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Quorum Sensing Inhibitors of *Staphylococcus aureus* from Italian Medicinal Plants

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- quorum sensing
- MRSA
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- δ -hemolysin
- *agr*

Abstract

Morbidity and mortality estimates due to methicillin-resistant *Staphylococcus aureus* (MRSA) infections continue to rise. Therapeutic options are limited by antibiotic resistance. Anti-pathogenic compounds, which inhibit quorum sensing (QS) pathways, may be a useful alternative to antibiotics. Staphylococcal QS is encoded by the *agr* locus and is responsible for the production of δ -hemolysin. Quantification of δ -hemolysin found in culture supernatants permits the analysis of *agr* activity at the translational rather than transcrip-

tional level. We employed reversed phase high performance chromatographic (RP-HPLC) techniques to investigate the anti-QS activity of 168 extracts from 104 Italian plants through quantification of δ -hemolysin. Extracts from three medicinal plants (*Ballota nigra*, *Castanea sativa*, and *Sambucus ebulus*) exhibited a dose-dependent response in the production of δ -hemolysin, indicating anti-QS activity in a pathogenic MRSA isolate.

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Introduction

Emerging infections due to methicillin-resistant *Staphylococcus aureus* (MRSA) pose a significant threat to hospital patients as the rates of nosocomial infection steadily rise [1]. Healthcare-associated MRSA (HA-MRSA) is often multidrug-resistant (MDR), and therapeutic options are rapidly becoming more limited as new resistant phenotypes arise. Even more alarming, perhaps, is the recent emergence of highly virulent community-acquired MRSA (CA-MRSA) [2,3]. Many of these CA-MRSA strains, most notably those of the USA300 clonal lineage, have the capacity to cause a serious, life-threatening infection even in otherwise healthy individuals [4]. This accounts in large part for the observation that, in the United States alone in 2005, an estimated 94 360 patients suffered from invasive infection caused by MRSA, with approximately 18 650 resulting in a fatal outcome [5].

One approach to drug discovery for the treatment of staphylococcal infections is through the study of natural products from traditional remedies, such as those made from plants. Plants are engaged in a struggle for survival that involves the production and release of secondary metabolites

into their immediate environment both as a means of defense against potential pathogens and offense against competing species. If viewed in the light of chemical ecology, it is logical then that certain plants would be geared towards the production of antimicrobial compounds that limit the ability of microbes to produce the factors required for virulence and successful colonization. Most research on the activity of botanical natural products towards *S. aureus* is focused on growth inhibition, while some have focused on inhibition of the MDR mechanisms, such as efflux pumps [6–9]. No studies on the *agr*-inhibiting or quorum sensing inhibiting (QSI) activity of botanical natural products on *S. aureus* have been conducted thus far. Inhibition of staphylococcal QS pathways could potentially limit the degree of pathogenicity posed by some *S. aureus* strains by blocking the production of certain virulence factors. Moreover, the inhibition of staphylococcal pathogenesis could be accomplished without growth inhibition, thus potentially avoiding selective pressures for drug resistance.

The staphylococcal QS system is a cell-density-dependent mechanism for controlling protein expression, including the production of staphylococcal virulence factors such as α -, β -, and δ -he-

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molysins. It is encoded by the *agr* locus, which is a quorum-sensing gene cluster of five genes (*hld*, *agrA*, *agrB*, *agrC*, and *agrD*) [10].

Staphylococcal δ -hemolysin, or δ -toxin, is a translational protein product of RNAIII. It is a 26-amino-acid polypeptide with surfactant-like properties [11]. Translation of *hld*, the gene for δ -hemolysin, occurs about one hour after transcription of RNAIII. There are two forms of δ -toxin that can be found in the culture supernatant: formylated (with an N-terminal methionine) and deformylated. These forms are represented by two distinct peaks in the reversed phase high-performance chromatography (RP-HPLC) chromatogram (Fig. 1S). δ -Toxin accumulates in the culture medium in both forms and is approximately 90% formylated and 10% deformylated. This ratio is due to the arrest of deformylated δ -toxin production during the post-exponential growth phase, whereas formylated δ -toxin continues to accumulate. Somerville et al. [12] suggest that this change may be linked to iron availability in the culture medium.

Quantification of δ -toxin produced by *S. aureus* and found in the culture supernatants allows for the analysis of *agr* activity at the translational rather than transcriptional level. The identification of *agr*-inhibiting drugs or staphylococcal QS-inhibitors has been proposed by several research groups as a potential anti-staphylococcal therapy [13–17]. In 2000, Otto and Götz [11] provided a fast method for δ -toxin quantification using RP-HPLC techniques for the analysis of staphylococcal culture filtrates. We apply this method for the first time as a screening tool for identifying plant extracts with QSI activity concerning a strain of HA-MRSA known as pulsed-field type (PFT) USA500.

