

Yield improvement of enediyne yangpumicins in *Micromonospora yangpuensis* through ribosome engineering and fermentation optimization

Zilong Wang¹, Runze Sun¹, Miao Li¹, Ling Liu¹, Yanwen Duan¹, and Yong Huang¹

¹Central South University

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Abstract

Yangpumicins (YPMs), eg. YPM A, F, and G, are newly discovered enediynes from *Micromonospora yangpuensis* DSM 45577, which could be exploited as promising payloads of antibody-drug conjugates. However, the low yield of YPMs in the wild-type strain (~ 1 mg/L) significantly hampers their further drug development. In this study, a combined ribosome engineering and fermentation optimization strategy has been used for yield improvement of YPMs. One gentamycin-resistant *M. yangpuensis* DSM 45577 strain (MY-G-1) showed higher YPMs production (7.4 ± 1.0 mg/L), while it exhibits delayed sporulation and slender mycelium under scanning electron microscopy. Whole genome re-sequencing of MY-G-1 reveals several deletion and single nucleotide polymorphism mutations, which were confirmed by PCR and DNA sequencing. Further Box-Behnken experiment and regression analysis determined that the optimal medium concentrations of soluble starch, mannitol, and pharmamedia for YPMs production in shaking flasks (10.0 ± 0.8 mg/L). Finally, the total titer of YPM A/F/G in MY-G-1 reached to 15.0 ± 2.5 mg/L in 3-L fermenters, which was about 11-fold higher than the original titer of 1.3 ± 0.3 mg/L in wild-type strain. Our study may be instrumental to develop YPMs into a clinical anticancer drug, and inspire the use of these multifaceted strategies for yield improvement in *Micromonospora* species.

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