Complete genome sequence of biofilm-producing strain Staphylococcus xylosus S170

Jisoo Hong and Eunjung Roh*

Microbial Safety Team, National Institute of Agricultural Sciences, Rural Development Administration, Wanju 55365, Republic of Korea

생물막 생성 Staphylococcus xylosus S170 균주의 유전체 분석연구

홍지수 · 노은정* 🗅

농촌진흥청 국립농업과학원

(Received April 17, 2018; Revised May 15, 2018; Accepted May 15, 2018)

Here we report the complete genome sequence of *Staphylococcus xylosus* S170, strong biofilm-producing strain, which comprised a single circular 2,910,005 bp chromosome and 32.97% G+C content. The genome included 2,674 protein-coding sequences, 22 rRNA genes, and 57 tRNA genes. Gene analysis of *S. xylosus* S170 could contribute to better understanding of biofilm-forming mechanisms.

Keywords: Staphylococcus xylosus, biofilm

Staphylococcus xylosus is common bacteria from the skin microflora of human and animals. S. xylosus also persists on surfaces in food-processing plants and on medical devices (Dordet-Frisoni et al., 2008), and possibly colonizes the skin and surfaces by forming a biofilm (Planchon et al., 2006). Biofilm infections on indwelling medical devices are serious problems because biofilms are more resistant to antibiotics than planktonic cells. Among the biofilm-forming staphylococci, Staphylococcus aureus and Staphylococcus epidermidis are the most frequent causes of biofilm-associated infections on medical devices (Otto, 2013). For those two species, biofilm-forming mechanisms are well characterized, unlike for other

species such as S. xylosus. Although S. xylosus is considered to be nonpathogenic bacteria, several studies have shown opportunistic infections associated with S. xylosus in animals and humans (Conrad and West, 1984; Fthenakis et al., 1994; Bingel, 2002; Koksal et al., 2009). Production of biofilm-associated components is dependent on the presence of biofilm-essential genes such as the *ica* (intercellular adhesion) operon or *bap* (biofilm associated protein) gene (Ploneczka-Janeczko et al., 2014). In 55 staphylococcal strains isolated from leaf vegetables (Kim et al., 2018), S. xylosus S170 was chosen as s strong biofilm producer. To investigate biofilm control strategies, complete genomic sequencing of S. xylosus S170 was performed. Genomic DNA was extracted using the Wizard Genomic DNA Isolation Kit (Promega). Sequencing was performed using a combination of the Illumina MiSeq platform and the Pacific Biosciences (PacBio) single-molecule real-time (SMRT) sequencing platform at ChunLab. The sequencing reads were assembled using the CLC Genomics Workbench 7.5.1 and the PacBio SMRT Analysis 2.3.0 software. Annotation of the genome sequence was performed with the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Automatic Annotation Pipeline. The complete genome of S. xylosus S170 is comprised of 2,910,005 base pairs with 32.97% G + C content. A total of 2,674 protein-coding sequences (CDSs), 22

Table 1. Genome features of S. xylosus S170

Genome information	Total
Genome size (bp)	2,910,005
G + C content (%)	32.97
CDS (total)	2,674
rRNA	22
tRNA	57

rRNAs, and 57 tRNAs were annotated (Table 1). Genome analysis revealed that there was an *ica* operon and *bap* gene, both of which have been reported to play an important role in biofilm formation in staphylococci. The global regulators *agr* (accessory gene regulator) and *sar*A (staphylococcal accessory regulator), the major autolysin gene *atl* (autolysin), and the two-component gene system *arl*RS, involved in the regulation of adhesion and autolysis, were found in the sequence of *S. xylosus* S170. Sequencing of *S. xylosus* S170, a biofilm-overproducing strain, could contribute to better understanding of biofilm-forming mechanisms.

Nucleotide sequence accession number

The genome sequence of *Staphylococcus xylosus* S170 has been deposited in NCBI GenBank under accession number NZ_CP013922. The strain was deposited in the Korean Agricultural Culture Collection (KACC 18730).

적 요

Staphylococcus xylosus는 일반적으로 포유동물의 피부에 존재하며 식품가공설비와 의료기기 등에서도 발견이 보고되었다. 본 연구에서는 강력한 생물막 생성 특성을 가지는 Staphylococcus xylosus S170의 전체 유전체 서열을 분석하여보고한다. 이 유전체는 2,910,005 bp 크기, 2,674개의 단백질 코딩 서열과 22개의 rRNA, 57개의 tRNA유전자를 포함한다. 본연구에서 제공하는 유전체 정보는 생물막 관련 유전자 분석으로 생물막 형성 기작을 좀 더 잘 이해하는데 도움이 될 수 있다.

Acknowledgements

This work was supported by a grant (PJ011930) from the Rural Development Administration, Republic of Korea.

References

- Bingel, S.A. 2002. Pathology of a mouse model of X-linked chronic granulomatous disease. *Contemp. Top. Lab. Anim. Sci.* 41, 33– 38.
- Conrad, S.A. and West, B.C. 1984. Endocarditis caused by *Staphylococcus xylosus* associated with intravenous drug abuse. *J. Infect. Dis.* **149**, 826–827.
- Dordet-Frisoni, E., Gaillard-Martinie, B., Talon, R., and Leroy, S. 2008. Surface migration of *Staphylococcus xylosus* on low-agar media. *Res. Microbiol.* 159, 263–269.
- Fthenakis, G.C., Marples, R.R., Richardson, J.F., and Jones, J.E. 1994. Some properties of coagulase-negative staphylococci isolated from cases of ovine mastitis. *Epidemiol. Infect.* **112**, 171–176.
- Kim, J., Hong, J., Lim, J.A., Heu, S., and Roh, E. 2018. Improved multiplex PCR primers for rapid identification of coagulasenegative staphylococci. *Arch. Microbiol.* 200, 73–83.
- Koksal, F., Yasar, H., and Samasti, M. 2009. Antibiotic resistance patterns of coagulase-negative staphylococcus strains isolated from blood cultures of septicemic patients in Turkey. *Microbiol. Res.* 164, 404–410.
- Otto, M. 2013. Staphylococcal infections: Mechanisms of biofilm maturation and detachment as critical determinants of pathogenicity. *Annu. Rev. Med.* 64, 175–188.
- Planchon, S., Gaillard-Martinie, B., Dordet-Frisoni, E., Bellon-Fontaine, M.N., Leroy, S., Labadie, J., Hebraud, M., and Talon, R. 2006. Formation of biofilm by *Staphylococcus xylosus*. *Int. J. Food Microbiol*. 109, 88–96.
- Ploneczka-Janeczko, K., Lis, P., Bierowiec, K., Rypula, K., and Chorbinski, P. 2014. Identification of bap and icaA genes involved in biofilm formation in coagulase negative staphylococci isolated from feline conjunctiva. Vet. Res. Commun. 38, 337– 346.