RESEARCH PAPER

Physiological Stress Tolerance of Culturable Bacterial Isolates Associated with Kappaphycus alvarezii: Evaluation of UV Tolerance, Salt Tolerance and Catalase Activity

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Abstract

Marine macroalgae provide diverse ecological niches for bacterial communities that may possess physiological adaptations to environmental stresses. The present study investigated selected stress-tolerance characteristics of culturable bacterial isolates associated with the red seaweed *Kappaphycus alvarezii*, with particular emphasis on ultraviolet (UV) tolerance, salt tolerance and catalase activity. Eight bacterial isolates, designated KA1–KA8, were recovered from *K. alvarezii* and subjected to physiological characterization. UV tolerance was evaluated following exposure to UV radiation at 230 nm using a resazurin-based viability assay. Salt tolerance was assessed by determining bacterial growth at 3%, 5%, 7% and 10% NaCl. Catalase activity was determined qualitatively using a 3% hydrogen peroxide slide assay. Considerable variation was observed among the isolates in their responses to the three stress conditions. KA3 exhibited the highest relative viability following UV exposure, followed by KA2 and KA1, whereas KA6 showed the lowest relative viability. In the salt-tolerance assay, KA2–KA8 demonstrated growth at all tested NaCl concentrations, including 10%, while KA1 failed to grow at the tested concentrations. Catalase activity was detected only in KA6 and KA7, whereas the remaining six isolates showed negative catalase reactions. The findings demonstrate substantial physiological diversity among the *K. alvarezii*-associated bacterial isolates, with salt tolerance being widespread but catalase activity restricted to a smaller proportion of isolates. The contrasting UV and catalase responses, particularly the low UV viability of catalase-positive isolate KA6, further suggest that tolerance to different environmental stresses may involve distinct physiological mechanisms. These findings provide a preliminary basis for selecting *K. alvarezii*-associated bacterial isolates for further physiological, biochemical and molecular characterization.

Keywords: *Kappaphycus alvarezii*; seaweed-associated bacteria; UV tolerance; salt tolerance; catalase; oxidative stress; marine bacteria.

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1. Introduction

Marine macroalgae are complex biological systems that harbour diverse microbial communities and maintain intimate associations with bacteria throughout their life cycle. These microorganisms can colonize the surface and internal tissues of macroalgae and contribute to several aspects of host physiology, including nutrient acquisition, growth promotion, chemical signalling, defence against competing organisms and adaptation to environmental fluctuations. Consequently, seaweeds and their associated microorganisms are increasingly considered integrated ecological units or holobionts rather than independent organisms (Egan et al., 2013). The bacterial communities associated with macroalgae are shaped by both host-derived factors and surrounding environmental conditions, resulting in microbial assemblages with considerable taxonomic and functional diversity.

Kappaphycus alvarezii is an economically important red macroalga belonging to the family Solieriaceae and is extensively cultivated because of its high carrageenan content and commercial value. In addition to its importance as a source of phycocolloids, *K. alvarezii* provides a suitable ecological niche for diverse bacterial communities. Culture-dependent and molecular investigations have demonstrated the occurrence of numerous bacterial taxa associated with healthy, diseased and endophytic tissues of *K. alvarezii*. For example, culture-based studies have recovered diverse bacterial groups from *K. alvarezii*, while 16S rRNA gene-based characterization of endophytic communities has identified members of *Bacillus*, *Cytobacillus*, *Priestia*, *Vibrio* and *Micrococcus* among isolates associated with healthy and diseased seaweed tissues (Mangun et al., 2023). More recent culture-dependent investigations have further demonstrated substantial bacterial diversity associated with *K. alvarezii*, highlighting the ecological importance of its culturable microbiota.

