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Draft genome sequence of *Streptomyces* sp. P3 isolated from potato scab diseased tubers

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감자 더뎅이병 이병괴경으로부터 분리한 *Streptomyces* sp. P3 균주의 유전체 해독

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Streptomyces sp. P3 was isolated from potato scab diseased tubers in Pyeongchang, Gangwon-do, Republic of Korea in 2017. Here, we report the draft genome sequences of P3 with 9,851,971 bp size (71.2% GC content) of the chromosome. The genome comprises 8,548 CDS, 18 rRNA and 66 tRNA genes. Although strain P3 did not show pathogenicity both potato tuber assay and radish seedling assay, it possesses tomatinase (*tomA*) gene among conserved pathogenicity-related genes in well characterized pathogenic *Streptomyces*. Thus, the genome sequences determined in this study will be useful to understand for pathogenic evolution in *Streptomyces* species, which already adapted to potato scab pathogens.

Keywords: *Streptomyces*, pathogenicity island, potato scab disease, tomatinase

Members of the genus *Streptomyces* are aerobic, filamentous, and Gam-positive bacteria, which are soil-inhabiting saprophytes that have ability to produce valuable compounds and hydrolytic enzymes (Joshi and Loria, 2007). Among them, a few strains are deposited into phytopathogens that cause potato scab disease on potato tubers (Loria *et al*., 2006). In order to induce a necrogenic symptoms on tuber tissue, which are early symptoms resulting from interactions between potato tubers and pathogenic *Streptomyces* strains, they must have pathogenicity factors representing thaxtomins (King *et al*., 1989). The biosynthetic genes of thaxtomins are located on mobilizable pathogenicity island (PAI) in chromosome and these are conserved in *Streptomyces scabies*, *Streptomyces acidiscabies*, and *Streptomyces turgidiscabies*, which are best characterized pathogenic *Streptomyces* species (Kers *et al*., 2005). In addition to thaxtomins, necrogenic protein called Nec1 had been reported as determinant of virulence such as colonization in the host tissue and *nec1* gene also is located on PAI of well characterized three species (Bukhalid *et al*., 2002). Furthermore, tomatinase gene, *tomA*, is reported to suppress the induced plant defense response and its genomic location had been also conserved on PAI in the three pathogenic *Streptomyces* (Kers *et al*., 2005). Taken together, the *nec1*, *tomA*, and thaxtomin biosynthetic genes are located on PAI, which is a large and mobilizable genetic cluster in three pathogenic *Streptomyces* sp. This fact suggests that at least three virulence genes are transfer together by lateral gene transfer mechanism from pathogens to non-pathogens. However, we found new fact, which contrary to above hypothesis that *Streptomyces* sp. P3 has only *tomA* gene among three pathogenicity genes

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based on PCR confirmation as preliminary experiment. Thus, we present the genome sequence of this strain in this study and hope to further understand the distinct characterization of evolution of the pathogenic *Streptomyces* by pathogenicity genes flow.

The new *Streptomyces* sp. P3 was isolated from potato scab diseased tubers in Pyeongchang, Gangwon-do, Republic of Korea in 2017. Draft genome sequencing of *Streptomyces* strain P3 was performed using Pacific Biosciences RSll sequencing platform (Pacific Biosciences) with a 20 kb SMRTbell™ templates library at ChunLab, Inc. Sequences were assembled using the HGAP2 protocol (Pacific Biosciences) and the sequencing depth was 98.2 × coverage of the genome. Genes encoding tRNAs and rRNA operons were searched using the tRNA-scan-SE 1.3.1 (Schattner *et al*., 2005) and Rfam 12.0 database (Nawrocki and Eddy, 2013), respectively. Genes of the draft genome sequence were annotated with Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) of the National Center for Biotechnology Information (NCBI) for annotation. The draft genome size of strain P3 was 9,851,971 bp chromosome with 71.28% G + C content (Table 1). A total of 8,548 CDS, 18 rRNA and 66 tRNA genes were identified. As expected, its genome sequences did not have *nec1* and thaxtomin biosynthetic genes. Instead, *tomA* cluster that *tomA* gene is linked to a cluster of glycoside hydrolases was found with array of *tomA* (tomatinase), *blgA* (ß-glucosidase), hypothetical protein, *tetR* (transcriptional regulator), three genes related to ABC transporter system, ß-glucosidase, and glycosyl hydrolase genes from left to right. These data suggest that *tomA* cluster in genome of P3 was *tomA* cluster 2, which was found in *S. turgidiscabies* rather than *tomA* cluster 1 (Huguet-Tapia *et al*., 2016). Actually, *tomA* cluster 1 involved with *nec1*, *tomA*, and thaxtomin biosynthetic genes was deposited in large, mobilizable PAI. Interestingly, pathogenic *Streptomyces* have *tomA* cluster 1 only or multiple copies of *tomA* cluster 1 and 2 in previous report (Huguet-Tapia *et al*., 2016). Whereas, existence of sole *tomA* cluster 2 is first case here, and transposase genes are located at left and right flanking regions from *tomA* gene with 2.4 kb and 172.8 kb distance, respectively. It indicates that *tomA* cluster 2 of P3 genome is acquired from another pathogenic *Streptomyces* by lateral gene transfer and thus strain P3 may have possibility to evolve as complete pathogenic *Streptomyces* at some point.

Table 1. Genome features of *Streptomyces* sp. strain P3

Genome features	Value
Genome size (bp)	9,851,971
G + C content (%)	71.28
tRNA	66
rRNA	18
CDS	8,548
No. of contigs	6
Sequencing depth of coverage	98.2 ×

Nucleotide sequence accession number

The draft genome sequences of a chromosome of *Streptomyces* sp. strain P3 have been deposited in the GenBank database under accession number CP028369. The strain was deposited in the Korean Agricultural Culture Collection (KACC) under the number of KACC 19680.

적 요

Streptomyces sp. P3 균주는 대한민국 강원도 평창의 더덩이병 이병괴경으로부터 2017년 분리되었다. 이 논문에서는 9,851,971 bp (71.2% G + C 함량)로 구성된 P3 균주의 전체염기서열을 보고한다. 지놈은 8,548개의 코딩서열, 18개의 rRNA 그리고 66개의 tRNA 유전자를 포함하고 있다. 특히 P3 균주는 감자표면과 무종자를 이용한 병원성 검정에서 병원성을 나타내지는 않았지만, 감자 더뎅이병 유발 *Streptomyces*들이 보유한 병원성 유전자 중 *tomA* 유전자만이 존재하였다. 따라서 본 논문에 제공되는 전체염기서열은 감자 더뎅이병원세균들의 병원성 획득을 위한 진화단계에서의 이해를 높이기 위한 중요한 단서가 될 것이다.

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