USA500 isolates are SCCmecIV and MLST ST8. USA500 demonstrates high virulence in animal infection models and has a high capacity to evade host defense mechanisms, including the lysis of neutrophils [18]. USA500 isolates are highly multidrug-resistant and tend to be associated with nosocomial transmission [19,20]. They are also associated with the production of many virulence factors, including δ -hemolysin cytolytic toxins and phenol-soluble modulins (including α -toxin), among others. A recent genetic study has demonstrated that the emerging highly virulent CA-MRSA USA300 lineage actually evolved from USA500 [18]. There is a critical need for novel therapeutic options in the treatment of highly virulent MDR staphylococcal infection, such as those caused by USA500.

We have quantified the amount of δ -hemolysin found in the supernatant of *S. aureus* cultures treated with plant extracts as a means of measuring the impact of plant products on the staphylococcal quorum sensing (QS) system. We examined 168 crude extracts made from 104 Italian plants, representing 44 plant families.

Materials and Methods

Plant material and extraction

Ethnobotanical surveys of plants used in the traditional pharmacopoeia of the Vulture-Alto Bradano region of Basilicata, southern Italy were conducted, and the results are described in previous works [21–24]. Bulk and voucher specimens were collected and identified in 2006 by C.L. Quave. Voucher specimens of plants were deposited at the Herbarium Lucanum (HLUC) in Potenza, Italy and Fairchild Tropical Botanic Gardens (FTG) in Miami, FL, USA.

Dry plant materials were ground into a fine powder using a homogenizer. Ethanolic extracts of all plant samples were made by soaking in 95% denatured EtOH using a ratio of 1 g (plant material):10 mL (EtOH) for 72 h. Flasks were agitated daily. Water extracts were made by boiling 1 g (plant material): 50 mL (dH₂O) for 30 minutes. Extracts were vacuum filtered and rotary evaporated, then frozen and lyophilized. Stock concentrations of 10 mg/mL of dry extract in the excipient (DMSO or dH₂O) were prepared, sterile filtered (0.2 μ m) and stored in the dark at 4 °C. The excipient (DMSO or dH₂O) made up less than 5.1% of the final test solution for MIC assays and less than 2.5% for δ -toxin assays.

Bacteria and culture conditions

HA-MRSA PFT USA500 (NRS385) was obtained from the Network on Antimicrobial Resistance in *S. aureus* (NARSA) repository [19]. We screened 10 different *S. aureus* isolates from our lab collection for δ -hemolysin production and selected this particular strain based on the high levels of δ -hemolysin detected in the RP-HPLC method detailed below. Bacteria were grown on tryptic soy broth (TSB) or agar plates (TSA) for 18 h at 37 °C. A 1 : 20 dilution of a standardized inoculum (0.5 McFarland Standard) was used to create final inoculum densities of $5\text{--}8 \times 10^5$ CFU/mL from overnight cultures using the direct suspension method [25] for MIC and δ -toxin assays. Inoculum densities were confirmed by taking colony counts using the spread plate method at the time of inoculation.

Determination of minimum inhibitory concentrations (MIC)

MIC's were determined following the NCCLS standard broth microdilution methods [26] in sterile flat-bottom 96-well polystyrene plates. Briefly, test strains were inoculated into 0.1 mL tryptic soy broth (TSB) containing the extract at concentrations ranging from 8–512 μ g/mL. The optical density (OD₆₀₀) was assessed immediately after inoculation and again after 18 hrs using a KC4 microplate reader. Corrections for extract color, which can alter the OD output, were done as previously described [27]. We included negative controls (cells + TSB), positive controls (cells + TSB + antibiotics – vancomycin, ampicillin, and trimethoprim-sulfamethoxazole; MP Biomedicals, > 98% purity for all antibiotics), vehicle controls (cells + TSB + DMSO), and media controls (TSB). All tests were performed in triplicate. Results are reported as the MIC for growth at 18 hours post-inoculation.

Quantification of δ -toxin production

Polystyrene 24-well culture plates were prepared with a total volume of 1 mL per well of TSB, an initial sub-MIC test concentration of 64 μ g of extract suspended in DMSO (< 1% DMSO in total well volume) and bacteria. We chose this concentration as it was well below the MIC for all of the extracts examined. By testing at concentrations too low to significantly impact growth, we could gain a better assessment of how δ -toxin production was affected. Screening at concentrations high enough to inhibit growth will yield more false-positives as δ -toxin production is lower in cultures that do not grow well.