The physicochemical characteristics of the marine environment exert strong selective pressure on microorganisms associated with macroalgae. Among these factors, salinity is particularly important because

bacterial cells must maintain cellular water balance and macromolecular stability in an environment containing relatively high concentrations of dissolved salts. Marine bacteria may also experience temporal fluctuations in salinity associated with rainfall, evaporation, tidal exposure, freshwater influx and other environmental processes. Consequently, the ability to tolerate changes in external salt concentration can represent an important physiological characteristic for bacteria inhabiting marine and seaweed-associated environments.

Elevated salinity imposes osmotic stress on bacterial cells. An increase in external NaCl concentration reduces water activity and creates an osmotic gradient that promotes the movement of water out of the cell, potentially resulting in loss of turgor pressure and cellular dehydration. To maintain cellular homeostasis under such conditions, bacteria have evolved several osmoadaptation strategies. These include regulation of intracellular inorganic ions and the synthesis or uptake of low-molecular-weight organic compounds known as compatible solutes (Roberts, 2005; Wood et al., 2001). Compatible solutes can accumulate to high intracellular concentrations without disrupting essential cellular processes and contribute to the restoration of osmotic balance while also stabilizing proteins and other macromolecular structures.

Bacterial responses to salinity are generally flexible and can involve both immediate and long-term adaptive mechanisms. Potassium ions can contribute to the initial response to osmotic stress, whereas compatible solutes such as glycine betaine, proline, ectoine and related compounds can provide longer-term osmoprotection (Roberts, 2005; Gregory and Boyd, 2021). In marine bacteria, the uptake and biosynthesis of compatible solutes are particularly important because these organisms may encounter both relatively stable marine salinity and transient changes in osmolarity. The diversity of osmoadaptation mechanisms enables bacteria to maintain cellular integrity over a broad range of environmental conditions.

The physiological response to salinity varies considerably among bacterial species and even among strains belonging to the same species. Some microorganisms are adapted to high-salt environments and require elevated salt concentrations for optimal growth, whereas halotolerant microorganisms can withstand high concentrations of salt without necessarily requiring them for growth. Therefore, the ability of an isolate to grow at a particular NaCl concentration provides an important preliminary indication of its salt tolerance, although qualitative growth alone cannot establish whether an organism is truly halophilic or halotolerant in the strict physiological sense.

Salt tolerance is particularly relevant when investigating bacteria associated with *K. alvarezii*. The surface and internal microenvironments of seaweed can differ from the surrounding seawater and may expose associated bacteria to localized changes in osmotic conditions. Bacteria capable of maintaining growth under elevated salinity may therefore possess physiological characteristics that favour their persistence within the seaweed-associated habitat. Recent investigations of *K. alvarezii*-associated bacteria have demonstrated considerable diversity among culturable isolates, supporting the possibility that individual members of the bacterial community possess distinct physiological adaptations to their environment (Mangun et al., 2023; Emerson et al., 2026).

In addition to osmotic stress, marine-associated bacteria are exposed to oxidative challenges. Reactive oxygen species (ROS), including superoxide, hydrogen peroxide and hydroxyl radicals, can arise from cellular metabolism and environmental processes. Although low levels of ROS can participate in normal cellular signalling and physiological processes, excessive accumulation can damage nucleic acids, proteins, membrane lipids and other cellular components. Bacterial survival therefore depends on efficient mechanisms for maintaining redox homeostasis and eliminating potentially damaging reactive oxygen species.

Hydrogen peroxide (H_2O_2) is an important reactive oxygen species encountered by aerobic bacteria. It can be generated intracellularly during normal aerobic metabolism and may also originate from extracellular environmental sources. Because excessive H_2O_2 is toxic, bacteria possess several enzymatic systems for its removal. Catalases and peroxidases are among the principal enzymes involved in hydrogen-peroxide detoxification (Mishra and Imlay, 2012). The importance of these enzymes is reflected by the observation that bacterial mutants deficient in major peroxide-scavenging systems can exhibit impaired growth, increased mutagenesis and reduced survival under oxidative stress.

