

## Note (Genome Announcement)

# Complete genome sequence of *Acidovorax citrulli* strain KACC17005, a causal agent for bacterial fruit blotch on watermelon

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## 수박에 과실썩음병을 일으키는 *Acidovorax citrulli* strain KACC17005의 유전체 해독

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*Acidovorax citrulli* is a causal agent for bacterial fruit blotch on watermelon. Here, we report the complete genome sequence of *A. citrulli* strain KACC17005. The genome contains 5,349,924 bp with G + C contents of 68.54%, including 4,520 protein coding genes in a circular chromosome. It also possesses at least 15 genes encoding putative type III effector proteins, which may contribute to promoting virulence in susceptible hosts or triggering immune responses in resistant hosts.

**Keywords:** *Acidovorax citrulli* KACC17005, bacterial fruit blotch, PacBio RS II, watermelon

*Acidovorax citrulli* is Gram-negative, curved rod-shaped, and motile with a single flagellum (Willems *et al.*, 1992). The bacterium is a causal agent for bacterial fruit blotch (BFB), which is one of the most destructive diseases on watermelon, and has been found in all watermelon producing countries including Korea (Latin and Hopkins, 1995). In favorable conditions, BFB can cause up to 90% yield loss in watermelon production. The bacterium can infect any aerial parts of water-

melon through natural openings and wounds (Burdman and Walcott, 2012). Specifically, seedlings and fruits are extremely susceptible to the bacterium. Infected seedlings show water-soaked symptoms on cotyledons and necrotic lesions on the hypocotyl, and eventually die. Symptoms on fruits are characterized by small, asymmetrical, water-soaked lesions extending through the rind, and later become brown and crack (Burdman and Walcott, 2012). In this report, we present the complete genome sequence of *A. citrulli* strain KACC17005 provided by Korean Agricultural Culture Collection and originally isolated from watermelon at Suwon, Republic of Korea.

The bacterial cells were grown to an OD<sub>600</sub> of 0.6 in tryptic soy broth and their genomic DNA was extracted with the DNeasy Blood & Tissue Kit (Qiagen). The extracted DNA was used to generate 20 kb SMRTbell™ template libraries. The whole genome sequencing of *A. citrulli* KACC17005 was performed using PacBio RS II platform (Pacific Biosciences). The 71,359 sequencing reads were gained, and *de novo* assembly was performed using Hierarchical Genome Assembly Process (HGAP, Version 2.3) combined with Quiver for consensus polishing (Chin *et al.*, 2013). About 614.5 Mbp were produced

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**Table 1.** Genome features of *A. citrulli* KACC17005

Genome features	Value
Genome size (bp)	5,349,924
G + C content (%)	68.54
rRNA (5S, 16S, 23S)	9 (3, 3, 3)
tRNA	53
ncRNA	3
Protein coding genes	4,520
Pseudo-genes	299

with 100X average coverage. Finally, all contigs were checked and trimmed for manual genome closure using MUMmer 3.5 (Kurtz *et al.*, 2004), resulting in one circular contig that contains 5,349,924 bp with 68.54% G + C contents (Table 1). The complete genome sequence of *A. citrulli* KACC17005 includes 4,520 protein coding genes, 9 rRNA genes, 53 tRNA genes, 3 ncRNA genes, and 299 pseudogenes, predicted by NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAPP) (Angiuoli *et al.*, 2008) combined with GeneMark S<sup>+</sup> (Borodovsky and Lomsadze, 2014). Functional annotation revealed that *A. citrulli* KACC17005 possesses one type III secretion system, which is a channel for secretion of type III effectors (T3Es) proteins in Gram negative bacteria (Alfano and Collmer, 2004). In most plant pathogenic bacteria, it is well known that T3Es promote virulence in susceptible hosts and trigger innate immune responses in resistant hosts or nonhost plants. The genome of *A. citrulli* KACC17005 contains at least putative 15 T3Es, suggesting that the bacterium also use T3Es to cause disease on watermelon. This report will provide fundamental information to elucidate biological functions of proteins/genes in *A. citrulli* at the molecular level.

#### Nucleotide sequence accession numbers

The complete genome sequence of *A. citrulli* KACC17005 has been deposited in GenBank under the accession no. CP023687.

## 적 요

*Acidovorax citrulli* 병원세균은 수박에 과실썩음병을 일으킨다. 이 논문에서는 *A. citrulli* strain KACC17005 균주의 완전한 게놈 서열을 분석하여 보고한다. 게놈은 총 5,349,924 bp 로 구성

되어 있으며 G + C 함량이 68.54%이다. 단백질을 coding하는 유전자가 총 4,520개이고, 이들 중 적어도 15개의 유전자들은 감수성 식물에서 병원성을 증가시키거나 저항성 식물에서 면역반응을 유도하는데 중요한 제3형 effector 단백질을 코딩하고 있다.

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