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Ahmad, S.J.[a b] , Zin, N.M.[b] , Mazlan, N.W.[c] , Baharum, S.N.[d] , Baba, M.S.[e] , Lau, Y.L.[f]

Metabolite profiling of endophytic Streptomyces spp. And its antiplasmodial potential
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[a] Faculty of Health Sciences, University of Sultan Zainal Abidin, Kuala Nerus, Terengganu, Malaysia
[b] Center for Diagnostic, Faculty of Health Sciences, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia
[c] Analytical and Environmental Chemistry, Faculty of Science and Marine Environment, Universiti Malaysia Terengganu, Kuala Nerus, Terengganu, Malaysia
[d] Institute of Systems Biology, Universiti Kebangsaan Malaysia, Bangi, Selangor, Malaysia
[e] Department of Biomedical Science, Kulliyyah of Allied Health Sciences, International Islamic University, Kuantan, Pahang, Malaysia
[f] Department of Parasitology, Faculty of Medicine, Universiti Malaya, Kuala Lumpur, Malaysia

Abstract
Background: Antiplasmodial drug discovery is significant especially from natural sources such as plant bacteria. This research aimed to determine antiplasmodial metabolites of Streptomyces spp. against Plasmodium falciparum 3D7 by using a metabolomics approach. Methods: Streptomyces strains' growth curves, namely SUK 12 and SUK 48, were measured and P. falciparum 3D7 IC50 values were calculated. Metabolomics analysis was conducted on both strains' mid-exponential and stationary phase extracts. Results: The most successful antiplasmodial activity of SUK 12 and SUK 48 extracts shown to be at the stationary phase with IC50 values of 0.8168 ng/mL and 0.1963 ng/mL, respectively. In contrast, the IC50 value of chloroquine diphosphate (CQ) for antiplasmodial activity was 0.2812 ng/mL. The univariate analysis revealed that 854 metabolites and 14, 44 and three metabolites showed significant differences in terms of strain, fermentation phase, and their interactions. Orthogonal partial least square-discriminant analysis and S-loading plot putatively identified pavettine, aurantioclavine, and 4-butyldiphenylmethane as significant outliers from the stationary phase of SUK 48. For potential isolation, metabolomics approach may be used as a preliminary approach to rapidly track and identify the presence of antimalarial metabolites before any isolation and purification can be done. Copyright 2021 Ahmad et al.

Author Keywords
Anti-plasmodial; Metabolomics; Multivariate analysis; Plasmodium falciparum; Streptomyces

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Correspondence Address
Ahmad S.J.; Faculty of Health Sciences, Malaysia; email: junaidahahmad@unisza.edu.my

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