Catalase is a major hydrogen-peroxide-scavenging enzyme found across diverse groups of microorganisms. The enzyme catalyses the disproportionation of hydrogen peroxide into water and molecular oxygen according to the reaction:

$$\mathbf{2H_2O_2 \rightarrow 2H_2O + O_2}$$

This reaction enables bacterial cells to rapidly reduce potentially toxic concentrations of hydrogen peroxide. Catalases occur in several structural and evolutionary forms, including typical heme catalases, catalase-peroxidases and manganese catalases (Zamocky et al., 2008). Although these enzymes differ in structure and catalytic properties, their common physiological significance is the removal or reduction of hydrogen peroxide.

The catalase reaction forms the basis of a widely used qualitative biochemical test in microbiology. When bacterial biomass possessing catalase activity is exposed to hydrogen peroxide, the enzymatic release of molecular oxygen produces visible effervescence. The slide catalase assay therefore provides a rapid preliminary method for determining whether an isolate possesses detectable catalase activity. However, a positive catalase reaction should not be considered synonymous with complete resistance to oxidative stress because bacterial peroxide defence involves

multiple enzymes and regulatory systems (Mishra and Imlay, 2012).

The oxidative-stress response of marine bacteria is particularly relevant because the marine environment can expose microorganisms to multiple simultaneous stressors. Salinity, temperature fluctuations, oxygen availability, irradiation and chemical interactions can alter bacterial physiology and potentially influence oxidative balance. Microorganisms that persist within macroalgal-associated habitats may consequently require physiological mechanisms that allow them to cope with both osmotic and oxidative challenges.

The interaction between salinity and oxidative stress is also biologically relevant. High salinity can impose energetic and metabolic demands on bacterial cells because maintenance of osmotic balance requires regulation of ions and compatible solutes. Changes in cellular metabolism under stress conditions may influence redox homeostasis, while oxidative damage can in turn affect proteins and membrane systems involved in osmoadaptation. Nevertheless, salt tolerance and oxidative-stress resistance should be considered distinct phenotypic characteristics unless experimental evidence demonstrates a direct relationship between them.

Although molecular investigations have greatly expanded knowledge of seaweed-associated microbiomes, culture-dependent physiological characterization remains important because individual bacterial isolates can be subjected to controlled stress conditions and subsequently examined for functional characteristics. Culture-dependent approaches have been used to recover bacterial isolates from *K. alvarezii* and characterize their taxonomic and functional properties (Mangun et al., 2023). Such isolates provide a valuable resource for investigating physiological adaptation to the marine environment and for subsequent molecular characterization.

Recent research has also emphasized the functional significance of bacteria associated with red seaweeds. Bacteria isolated from *K. alvarezii* and other red macroalgae have been investigated for enzymatic activities, including agarolytic and carrageenolytic capabilities, demonstrating that seaweed-associated microorganisms can possess characteristics relevant to both ecological interactions and biotechnology. These observations reinforce the importance of examining physiological properties of individual bacterial isolates rather than focusing exclusively on community composition.

Despite increasing interest in the microbiology of *K. alvarezii*, the physiological stress tolerance of individual culturable isolates remains comparatively less characterized than their taxonomic diversity. In particular, determining the ability of isolates to tolerate elevated NaCl concentrations provides a straightforward approach for identifying bacterial phenotypes adapted to saline conditions. Similarly, screening for catalase activity provides an initial indication of the ability of isolates to enzymatically decompose hydrogen peroxide.

Therefore, the present study was undertaken to characterize culturable bacterial isolates associated with *Kappaphycus alvarezii* based on two complementary physiological characteristics: salt tolerance and catalase activity. Salt tolerance was evaluated by assessing bacterial growth at increasing NaCl concentrations of 3%, 5%, 7% and 10%, while catalase activity was determined using the conventional hydrogen peroxide slide assay. The study provides a preliminary phenotypic assessment of the ability of *K. alvarezii*-associated bacterial isolates to persist under elevated saline conditions and their capacity to exhibit catalase-mediated hydrogen-peroxide detoxification. Such characterization may provide a foundation for subsequent taxonomic, biochemical and molecular investigations of stress-adapted bacteria associated with marine macroalgae.