Extracts demonstrating activity, as exhibited by lower δ -toxin levels, were also investigated at a range of test concentrations from 8–256 μ g/mL. Controls for media, growth, and growth in the carrier solvent (DMSO) were also performed. Liquid test cultures were grown for 15 hours at 37 °C and aerated by shaking at 150 rpm. All tests were performed in triplicate.

Aliquots of bacteria (2 mL) were centrifuged for 5 min at 14000 × g with a microcentrifuge. Supernatants were removed and stored at -20 °C until HPLC analysis. The concentration of δ -toxin was measured by RP-HPLC with a 1-mL Resource PHE column (GE Healthcare) as previously described [11], except that 200 μ L of supernatant (as opposed to 500 μ L) was injected onto the column using a Thermo Spectra-System HPLC apparatus, equipped with a Diode Array Detector and autosampler (Thermo Electron Corporation) as well as ChromQuest 4.1 software.

δ -Hemolysin eluted at a retention time of about 6.4 minutes (deformylated) and 6.8 minutes (formylated) after sample injection as two distinct peaks. Integration of the δ -toxin peak area was performed at 280 nm. We confirmed the identity of δ -toxin peaks by peak fractionation and LC-mass spectrometry (Fig. 1S) using a Thermo Finnigan Deca XP max ion trap mass spectrometer and surveyor LC with autosampler and diode array detector (Thermo Electron Corporation) using conditions previously described [12]. The peak areas for both the formylated and deformylated forms of δ -hemolysin were calculated using ChromQuest software. The sum of both peaks was calculated and used to calculate the mean percent inhibition of δ -toxin production for the replicate tests in relation to the mean peak area of the excipient (DMSO) growth controls.

Regarding the issue of plant color in the protocol for δ -toxin detection, we ran controls with extract and media alone using the same RP-HPLC conditions described above, and no peaks were observed, indicating that extract does not interfere with the results of this particular test.

Statistical analysis

All experiments were carried out in triplicate. Pairwise testing was performed based on t-tests as formatted in Microsoft Excel and SPLUS software with p values < 0.05 considered significant.

Supporting information

A HPLC chromatogram of the *S. aureus* supernatant showing both δ -hemolysin peaks (formylated and deformylated) is provided with accompanying LC-MS spectrograms, confirming the peak identities (Fig. 1S). In addition, HPLC chromatograms of supernatants collected after treatment with a range of 8–256 μ g/mL of extract (*Ballota nigra* stems, *Castanea sativa* leaves, and *Sambucus ebulus* leaves) are provided and demonstrate a dose-dependent response in δ -hemolysin production (Fig. 2S).

Results

There was a broad low level response of δ -toxin inhibition to the screening test concentration of 64 μ g/mL. QSI activity was apparent in 90% of the extracts tested (Table 1). No QSI activity was apparent in aqueous extracts. This suggests that the active QSI components are predominantly low to medium in polarity. Extracts were not effective at inhibiting growth of this multidrug-resistant strain of HA-MRSA (USA500/NRS385). Only 6% of extracts demonstrated a MIC₅₀ at concentrations of 256–512 μ g/mL. None demonstrated a MIC₉₀ at concentrations \leq 512 μ g/mL. Cytotoxicity of the extracts against a CCRF-CEM human T lymphoblastoid cell line (ATCC CCL-119) was assessed using an MTT cell proliferation assay and has been previously reported [28].

A total of 15 ethanolic extracts inhibited the production of δ -toxin by \geq 50% in comparison to controls at the preliminary screen concentration of 64 μ g/mL: *Sambucus ebulus* (leaves), *Achillea*

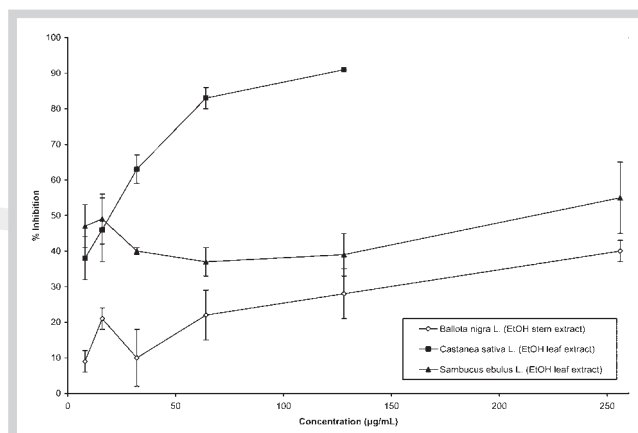


Fig. 1 Percent inhibition of δ -toxin peak area after treatment with extracts of *Ballota nigra*, *Castanea sativa*, and *Sambucus ebulus*.

