Isolation of xylanolytic bacteria from agricultural resources and cloning of xylanase gene

김중곤*, 안승현, 박유리, 차영록, 안기홍, 박선태, 문윤호,
최용환, 구본철, 박광근
농촌진흥청 국립식량과학원 바이오에너지 작물센터
(kjk9207@korea.kr*)

Eleven microorganisms, expected to be xylanolytic microorganisms were isolated from agricultural resources, such as soil of sweet sorghum field, compost, decayed sweet sorghum and decayed wood. These strains were screened at 35℃ by using plate count agar containing 1% (w/v) xylan (from the beech wood) instead of glucose. Among the strains, SS8 and SS10 microbial strains, which have high xylanase activities, were characterized and identified as *Staphylococcus* sp. by analysis of 16S rDNA sequence and biochemical studies, and named as *Staphylococcus* sp. SS8 and SS10, respectively. The xylanase gene was cloned from SS8 and SS10 genomic DNA by polymerase chain reaction (PCR). The amplified PCR products were ligated with the T&A cloning vector system and the constructed plasmids were transformed into *E. coli* DH5α. The sequence analysis of the insert DNAs revealed the identification of a 640-bp region containing xylanase open reading frame. According to xylanase gene sequence analysis, both strains had gene sequence similarity of 99% with *Bacillus subtilis* Xyl gene for xylanase (AB457186.1).