Ultraviolet (UV) radiation is another important environmental stressor influencing microbial communities in marine surface environments. UV exposure can cause direct DNA damage and can also promote the formation of reactive oxygen species, resulting in cellular damage and loss of viability. Marine bacterial isolates exhibit considerable interspecific variation in their sensitivity to UV radiation and in their ability to recover following irradiation (Arrieta et al., 2000; Matallana-Surget et al., 2012). Such variation may reflect differences in DNA-repair capacity, photoreactivation and other protective mechanisms. Therefore, assessment of UV tolerance, together with salt tolerance and catalase activity, provides a broader phenotypic perspective of the stress-adaptation potential of bacteria associated with marine macroalgae.

2. Materials and Methods

2.1 Isolation of Bacterial from *Kappaphycus alvarezii*

Fresh thalli of the red seaweed *Kappaphycus alvarezii* were collected and transported to the laboratory under appropriate conditions for microbiological processing. The collected seaweed material was washed three times with sterile seawater to remove loosely attached debris and non-associated microorganisms. The washed thalli were subsequently processed aseptically using a sterile mortar and pestle to obtain a homogenized seaweed suspension.

The homogenized material was serially diluted using sterile seawater. Serial dilutions were prepared from 10^{-1} to 10^{-6}, and aliquots of the appropriate dilutions were inoculated onto suitable bacteriological growth media using the spread-plate technique. The inoculated plates were incubated under the conditions used for recovery of the associated bacterial population.

Following incubation, morphologically distinct bacterial colonies were selected based on differences in colony morphology, including size, shape, pigmentation, elevation and surface characteristics. Individual colonies were subcultured repeatedly onto fresh medium to obtain pure bacterial cultures. The purified isolates were designated KA1 to KA8 and were maintained for subsequent physiological characterization.

The isolation procedure was based on the experimental protocol described for *K. alvarezii*-associated bacterial isolates in the present study, in which the seaweed

material was washed with sterile seawater, crushed, serially diluted and plated for bacterial recovery.

2.1.1 Purification and maintenance of isolates

The morphologically distinct colonies obtained from the isolation plates were individually transferred to fresh growth medium and subjected to repeated sub-culturing until pure cultures were obtained. Purity was assessed based on uniform colony morphology and microscopic characteristics.

The purified bacterial isolates were assigned the codes KA1–KA8 and subsequently used for physiological characterization. The isolates were maintained on appropriate culture medium until further analysis.

2.1.2 Selection of isolates for physiological characterization

Eight purified bacterial isolates, designated KA1, KA2, KA3, KA4, KA5, KA6, KA7 and KA8, were selected for further characterization. These isolates were subjected to salt-tolerance testing at increasing NaCl concentrations and qualitative catalase testing to assess their physiological responses to saline and oxidative stress, respectively.

2.2 Salt Tolerance Assay

The salt tolerance of the bacterial isolates was evaluated by determining their ability to grow at increasing concentrations of sodium chloride (NaCl). A basal growth medium was prepared and supplemented with NaCl at concentrations of **3%, 5%, 7% and 10% (w/v)** to provide progressively increasing saline conditions. Each bacterial isolate was inoculated onto the surface of the respective NaCl-supplemented media by streaking. The inoculated plates were incubated at **28–30°C for 24–48 h**. Following incubation, bacterial growth was assessed based on the formation of visible colonies and recorded as positive (+) for growth and negative (−) for no visible growth. The salt tolerance of each isolate was determined based on its ability to grow across the tested range of NaCl concentrations, with growth at **10% NaCl**, the highest concentration tested, considered indicative of a high salt-tolerance phenotype under the experimental conditions. This interpretation was restricted to the tested concentration range and did not represent the absolute maximum salt concentration tolerated by the isolates.