ageratum (aerial parts), *Borago officinalis* (whole plant), *Cerinth major* (whole plant), *Knautia arvensis* (aerial parts), *Acacia dealbata* (inflorescence), *Castanea sativa* (leaves), *Ballota nigra* (stems), *Rosmarinus officinalis* (aerial parts), *Salvia pratensis* (inflorescence), *Malva sylvestris* (flowers), *Aceras anthropophora* (whole plant), *Orchis purpurea* (whole plant), *Orchis italica* (whole plant), and *Crataegus monogyna* (aerial parts). However, upon further testing of these extracts at a concentration range of 8–256 μ g/mL, we found that only three of these demonstrated significant dose-dependent δ -toxin inhibition independent of any growth-inhibitory effects: *B. nigra*, *C. sativa*, and *S. ebulus* (Fig. 1 and 2S).

Discussion

Quantification of δ -hemolysin in the supernatant of staphylococcal cultures can be used as a measure of *agr* system or QS activity [11–13]. The *agr* system controls approximately 150 genes and is critical to *S. aureus* virulence [29]. Although blocking certain virulence pathways (such as *agr*-regulated toxin production) would not necessarily prevent *S. aureus* from entering and growing in a host, it could impede processes related to colonization and delay the establishment of infection, affording the host immune response more time to combat the pathogen.

While the staphylococcal QS system is a useful target for the discovery and development of new anti-pathogenic drugs, the dynamic nature of the *agr* system must not be overlooked. There is the risk that downregulation or manipulation of certain gene promoters could result in the unintended consequence of up-regulating the production of another virulence factor. In particular, a better understanding of the effect that *agr* manipulation can have on the development of infection *in vivo* is necessary. For example, inhibiting *agr* activity during certain times in the infection process can lead to deleterious effects, such as increased biofilm formation [30].

In a previous study of these same extracts, we examined the anti-biofilm and bacteriostatic activity against another strain of *S. aureus* (ATCC 33593) [27]. We found that none of the most promising QS inhibitors reported here (*B. nigra*, *C. sativa*, and *S. ebulus*) exhibited any anti-biofilm activity, and they did not appear to promote biofilm formation in an *in vitro* context. However, in order

Table 1 Inhibition of δ -toxin and minimal inhibitory concentrations of plant extracts against MRSA (strain I. D. NRS385/PFT USA500).

