Common medicinal plants with topical use : a metabolomic and proteomic approach targeting cutaneous microbiota

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Résumé

The skin microbiota is essential for skin health. Some bacteria, like Staphylococcus epidermidis or Staphylococcus hominis, help maintain the cutaneous barrier and reduce inflammation after skin wound (1). Dysbiosis can lead to dermatological inflammatory conditions, like dermatitis. That shows the importance of maintaining the homeostasis (2). The effect of dermal products prepared with medicinal plants on microbiota is not fully investigated and do not cover growth, metabolomic and proteomic aspects of skin microbiota after topical application. To gain a comprehensive understanding, special attention will be given to how plant molecules metabolized by the microbiota interact with the skin and other bacteria (3). In this project, we screen the effects of twenty traditional medicinal plants all already sourced such as Aloe vera, Arnica montana, Calendula officinalis, or Hamamelis virginiana. First, on skin bacteria and human healthy keratinocyte lines viability assays, then on more complex in vitro models of skin microbiota (4). Alongside we perform extractions and chemical characterization of extracts using dereplication tools and molecular networking. Bioguided screening is performed on bacterial viability and growth by broth microdilution assay to determine MIC (Minimum Inhibitory Concentration) values and to target right fraction to purify allowing to find specific molecules responsible of bioactivity. Stress levels will also be measured by an innovative fluorescent solvatochromic probe method that can help us monitor changes in the bacterial cell envelope in response to stress (5) at sub-MIC concentrations. Proteomic analysis of bacterial metabolism will be used to detect changes between treated and untreated conditions, as bacterial metabolites can also affect the skin in response to external compounds.
This work could help create safer, more effective skin treatments and cosmetic products that respect both the skin and its natural microbial balance.

Mots-Clés: Cutaneous microbiota, homeostasis, traditional plants, dereplication, molecular networking, metabolomic, proteomic

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