2.3 Catalase Activity Assay

Catalase activity was determined using a rapid slide method to assess the ability of the bacterial isolates to decompose hydrogen peroxide. A loopful of bacterial biomass from each isolate was transferred onto a clean, sterile glass slide. A drop of **3% hydrogen peroxide (H_2O_2)** was then added directly to the bacterial biomass.

The reaction was observed immediately for the formation of visible effervescence. The appearance of bubbles was considered a positive catalase reaction, indicating the enzymatic decomposition of hydrogen peroxide with the release of molecular oxygen. Isolates showing no visible or weak bubble formation were considered negative for catalase activity.

2.4 UV Tolerance Assay

The UV tolerance of the bacterial isolates was evaluated using a resazurin-based viability assay following exposure to ultraviolet radiation. The isolates KA1–KA8 were initially cultured in Zobell Marine Broth overnight at **37°C**. The cultures were subsequently diluted with fresh medium to obtain an optical density of **0.6**. The diluted bacterial cultures were transferred into the wells of a sterile microtitre plate and exposed to ultraviolet radiation at a wavelength of **230 nm** for the specified exposure period. An unexposed culture maintained under identical conditions was used as the control.

Following UV exposure, 150 µL of nutrient broth and 10 µL of 0.675% resazurin solution were added to each well. The plates were incubated at 37°C for 4 h, and the reduction of resazurin from its oxidized blue form to the pink resorufin form was used as an indicator of bacterial metabolic activity and viability. Absorbance was measured at 492 nm, and the relative viability of each UV-exposed isolate was compared with the corresponding untreated control. Each isolate was analysed in three replicate wells, and the mean absorbance values were used to determine the relative viability following UV exposure.

Relative viability was expressed as the percentage of metabolic activity retained following UV exposure compared with the untreated control. Higher relative viability was interpreted as greater tolerance to the applied UV treatment, whereas lower relative viability indicated greater sensitivity under the experimental conditions.

3. Results

3.1 Isolation of Bacterial Isolates from *Kappaphycus alvarezii*

Bacterial isolates associated with *Kappaphycus alvarezii* were recovered following processing of the seaweed sample and serial dilution plating. The processed sample was serially diluted and plated, resulting in the recovery of distinct bacterial colonies. Morphologically distinct colonies were selected and purified by repeated subculturing. A total of eight purified bacterial isolates were selected for further physiological characterization and designated KA1–KA8. The isolates were subsequently evaluated for their ability to tolerate increasing NaCl concentrations and for catalase activity.

3.2 Salt Tolerance of Bacterial Isolates

The eight bacterial isolates were evaluated for their ability to grow at NaCl concentrations of 3%, 5%, 7% and 10%. Considerable variation was observed among the isolates. KA1 showed no visible growth at any of the tested NaCl concentrations, whereas KA2–KA8 exhibited visible growth at all concentrations tested. Thus, seven of the eight isolates were capable of growing at the highest NaCl concentration tested (10%).

The salt-tolerance profile of the isolates is presented in Table 1.

Table 1 : Salt tolerance of bacterial isolates associated with *Kappaphycus alvarezii*

Isolate	3% NaCl	5% NaCl	7% NaCl	10% NaCl
KA1	−	−	−	−
KA2	+	+	+	+

Isolate	3% NaCl	5% NaCl	7% NaCl	10% NaCl
KA3	+	+	+	+
KA4	+	+	+	+
KA5	+	+	+	+
KA6	+	+	+	+
KA7	+	+	+	+
KA8	+	+	+	+

+ = growth; − = no visible growth.

Figure 1 : Salt tolerance of bacterial isolates KA1–KA8 associated with *Kappaphycus alvarezii* at different NaCl concentrations.