Family	Botanic Name	Voucher ID	Plant Part	Ethno-botanical Use*	Extract Solvent	Percent Inhibition of δ -toxin Production**	MIC ₅₀ ***	
Adoxaceae	<i>Sambucus ebulus</i> L.	CQ-168	inflorescence	N	EtOH	45	–	
			leaves	S	EtOH	48	–	
			stems	N	EtOH	28	–	
	<i>Sambucus nigra</i> L.	CQ-151	woody parts	R	EtOH	29	–	
			leaves	S	EtOH	36	–	
					dH ₂ O	–	–	
			inflorescence	S; R	EtOH	38	–	
				dH ₂ O	–	–		
			infructescence	F	EtOH	34	–	
Alliaceae	<i>Allium cepa</i> L.	CQ-206	leaves; bulbs; roots	S; M; F	EtOH	22	–	
Apiaceae	<i>Daucus carota</i> L.	CQ-215	leaves; stems	N	EtOH	2	–	
			inflorescence; infructescence	N	EtOH	39	–	
	<i>Foeniculum vulgare</i> ssp. <i>piperitum</i> (Ucria) Coutinho	CQ-192	leaves; stems	M; F	EtOH	–	–	
	<i>Foeniculum vulgare</i> ssp. <i>vulgare</i> Mill.	CQ-196	leaves; stems	M	EtOH	8	–	
	<i>Tordylium apulum</i> L.	CQ-101	flowers; leaves; roots; stems	N	EtOH	25	–	
Apocynaceae	<i>Vinca major</i> L.	CQ-117	flowers; leaves; roots; stems	M	EtOH	26	–	
Araceae	<i>Arum italicum</i> Mill.	CQ-175	stems	N	EtOH	28	–	
			fruits	N	EtOH	15	–	
			stalks	N	EtOH	2	–	
			leaves	S	EtOH	22	–	
Asphodelaceae	<i>Asphodelus microcarpus</i> Salzm. & Viv.	CQ-109	inflorescence	N	EtOH	19	–	
			leaves	N	EtOH	17	–	
Asteraceae	<i>Achillea ageratum</i> L.	CQ-219	leaves; stems; flowers	M	EtOH	66	512	
			inflorescence	M	EtOH	41	–	
	<i>Achillea millefolium</i> L.	CQ-176	leaves; stems	M	EtOH	23	–	
			leaves; stems; flowers	M	EtOH	38	–	
			leaves; stems; flowers	M	EtOH	36	–	
	<i>Anacyclus tomentosus</i> DC.	CQ-167	leaves; stems; flowers	N	EtOH	36	–	
	<i>Cichorium intybus</i> L.	CQ-106	basal leaves; roots	F	EtOH	23	–	
					dH ₂ O	–	–	
				leaves; stems; flowers	F	EtOH	8	–
	<i>Matricaria recutita</i> L.	CQ-118	flowers; leaves; roots; stems	S; M	EtOH	29	512	
					dH ₂ O	–	–	
<i>Scolymus hispanicus</i> L.	CQ-199	leaves; stems; flowers	N	EtOH	23	–		
<i>Tussilago farfara</i> L.	CQ-202	leaves; stems; roots	S	EtOH	16	–		
<i>Urospermum dalechampii</i> (L.) Scop.	CQ-134	flowers; leaves; roots; stems	N	EtOH	14	–		
Boraginaceae	<i>Anchusa officinalis</i> L.	CQ-128	leaves; stems; flowers	N	EtOH	34	–	
	<i>Borago officinalis</i> L.	CQ-100	flowers; leaves; roots; stems	M	EtOH	54	–	
					dH ₂ O	–	–	
	<i>Cerinth major</i> L.	CQ-110	flowers; leaves; roots; stems	N	EtOH	48	–	
	<i>Echium italicum</i> L.	CQ-162	leaves; stems; flowers	N	EtOH	32	–	
Brassicaceae	<i>Brassica rapa</i> subsp. <i>rapa</i>	CQ-104	flowers; leaves; roots; stems	F	EtOH	27	–	
	<i>Cardaria draba</i> (L.) Desv.	CQ-140	flowers; leaves; roots; stems	N	EtOH	12	–	
	<i>Eruca sativa</i> Mill.	CQ-102	flowers; leaves; roots; stems	N	EtOH	13	–	
	<i>Sisymbrium officinale</i> (L.) Scop.	CQ-131	flowers; leaves; roots; stems	N	EtOH	20	–	
Caprifoliaceae	<i>Lonicera alpigena</i> L.	CQ-213	woody parts	N	EtOH	28	–	
			leaves	N	EtOH	25	–	
Caryophyllaceae	<i>Saponaria officinalis</i> L.	CQ-210	leaves; stems; flowers	N	EtOH	4	–	
	<i>Silene alba</i> (Mill.) E. H. L. Krause	CQ-123	leaves; stems; flowers	N	EtOH	43	–	
	<i>Silene nutans</i> L.	CQ-125	leaves; stems; flowers	N	EtOH	43	–	
Cucurbitaceae	<i>Ecballium elaterium</i> (L.) A. Richard	CQ-169	leaves; stems; flowers	S	EtOH	21	–	
Dennstaedtiaceae	<i>Pteridium aquilinum</i> (L.) Kuhn	CQ-211	leaves	N	EtOH	–	–	
			stems	N	EtOH	24	–	
Dipsacaceae	<i>Dipsacus fullonum</i> L.	CQ-201	leaves; stems	N	EtOH	28	–	
			flowers	N	EtOH	28	–	
	<i>Knautia arvensis</i> Coult.	CQ-190	leaves; stems; flowers	N	EtOH	48	–	
	<i>Knautia lucana</i> Lacaíta & Szabo	CQ-166	leaves; stems; flowers	N	EtOH	6	–	

continued next page

Table 1 Inhibition of δ -toxin and minimal inhibitory concentrations of plant extracts against MRSA (strain I.D. NRS385/PFT USA500). *continued*

