Scientific paper

Antimicrobial and anticancer evaluation of *Juniperus chinensis* seed oil with molecular docking of α-cedrol–AKT1

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Abstract

In this study, the essential oil of *Juniperus chinensis* L. seeds was analyzed by GC-MS, identifying 25 comprising comprising 99.78% of the oil. α-Pinene (79.63 ± 0.45%) was the major component, followed by β-myrcene, β-pinene, and DL-limonene. The oil exhibited antimicrobial activity with inhibition zones of 11 mm (*S. aureus*), 6 mm (*E. coli*), and 4 mm (*S. mutans*). Antifungal effects were noted against *Fusarium solani* and *Aspergillus niger*. Cytotoxicity assays revealed selective effects on MDA-MB-231 breast cancer cells (IC_{50}: 38 µg/mL), with no toxicity to MCF-10A normal cells. Molecular docking demonstrated strong binding affinity of α-cedrol to AKT-1 protein (–7.5 kcal/mol), supported by RMSD stability analysis and hydrogen bonding. ADME profiling confirmed favorable drug-likeness of α-cedrol. These results suggest that *J. chinensis* L. seed essential oil, particularly as a complex phytochemical mixture containing α-cedrol, holds promise as a natural source for antimicrobial and anticancer agents.

Keywords: *Juniperus chinensis* L., seed oil, GC–MS, α-cedrol, antimicrobial efficacy, molecular docking, anticancer potential

1. Introduction

The *Juniperus* genus, a member of the *Cupressaceae* family, encompasses approximately 75 species distributed across various regions worldwide. Many of these species have been employed in traditional medicine systems for their antiseptic, diuretic, and anti-inflammatory properties. Among them, *Juniperus chinensis* L. (commonly known as *Chinese juniper*) is a perennial conifer native to East Asia. The essential oil derived from this species is particularly rich in monoterpenes and sesquiterpenes, including α-pinene, sabinene, limonene, and α-cedrol compounds that have been widely documented for their diverse biological and pharmacological activities.[1,2]

Although extensive phytochemical and pharmacological evaluations have been conducted on other *Juniperus* species such as *J. communis*, *J. oxycedrus*, and *J. Phoenicea* mainly from Mediterranean and Anatolian regions data focusing specifically on *J. chinensis*, especially its seed-derived oils and extracts, remain scarce. These other species have demonstrated promising antioxidant, antimicrobial, and cytotoxic properties in multiple *in vitro* and *in vivo* models.[3,4] In the context of ethnomedicine in Türkiye, preparations from *Juniperus* species have been traditionally utilized to treat ailments involving the digestive, dermatological, and respiratory systems.[5] Nevertheless, there is limited experimental data regarding the therapeutic efficacy of *J. chinensis* seeds, particularly concerning their antimicrobial and anticarcinogenic properties.

Breast cancer continues to represent the most commonly diagnosed malignancy in women worldwide and remains a major contributor to cancer-related mortality. It accounts for the highest incidence among women in over 140 countries and often exhibits a metastatic phenotype, spreading to distant organs such as bone, lung, liver, and brain, which complicates its clinical management.[6] Current research emphasizes the importance of improving diagnostic sensitivity through emerging technologies such as molecular imaging and liquid biopsies, while also exploring epigenetic regulation and novel immunotherapeutic approaches.[7,8]

One of the significant challenges in breast cancer treatment is the development of resistance to chemother-

apy, which undermines the success of conventional anticancer agents.[9] This limitation has intensified the search for novel therapeutic compounds with enhanced efficacy and lower toxicity profiles. Natural products, due to their structural diversity and multifaceted biological actions, have been recognized as a valuable resource for anticancer drug discovery.[10] In particular, essential oils (EOs) have attracted growing interest for their chemopreventive and cytotoxic activities in preclinical cancer models. Various EO constituents have shown potential to sensitize resistant cancer cells when used alongside established chemotherapy agents. Despite this, the precise cellular and molecular mechanisms by which EOs exert such effects are not yet fully elucidated.[11,12]

In a comprehensive study, HS-SPME-GC-MS was utilized to analyze the leaf essential oil of *J. chinensis*, identifying α-pinene (27.2%) as the major constituent among 37 detected compounds.[2] Significant antibacterial activity was also reported against both Gram-positive and Gram-negative bacterial strains, including *Staphylococcus* aureus, MRSA, and *Micrococcus luteus*. Likewise, LC-QTOF-MS and LC-MS/MS were applied to the ethanolic extract of *J. chinensis* leaves, leading to the identification of abundant flavonoid and lignan derivatives, such as quercetin-3-O-α-L-rhamnoside and amentoflavone, which contributed to the observed antimicrobial effects, notably against *Bordetella pertussis*.[1]

Computational tools such as molecular docking offer valuable insights into the potential interactions between bioactive small molecules and their biological targets, including proteins involved in disease progression. When complemented with pharmacokinetic modeling techniques such as ADME (Absorption, Distribution, Metabolism, and Excretion) analysis, these methods provide a comprehensive platform for early-stage drug development.