Among the eight isolates, **87.5% (7/8)** exhibited growth at 10% NaCl, while **12.5% (1/8)** failed to grow at the tested salt concentrations. The results indicate that the majority of the isolates exhibited a high salt-tolerance phenotype under the conditions examined. Since 10% NaCl was the highest concentration tested, the actual upper limit of salt tolerance of KA2–KA8 could not be determined from the present assay.

3.3 Catalase Activity of Bacterial Isolates

Catalase activity was determined among the eight bacterial isolates using the 3% hydrogen peroxide slide assay. The isolates exhibited variation in their catalase reaction. KA6 and KA7 showed positive catalase reactions, characterized by immediate visible effervescence following the addition of hydrogen peroxide**.** In contrast, KA1, KA2, KA3, KA4, KA5 and KA8 showed negative catalase reactions, with no visible bubble formation. Thus, only two of the eight isolates (25%) exhibited detectable catalase activity, whereas six isolates (75%) were catalase negative.

Table 2. Catalase activity of bacterial isolates associated with *Kappaphycus alvarezii*

Isolate	Catalase activity
KA1	−
KA2	−
KA3	−
KA4	−
KA5	−
KA6	+
KA7	+
KA8	−

+ = catalase positive; − = catalase negative.

The predominance of catalase-negative isolates indicates that detectable catalase activity was restricted to KA6 and KA7 under the conditions of the qualitative assay. However, catalase negativity does not necessarily indicate an inability to withstand oxidative stress, as bacteria may possess alternative hydrogen-peroxide-scavenging systems, including peroxidases and other antioxidant enzymes (Mishra & Imlay, 2012).

3.4 UV Tolerance of Bacterial Isolates

The UV tolerance of bacterial isolates KA1–KA8 was evaluated following exposure to UV radiation at 230 nm, and the relative viability of the isolates was determined using the resazurin reduction assay. A reduction in metabolic activity was observed following UV exposure, indicating that the treatment exerted a stress effect on the bacterial isolates. However, considerable variation was observed among the isolates in their relative viability following exposure.

Among the tested isolates, KA3 exhibited the highest relative viability, followed by KA2 and KA1, indicating comparatively greater tolerance to the applied UV treatment. In contrast, KA6 showed the lowest relative viability, indicating comparatively greater sensitivity to UV exposure under the experimental conditions. The remaining isolates showed intermediate responses.

The observed variation demonstrates that the bacterial isolates differed in their capacity to withstand UV-induced stress. The relative viability values obtained from the resazurin assay are presented in Figure 2.

Figure 2. Relative viability of Kappaphycus alvarezii-associated bacterial isolates following exposure to UV radiation at 230 nm.

4. Discussion

The present study demonstrated considerable variation in the response of *Kappaphycus alvarezii*-associated bacterial isolates to UV radiation. Following exposure to UV radiation at 230 nm, KA3 exhibited the highest relative viability, followed by KA2 and KA1, whereas KA6 showed the lowest relative viability. This variation indicates that the bacterial isolates differed in their ability to withstand the applied UV stress. UV radiation can affect bacterial cells through direct DNA damage as well as oxidative damage. Marine bacterial isolates have previously been shown to exhibit substantial interspecific variation in UV sensitivity and recovery following irradiation (Arrieta et al., 2000; Matallana-Surget et al., 2012). The comparatively higher viability observed in KA3, KA2 and KA1 may therefore reflect differences in cellular mechanisms involved in UV damage tolerance and recovery. However, DNA repair and photoreactivation mechanisms were not examined in the present study and therefore cannot be directly attributed to the observed responses.