Family	Botanic Name	Voucher ID	Plant Part	Ethno-botanical Use*	Extract Solvent	Percent Inhibition of δ -toxin Production**	MIC ₅₀ ***	
Equisetaceae	<i>Equisetum arvense</i> L.	CQ-226	stems; leaves	N	EtOH	22	–	
Fabaceae	<i>Acacia dealbata</i> Link	CQ-115	inflorescence	O	EtOH	56	–	
			stems	O	EtOH	38	–	
			leaves; stems	O	EtOH	21	–	
	<i>Anthyllis vulneraria</i> L.	CQ-147	leaves; stems; flowers	N	EtOH	28	–	
	<i>Astragalus monspessulanus</i> L.	CQ-112	leaves; stems; flowers; roots	N	EtOH	36	–	
	<i>Coronilla emerus</i> L.	CQ-137	leaves; flowers	N	EtOH	33	–	
			woody stems	N	EtOH	14	–	
	<i>Melilotus alba</i> Medik.	CQ-193	leaves; stems; flowers	N	EtOH	43	–	
	<i>Robinia pseudoacacia</i> L.	CQ-155	woody parts	N	EtOH	32	–	
			leaves	N	EtOH	–	–	
			inflorescence	N	EtOH	21	–	
	<i>Spartium junceum</i> L.	CQ-144	leaves; stems; flowers	A	EtOH	22	–	
	<i>Trifolium repens</i> L.	CQ-138	leaves; stems; flowers; roots	N	EtOH	4	–	
	<i>Vicia craca</i> L.	CQ-149	leaves; stems; flowers; roots	N	EtOH	19	–	
	<i>Vicia faba</i> L.	CQ-103	leaves; stems; flowers; roots	F	EtOH	14	–	
	<i>Vicia sativa</i> subsp. <i>angustifolia</i>	CQ-124	leaves; stems; flowers	N	EtOH	22	512	
	<i>Vicia sativa</i> subsp. <i>sativa</i>	CQ-119	leaves; stems; flowers	N	EtOH	29	–	
	<i>Wisteria sinensis</i> (Sims) Sweet	CQ-126	inflorescence	O	EtOH	36	–	
			stems	O	EtOH	39	–	
			leaves	O	EtOH	41	–	
Fagaceae	<i>Castanea sativa</i> Mill.	CQ-191	inflorescence	N	EtOH	20	–	
			leaves	N	EtOH	70	512	
			woody parts	A	EtOH	32	512	
	<i>Quercus cerris</i> L.	CQ-228	leaves	N	EtOH	27	–	
			stems; fruits	N	EtOH	37	–	
Gentianaceae	<i>Centaurium pulchellum</i> (Sw.) Druce	CQ-217	leaves; stems; flowers; roots	N	EtOH	21	–	
Geraniaceae	<i>Erodium ciconium</i> (L.) L'Hér.	CQ-142	leaves; stems; flowers; roots	N	EtOH	34	–	
	<i>Erodium malacoides</i> (L.) L'Hér. ex Aiton	CQ-121	leaves; stems; flowers	N	EtOH	7	512	
	<i>Geranium columbinum</i> L.	CQ-129	leaves; stems; flowers	N	EtOH	–	–	
Hyacinthaceae	<i>Leopoldia comosa</i> (L.) Parl.	CQ-105	bulbs	M; F	EtOH	21	–	
			leaves; inflorescence	N	EtOH	31	–	
Hypericaceae	<i>Hypericum perforatum</i> L.	CQ-183	leaves; stems; flowers	S	EtOH	36	–	
Juglandaceae	<i>Juglans regia</i> L.	CQ-181	immature fruits	S; C	EtOH	–	–	
			leaves	R	EtOH	39	–	
			woody parts	N	EtOH	17	–	
Juncaceae	<i>Juncus articulatus</i> L.	CQ-216	leaves; fruits	N	EtOH	32	–	
Lamiaceae	<i>Ballota nigra</i> L.	CQ-160	stems	S; M	EtOH	76	–	
			roots	N	EtOH	37	–	
			leaves	S; M	EtOH	47	–	
			leaves; stems; flowers	S; M	EtOH	47	–	
						dH ₂ O	–	–
						EtOH	40	–
	<i>Clinopodium vulgare</i> L.	CQ-182	leaves; stems; flowers	N	EtOH	40	–	
	<i>Marrubium vulgare</i> L.	CQ-170	leaves; stems; flowers	S; M	EtOH	40	–	
					dH ₂ O	6	–	
			roots	N	EtOH	40	–	
	<i>Mentha pulegium</i> L.	CQ-200	leaves; stems; flowers; roots	F	EtOH	36	–	
	<i>Mentha spicata</i> L.	CQ-224	leaves; stems; flowers	F	EtOH	28	–	
	<i>Origanum heracleoticum</i> L.	CQ-207	leaves; stems; flowers	F	EtOH	30	–	
	<i>Phlomis herba-venti</i> L.	CQ-168	leaves; stems; flowers	N	EtOH	16	–	
	<i>Rosmarinus officinalis</i> L.	CQ-113	leaves; stems; flowers	F; S	EtOH	58	256	
	<i>Salvia pratensis</i> L.	CQ-165	leaves; stems	N	EtOH	23	–	
			inflorescence	N	EtOH	58	–	
	<i>Salvia virgata</i> Jacq.	CQ-127	leaves; stems; flowers	N	EtOH	42	256	
	<i>Stachys tymphaea</i> Hausskn.	CQ-189	leaves; stems; flowers	N	EtOH	41	–	
Liliaceae	<i>Lilium candidum</i> L.	CQ-174	leaves; stems	N	EtOH	37	–	
			inflorescence	N	EtOH	30	–	

