



## Genome Announcement

# Draft genome sequence of *Xanthomonas axonopodis* pv. *glycines* 8ra possessing transcription activator-like effectors used for genetic engineering



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## ABSTRACT

*Xanthomonas axonopodis* pv. *glycines* 8ra is a causal agent of bacterial pustule disease in soybean. This bacterium possesses transcription activator-like (TAL) effectors which are useful for genetic/protein engineering applications in higher organisms including plants and humans. Here, we report that the draft genome sequence consists of 5,337,885-bp double-stranded DNA encoding 4674 open reading frames (ORFs) in 13 different contigs. This genome sequence would be useful in applications of TAL effectors in genetic engineering and in elucidating virulence factors against plants.

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*Xanthomonas axonopodis* pv. *glycines* is a Gram-negative, aerobic, motile, and plant pathogenic bacterium causing bacterial pustules (BP) diseases in soybean (Jones and Fett, 1987; Vauterin et al., 1995). The strain 8ra was first isolated from Iowa, USA in 1980 and has been widely used as a model strain for various genetic studies (Groth and Braun, 1989; Han et al., 2007; Kim et al., 2003, 2004; Pham et al., 2004). The transcription activator-like (TAL) effectors of this species are important because they specifically regulate host gene expression (especially, resistance/susceptibility-related genes) and are highly useful in transcription activator-like effector nuclease (TALEN) technology by customizing their amino acid repeat region. This technique is very important in genetic engineering and industrial applications to control plant diseases including the BP (Boch et al., 2009; Scholze and Boch, 2011; Schornack et al., 2013; Zhang et al., 2011). Three other genome sequences of the species have been previously reported (Chatnapat et al., 2012; Darrasse et al., 2013). However, the genome information of the model strain, 8ra, has been unavailable. Therefore we sequenced and analyzed the genome of 8ra to elucidate the TAL effectors and their genetic characteristics.

The genome of strain 8ra was sequenced with next generation sequencing technology using GS-FLX+ pyrosequencer and Illumina HiSeq2500, and assembled using the Newbler 2.3 program in Macrogen (Korea). ORF prediction was conducted using applications such as Glimmer3 (Delcher et al., 2007), GeneMarkS (Besemer et al., 2001), and FgenesB (Softberry, Inc., Mount Kisco, NY). Functional analysis of all predicted ORFs was performed using InterProScan (Zdobnov and Apweiler, 2001) and BLASTP (Altschul et al., 1990) including various protein domain databases. Metabolic pathway analysis was conducted using the KAAS program and the KEGG database (Kanehisa et al., 2014). tRNA genes were predicted using the tRNAscan-SE program (Schattner et al., 2005).

The draft genome sequences of 8ra composed 13 different contigs ranging from 2-kb to 1.17-Mb. They included 5,337,885-bp encoding 4674 ORFs, 3 rRNA genes (16S rRNA, 23S rRNA, and 5S rRNA), and 52 tRNA genes with a GC content of 64.5% (Table 1). ORF annotation and functional analysis showed that the total number of ORFs with a predicted function is 3085. This genome has most of genes required for flagellum assembly and bacterial chemotaxis. It also has secretion systems such as Types I, II, III, IV, VI, and Sec-type secretion systems. In particular, the type III secretion system is known as a secretion channel of TAL effectors during bacterial infection of plants (Boch et al., 2009). While previous studies have reported many TAL effectors in *Xanthomonas oryzae* species, the current strain's genome had at least one gene encoding TAL effector.

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**Table 1**  
Genome statistics.

Attribute	Value
Genome size (bp)	5,337,885
DNA G + C content	64.5%
Total contigs	13
Total genes	4674
rRNA genes	3
tRNA genes	52
Protein coding genes	4601
Genes with predicted function	3085

The presence of type III secretion system (XAR\_4141–XAR\_4160) and as a TAL effector gene (XAR\_4366; AvrBs3) suggests that the strain 8ra regulates host gene expression during infection. The genome sequence of *X. axonopodis* pv. *glycines* 8ra provides fundamental information for further studies on TAL effectors that control host specificity, and for genetic engineering using TAL effectors in plant–microbe interactions.

### Nucleotide sequence accession number

The draft genome sequence of *X. axonopodis* pv. *glycines* 8ra is now available in GenBank database under accession number JDSU00000000. The strain is available from the corresponding author upon request.

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