A pronounced salt-tolerance phenotype was also observed among the isolates. KA2–KA8 exhibited growth at all tested NaCl concentrations, including 10%, whereas KA1 showed no growth from 3% to 10% NaCl. Thus, seven of the eight isolates were capable of growing at the highest salt concentration tested. Increased salinity imposes osmotic stress by reducing water availability and disturbing cellular water balance. Bacteria respond through mechanisms involving ion regulation and the accumulation or uptake of compatible solutes such as glycine betaine, proline and ectoine (Wood et al., 2001; Roberts, 2005; Gregory & Boyd, 2021). The ability of KA2–KA8 to grow at 10% NaCl may therefore reflect physiological mechanisms that enable maintenance of cellular homeostasis under saline conditions. However, compatible-solute accumulation, ion transport and

osmoregulatory genes were not examined in this study, and the underlying mechanism cannot be established from the present results.

The response of KA1 was distinctly different from that of the other isolates. Its inability to grow even at 3% NaCl suggests greater sensitivity to osmotic stress. However, because concentrations below 3% were not tested, the optimum salinity or minimum salt requirement of KA1 cannot be determined. The high proportion of salt-tolerant isolates may be associated with their marine origin, as marine bacteria are naturally exposed to saline conditions and may possess physiological adaptations that support growth under elevated osmolarity. Previous studies have demonstrated considerable diversity among culturable bacteria associated with *K. alvarezii*, indicating that this macroalga supports physiologically diverse bacterial populations (Mangun et al., 2023; Emerson et al., 2026). The present findings further demonstrate variation in salt tolerance among individual isolates. Nevertheless, the isolates should be described as showing growth under high-salt conditions, rather than being classified as halophilic, because the optimum and minimum salt requirements were not determined (Ventosa et al., 1998; Oren, 2002).

Catalase activity was detected only in KA6 and KA7, whereas KA1–KA5 and KA8 showed negative reactions. Thus, detectable catalase activity was observed in 25% of the isolates under the conditions of the assay. Catalase protects bacterial cells from hydrogen peroxide by converting H_2O_2 into water and molecular oxygen and represents one component of the bacterial antioxidant defence system (Zamocky et al., 2008; Mishra & Imlay, 2012). The positive reactions observed for KA6 and KA7 indicate detectable hydrogen-peroxide-degrading activity. However, catalase negativity should not be interpreted as an absence of oxidative-stress defence because bacteria possess additional systems, including catalase-peroxidases and other peroxidases, for hydrogen-peroxide detoxification (Mishra & Imlay, 2012). Therefore, the qualitative catalase assay provides only a preliminary indication of one component of the antioxidant defence system.

The combined results of the three assays revealed distinct physiological profiles among the isolates. Salt tolerance was widespread, with KA2–KA8 growing at 10% NaCl, whereas catalase activity was restricted to KA6 and KA7. UV tolerance also varied, with KA3 exhibiting the highest relative viability and KA6 the lowest. Interestingly, KA6 was catalase positive but showed the lowest UV viability, indicating that detectable catalase activity did not correspond directly with UV tolerance. Conversely, the isolate with the highest UV viability, KA3, was not among the catalase-positive isolates. These observations suggest that tolerance to different environmental stresses may depend on distinct physiological mechanisms rather than representing a single generalized stress-tolerance phenotype.

Overall, the present study demonstrates physiological diversity among culturable bacteria associated with *K. alvarezii* in relation to UV exposure, elevated salinity and catalase activity. The findings provide a preliminary basis for selecting isolates for further characterization. Future studies involving molecular identification, genomic analysis and targeted investigation of osmoadaptation, DNA repair and oxidative-stress defence mechanisms would help elucidate the basis of the contrasting phenotypes observed among the isolates.

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Conflict of Interest

The authors declare that there is no conflict of interest.

Data Availability

All data generated and analysed during the present study are included in this article.

Author Contributions

The study was conceptualized by the authors. The experimental work, data collection, analysis and interpretation were carried out by the authors. The manuscript was prepared and reviewed by the authors.

Ethics Approval

This study did not involve human participants or experimental animals; therefore, ethical approval was not required.