continued next page

Table 1 Inhibition of δ -toxin and minimal inhibitory concentrations of plant extracts against MRSA (strain I. D. NRS385/PFT USA500). *continued*

Family	Botanic Name	Voucher ID	Plant Part	Ethnobotanical Use*	Extract Solvent	Percent Inhibition of δ -toxin Production**	MIC ₅₀ ***
Malvaceae	<i>Alcea rosea</i> L.	CQ-205	leaves; stems; flowers; roots	O	EtOH	18	–
	<i>Malva sylvestris</i> L.	CQ-156	stems	S; M	EtOH	22	–
			flowers	S; M	EtOH	53	–
			leaves	S; M	EtOH	34	–
					dH ₂ O	–	–
Moraceae	<i>Ficus carica</i> L.	CQ-173	leaves	N	EtOH	24	–
			woody parts	N	EtOH	21	–
			immature fruits	S; F	EtOH	41	–
Myrsinaceae	<i>Cyclamen hederifolium</i> Aiton	CQ-186	tubers	M	EtOH	10	–
Nyctaginaceae	<i>Mirabilis jalapa</i> L.	CQ-222	leaves; flowers; fruits	N	EtOH	16	–
Oleaceae	<i>Olea europaea</i> L.	CQ-197	leaves	N	EtOH	40	–
			woody parts	A	EtOH	24	–
Orchidaceae	<i>Aceras anthropophora</i> R. Br.	CQ-153	leaves; stems; flowers; roots	N	EtOH	51	–
	<i>Orchis italica</i> Poir.	CQ-133	inflorescence; leaves; stems	N	EtOH	49	–
	<i>Orchis purpurea</i> Huds.	CQ-132	inflorescence; leaves; stems	N	EtOH	57	–
Papaveraceae	<i>Fumaria officinalis</i> L.	CQ-107	leaves; stems; flowers; roots	N	EtOH	44	–
	<i>Papaver rhoeas</i> subsp. <i>rhoeas</i>	CQ-145	leaves; stems; flowers; roots	F	EtOH	25	–
	<i>Papaver somniferum</i> L.	CQ-178	leaves; stems; flowers; roots	M; R	EtOH	36	–
Plantaginaceae	<i>Digitalis ferruginea</i> L.	CQ-227	leaves; stems; flowers	N	EtOH	32	–
	<i>Linaria vulgaris</i> Hill	CQ-223	leaves; stems; flowers; roots	N	EtOH	25	–
	<i>Plantago major</i> L.	CQ-225	leaves; stems; flowers; roots	S; M	EtOH	12	–
Poaceae	<i>Agropyron repens</i> (L.) P. Beauv.	CQ-208	leaves; stems; roots	M	EtOH	19	–
	<i>Arundo donax</i> L.	CQ-146	stem internodes	A; R	EtOH	22	–
			stem nodes	S	EtOH	35	–
					dH ₂ O	–	–
			leaves; stems	A; R	EtOH	10	–
Polygonaceae	<i>Rumex crispus</i> L.	CQ-171	leaves; stems; fruits	S	EtOH	25	–
Pottiaceae	<i>Syntrichia ruralis</i> (Hedw.) Web. & Mohr	CQ-229	whole plant	N	EtOH	45	–
Ranunculaceae	<i>Delphinium fissum</i> Waldst. & Kit.	CQ-187	leaves; stems; flowers; fruits	N	EtOH	29	–
	<i>Ranunculus acris</i> L.	CQ-135	leaves; stems; flowers	N	EtOH	34	–
Rosaceae	<i>Crataegus monogyna</i> Jacq.	CQ-116	leaves; stems; flowers	M	EtOH	57	–
	<i>Prunus spinosa</i> L.	CQ-163	woody parts; leaves	M	EtOH	33	–
			fruits	N	EtOH	29	512
	<i>Rosa canina</i> var. <i>canina</i>	CQ-152	fruits	N	EtOH	16	–
			woody parts	N	EtOH	44	–
			leaves; stems	N	EtOH	14	512
	<i>Rubus ulmifolius</i> Schott	CQ-164	leaves; stems; flowers	S	EtOH	10	–
			leaves	S	EtOH	17	–
			roots	M	EtOH	21	–
			woody stems	N	EtOH	16	512
Rubiaceae	<i>Galium verum</i> L.	CQ-177	leaves; stems; flowers	N	EtOH	27	–
Scrophulariaceae	<i>Verbascum sinuatum</i> L.	CQ-218	leaves; stems; flowers	N	EtOH	34	–
	<i>Verbascum thapsus</i> L.	CQ-172	stems	M	EtOH	31	–
			leaves	M	EtOH	40	–
			inflorescence	M	EtOH	38	–
Ulmaceae	<i>Ulmus minor</i> L.	CQ-195	leaves	N	EtOH	23	–
			woody parts	M	EtOH	–	–
Urticaceae	<i>Parietaria diffusa</i> Mert. & Koch	CQ-212	leaves; stems; fruits; roots	M	EtOH	19	–
	<i>Urtica dioica</i> L.	CQ-179	leaves; stems; flowers	S; M; F	EtOH	36	–
Valerianaceae	<i>Centranthus ruber</i> (L.) DC.	CQ-143	leaves; stems; inflorescence	M	EtOH	31	–
Vitaceae	<i>Vitis vinifera</i> var. <i>aglanico</i>	CQ-209	wine	S; F	–	–	–
			stems	N	EtOH	–	–
			fruits	F	EtOH	21	–
			leaves	N	EtOH	22	–

