3,528	8	531	98
NZ_CP008714.1									
ICMP11055	1983	Iran	4,761,583	1	67.8	3,953	7	540	98
NZ_CP009750.1									

^a Lines indicate species, strain, and NCBI reference number.

^b Coding sequence.

^c Transcription activator-like effectors.

^d Average nucleotide identity (ANI) is relative to UPB886.

Table 2. RVD sequences of *Xanthomonas translucens* pvs. *undulosa* and *translucens*

TALE classes ^a	Strain ^b	RVD sequence alignment	Genome location:strand
TalAJ	UPB886	NN HD NG NI HD HD HD	4,505,717–4,508,111:–1
TalCT	DSM18974	NN HD HD HD NI NI NI NN HD HD NN NN NI NN HD	671,336–674,561:1
	UPB886	NN HD HD HD NI NI NI HN HD HD NN NN NI NN HD	4,482,729–4,485,960:–1
	XT4699	HN HD HD HD NI NI NI HN HD HD NN NN NI NN HD	3,253,498–3,256,723:–1
	ICMP11055	HN HD HD HD NI NI NI HN HD HD NN NN NI NN HD	1,470,456–1,473,681:1
TalCU	DSM18974	NG HD HD HN NG NI HG HG HD ND NN NN NI NH QD	3,565,727–3,568,955:–1
TalCV	DSM18974	NG NN HD HD NN NI HG HD ND HG NI NN HD	3,562,396–3,565,408:–1
	UPB886	NG NN HD HD NN NI HG HD ND HG NI NN HD	1,623,874–1,626,892:1
TalCW	DSM18974	NN NI HN HD NI NH NG HN HD HD NI QD	660,311–663,329:1
TalCX	DSM18974	NNHDNGNI HNKG NI HDNINH NG NN HD HDNI NN NI HD QD	663,647–667,295:1
TalCY	DSM18974	NI NG HN NN HD NG ND NK QD NH QD	668,858–671,207:1
TalCZ	XT4699	NH NN HD NN HD NH HD YK NG NH Y* HD NN NI NG QD NH NN	2,669,985–2,673,321:–1
	DSM18974	HD NN HD NH HD YK NG NH Y* HD NN NI NG QD NH NN HD NN	1,995,271–1,998,607:1
	ICMP11055	HD NH HD YK NG NH Y* HD NN NI NG Q	2,119,325–2,122,661:–1
TalDA	DSM18974	NN HD NG NG NG NN YK NG HD NG NG ND NG HD NH HD	627,243–630,573:1
	XT4699	HD YD NI NG NG NN YK NG HD NG NG ND NG QD NH HD	584,465–587,645:1
	ICMP11055	HD YD NI NG NG NN YK NG HD NG NG ND NG QD NH HD	627,709–630,889:1
TalDB	XT4699	NN HD NG HD HD HN NF NI NH HD HD HD HN HN HD	1,991,439–1,994,667:–1
TalDC	XT4699	NN NG HD HD HD KG NN Y* NG HD HD QD HN	3,257,061–3,260,076:–1
TalDD	UPB886	NN QD NG NN HN KG NI HD NI HN NG HN HD HD NI NN HD	4,486,088–4,489,529:–1
	XT4699	NN HD NG NN HN KG NI HD NI NN HD HN HD HD NI HN HD QD	605,042–608,582:1
	ICMP11055	NN HD NG NN HN KG NI HD NI HN HD HN HD Y* NG HD HD HN	648,160–651,691:1
TalDE	XT4699	NN HD NG NN HN HN NI NI NI HN NN HD NN NH HD HD	2,857,126–2,860,465:–1
TalDF	XT4699	HD HN HN HD NH NH HG HD KG NN Y* NG HD HD HN	2,861,842–2,865,061:–1
	ICMP11055	HD HN HN HD NH NH HG HD KG NN Y* NG HD HD HN	1,918,202–1,921,427:1
TalEV	ICMP11055	NN HD NG HD HD HG HD KG NN Y* NG NG HD HD QD HN	1,924,847–1,928,171:1
TalEW	ICMP11055	NN HD NG HD NG HD HD HG HD KG NN KG HD HN QD HN	1,466,788–1,470,118:1
TalEX	UPB886	NI NG HN NK HD NH HN HD HD HD QD	2,350,128–2,353,041:–1

^a Transcriptional activator-like effector (TALE) classes based on annoTALE (Grau et al. 2016).

^b *Xanthomonas translucens* strains.

studies to understand the mechanisms underlying disease development, improve tools for diagnostics, and assist barley breeding programs.

The whole genome was deposited at GenBank under BioSample accession number SAMN11831831.

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