



## Profile of antimicrobial potential of fifteen *Hypericum* species from Portugal



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### ABSTRACT

The aim of the present study was the search for the industrial exploitation potential of 15 *Hypericum* species crops from Portugal. Although *Hypericum perforatum* is well known worldwide, scarce studies have been published of *Hypericum* spp. identified in Portugal.

Extracts from 15 *Hypericum* species were screened for its antimicrobial activities against 2 Gram– and 2 Gram+ bacteria, 4 non-tuberculous *Mycobacterium* species, a reference strain H<sub>37</sub>Rv and 4 drug-resistant strains of *Mycobacterium tuberculosis*, as well as 4 drug-resistant clinical isolates.

In terms of Gram – standards, *H. humifusum* and *H. elodes* were the most active against *Agrobacterium tumefaciens*, with MIC of 2.5 µg/mL. *H. elodes* and *H. hircinum* subsp. *majus* extracts were the most active against MDR-TB strains and isolates, with MIC of 25–100 µg/mL and both exhibited significant effect against MDR-TB clinical isolates. With the exception of *H. androsaemum* and *H. linarifolium* all *Hypericum* species were active against *Staphylococcus aureus*, the *H. perforatum* and *H. elodes* at the level of 6 and 12 µg/mL, respectively, and none showed activity on *E. coli*.

Reference compounds isolated from *H. perforatum* were also tested and might contribute to the activities observed. The profile of the 15 *Hypericum* spp. as effective antimicrobial therapy against multidrug resistant pathogens is now available, providing scientific validation on a few available ethnopharmacological data resources.

This study may be a starting point for the research on the role of various *Hypericum* species in integrative medicine for infection control of *S. aureus* and MDR-MTB. *Hypericum* species may also constitute a source of new leads towards the discovery of either new candidates and biologically active compounds for pharmaceutical interest, for the treatment of multidrug resistant diseases.

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### 1. Introduction

Continuing search for effective antimicrobials is required to improve disease management against multidrug resistant pathogens. Gram-positive cocci have reemerged as predominant pathogens of human hosts within the past decade as an increasing cause of hospital-acquired infections. *Staphylococcus aureus* is a virulent and invasive pathogen that produces a variety of pyrogenic toxins and superantigens which contribute to its overall virulence. In the past several years Methicillin-resistant *S. aureus* were also

spreading clonally into the community leading to an increased use of vancomycin therapy. Vancomycin-resistant enterococci became a major hospital-acquired pathogen (Okuma et al., 2002).

Tuberculosis is still the leading killer infectious disease in the world, with one-third of the world's population infected with *Mycobacterium tuberculosis*. The World Health Organization estimates that 2 billion people have latent tuberculosis and 2 million people die each year worldwide because of this infection (WHO, 2008). Although a vaccine (BCG) and effective chemotherapy against tuberculosis were available 50 years ago, the increase in tuberculosis with the AIDS epidemic has resulted in the emergence of multidrug-resistant isolates of *Mycobacterium tuberculosis*. In spite of enormous efforts to find good leads, pharmacophore elucidation is still distant from a solution against the mechanism by which mutations induce drug resistance (Figueiredo et al., 2012). This fact demands the search for alternative antimycobacterial

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