* Ethnobotanical use of specific plant part(s) in the study region: S = medicinal application to skin; M = medicinal application not involving the skin; C = cosmetic applications; A = agricultural tool; O = ornamental; R = ritual or spiritual use; F = food; N = no reported use; ** Percent inhibition for δ -toxin based on an initial screening concentration of 64 μ g/mL for MRSA PFT USA500; *** MIC values are reported as μ g/mL for MRSA PFT USA500; – No inhibitory activity

to account for variations in staphylococcal genotypes and phenotypes, we strongly caution that additional testing against all of the major PFT strains (especially CA-MRSA isolates from the USA-300 lineage) should be undertaken with these active extracts and fractions thereof in regards to QSI, anti-biofilm, bacteriostatic, and bactericidal activity prior to the initiation of *in vivo* studies.

Interestingly, each of the three most promising extracts comes from species that are topically applied in south Italian folk remedies for skin and soft tissue infection and inflammation [24]. Specifically, the leaves of *S. ebulus* are used to wrap the feet before putting on shoes in order to prevent the formation of foot blisters and sores. The aerial parts (leaves, flowers, and stems) of *B. nigra* are prepared in an aqueous decoction and then used to wash the skin as an anti-inflammatory and hemostatic. The leaves of *C. sativa* are topically applied to decrease swelling from varicose veins. Other ethnobotanical studies in the Mediterranean have also documented the application of these species in traditional wound healing practices [31, 32].

Regarding the chemistry of these species, *B. nigra* is rich in phenolic compounds [33], including phenylpropanoid glycosides [34], phenylpropanoid derivatives [35, 36], and flavonoids [37]. *C. sativa* [38] and *S. ebulus* [39] are also rich in phenolics, specifically regarding flavonoid content. At this point, we have not conducted bioassay-guided fractionation tests for the isolation of the active constituent(s), but it is reasonable to hazard a guess that the activity may be related to phenolic compound(s) with a low to medium level of polarity. Based on analyses of δ -hemolysin production, we have offered the first reports of plant extracts interfering with QS pathways in *S. aureus*. These results indicate that some small degree of QSI activity is evident in 90% of the ethanolic plant extracts screened, including those extracts with no growth inhibitory activity. Future changes to the protocol that may afford a more selective hit rate could be to conduct the preliminary screen at a lower test concentration of 32 $\mu\text{g}/\text{mL}$.

The validity of plant-based therapies for infection that do not exhibit activity in the standard *in vitro* bacteriostatic or bactericidal assays is oftentimes questioned. These data, however, support the concept that other mechanisms of action may be in play, which do not necessarily impact bacterial growth, but virulence mechanisms instead. These data offer a level of validity to the use of south Italian folk remedies incorporating *B. nigra*, *C. sativa*, and *S. ebulus* for the treatment of skin and soft tissue infection when *S. aureus* is implicated. Further investigation, including the bioassay-guided fractionation and isolation of active components from these three species, is recommended.

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