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ORIGINAL ARTICLE

Peroxidase-producing actinobacteria from Algerian environments and insights from the genome sequence of peroxidase-producing *Streptomyces* sp. S19

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Abstract

Unique environments often serve as a source of novel microorganisms with novel chemistries. In this study, telluric samples collected from different regions of Algeria were processed for the isolation of novel peroxidase-producing actinobacterial strains. An agar-based screening identified 45 isolates with the ability to produce peroxidase. The 16S rRNA gene sequencing showed that most of the strains belong to the genus *Streptomyces*. Optimization of cultivation conditions was performed for the top five peroxidase-producing strains. Apart from strain 36 (optimal growth temperature of 30 °C) and strain 45 (optimal medium pH of 6.0), the strains exhibited optimal peroxidase production when cultivated for 5 days at 37 °C and in a medium at pH 7.0. Extracellular peroxidase production was induced by ferulic acid in three of the five strains, while the presence of canola lignocellulosic waste (CLW) induced peroxidase production in all strains. Strain 19 (S19) was selected for further optimization and the extracellular peroxidase purified using acid and acetone precipitation, followed by size exclusion chromatography. The purified fraction showed a single band on the polyacrylamide gel with an estimated molecular weight of 21.45 kDa. Genome analysis confirmed the assignment of S19 to the genus *Streptomyces*, the presence of genes encoding for peroxidases, and the presence of genes encoding for carbohydrate-active enzymes. The presence of biosynthetic gene clusters potentially encoding for biosurfactants further highlighted the great biotechnological potential of the strain.

Keywords Actinobacteria · Canola lignocellulosic waste · Genome sequencing · Optimization · Peroxidase · Purification

Introduction

The actinobacteria are a large group of mostly Gram-positive bacteria and are known to have a genomic G+C% of between 60 and 70%. They are widely distributed in nature and are found in almost all ecosystems including aquatic environments such as seawater (Subramani and Aalbersberg 2013), ocean sediments (Jensen et al. 2005; Solano et al. 2009), and in some plants and animals (Fiedler et al. 2005). However, soil remains the richest reservoir of actinobacteria. They are found in hot and dry desert soils, soils highly contaminated with heavy metals, frozen polar soils, highly alkaline lakes, and salt lakes (Kitouni 2007). Actinobacteria are known for their production of various metabolites and bioactive molecules such as antimicrobials, antidepressants, antitumor compounds, and immunosuppressants (Angehrn et al. 2004; Imada 2005) and are also able to degrade pesticides, herbicides, and hydrocarbons (Benimeli et al. 2003). This production and degradation potential give actinobacteria a wide range of potential industrial applications: food, pharmaceuticals, and agriculture. These bacteria are also widely and frequently exploited for their production of a variety of enzymes, such as peroxidases, that are increasingly sought after and applied in various industries.

Peroxidases represent a large family of oxidoreductases that catalyze the oxidation of a variety of organic and inorganic compounds using peroxides, such as hydrogen peroxide (H_2O_2) as a co-factor (Musengi et al. 2020). They have a molecular weight ranging from 30 to 150 kDa, and

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