Recent studies on *J. chinensis* L. seed essential oil have highlighted the relevance of these in silico approaches. The molecular docking data offer initial insights into the binding modalities of the identified drugs; nonetheless, these *in silico* predictions necessitate validation through additional experimental binding and functional experiments.[2] Furthermore, molecular dynamics simulations have confirmed the stability of these interactions, offering mechanistic insight at the atomic level.[13] Parallel ADME profiling has supported their favorable pharmacokinetic characteristics, such as good oral bioavailability and low predicted toxicity.[14]

Based on these findings, the present study was undertaken to (i) determine the chemical profile of essential oil derived from *J. chinensis* L. seeds collected from Afyonkarahisar, Türkiye, (ii) assess its antimicrobial and cytotoxic effects, particularly against the MDA-MB-231 triple-negative breast cancer cell line, and (iii) elucidate the binding interactions between its major bioactive constituents especially α-cedrol and the AKT-1 protein through molecular docking and dynamics analyses.

2. Materials and method

2. 1. Collection and identification of plant materials

Mature seeds of *J. chinensis* L. were collected in September 2024 from a natural population located on the ANS Campus of Afyon Kocatepe University (38.7575° N, 30.5343° E), Afyonkarahisar, Türkiye. The species was botanically identified by a field taxonomist, and a voucher specimen (Code: AKU-JC-2024) was deposited in the herbarium of the Department of Biology, Faculty of Arts and Sciences, Afyon Kocatepe University. The identification process was performed based on "Flora of Turkey and the East Aegean Islands," and further validated by herbarium comparison.

2. 2. Extraction of aqueous plant extract

Ten grams of air-dried *J. chinensis* L. seeds were thoroughly rinsed with deionized water and subjected to extraction using a Soxhlet apparatus with 300 mL of distilled water under reflux conditions. The extraction process lasted approximately six hours. After cooling, the extract was filtered and stored at 4 °C until use.[15] Prior to biological assays, the aqueous extract was concentrated under reduced pressure to remove excess solvent and subsequently reconstituted in dimethyl sulfoxide (DMSO) to obtain stock solutions.

2. 3. Essential oil extraction and GC-MS analysis

2. 3. 1. Hydrodistillation with clevenger apparatus

Twenty grams of crushed seeds were placed in a 500 mL round-bottom flask and subjected to hydrodistillation using a Clevenger-type apparatus with 250 mL of distilled water for 2.5 hours. The distillation was repeated in triplicate. The collected essential oil was extracted with 5 mL *n*-hexane, dried over anhydrous sodium sulfate (Na_2SO_4), and stored in sealed amber vials at 4 °C.[16] Residual *n*-hexane was completely removed under gentle nitrogen flow prior to biological evaluations. The essential oil was then dissolved in DMSO to prepare stock solutions.

2. 3. 2. GC-MS conditions

Analysis of essential oil composition was conducted using an Agilent 7890A GC system equipped with a 5975C mass detector and a CP-Wax 52 CB capillary column (50 m × 0.25 mm i.d., film thickness 0.2 μm). The oven temperature was programmed from 60 °C (held 2 min), raised to 220 °C at 2 °C/min, and held for 20 minutes. Injection and detector temperatures were set at 240 °C and 250 °C, respectively. Samples were dissolved in hexane (1:10), and 1 μL was injected in split mode.[17]

2. 4. Determination of antimicrobial activity

The antimicrobial activity of the aqueous extract and essential oil was evaluated using the agar well diffusion method against selected bacterial and fungal strains. The bacterial strains included *Staphylococcus aureus* ATCC 12600, *Escherichia coli* ATCC 35213, *Pseudomonas aeruginosa* ATCC 11778, *Streptococcus mutans* ATCC 25175, and *Listeria monocytogenes* (Uşak University Culture Collection). For antifungal evaluation, *Candida* spp., *Penicillium citrinum* NRRL 174127, *Aspergillus flavus* NRRL 980, *Fusarium solani* NRRL 13414, and *Aspergillus niger* 1094 strains were used.[18]

Bacterial suspensions were prepared and adjusted to a 0.5 McFarland standard, then spread onto Mueller-Hinton Agar (MHA) plates. Wells of 6 mm diameter were punched aseptically into the agar, and 200 µL of the extract or essential oil was added to each well. Plates were incubated at 37 °C for 24 h, after which inhibition zones were measured in millimeters.

For antifungal activity, mycelial growth inhibition assays were conducted on Potato Dextrose Agar (PDA). Fungal plugs were placed equidistantly from the central well containing the test sample. Following incubation at 27 °C for 7 days in the dark, radial growth was measured, and percentage inhibition was calculated relative to the control groups.[19] All samples were dissolved in DMSO, and the final DMSO concentration in agar wells did not exceed 0.01% (v/v), a level reported to be non-toxic to microbial and mammalian cells. A DMSO control (0.01%) was included in all experiments. Pure α-pinene was not included as a positive control because the primary objective of this study was to evaluate the antimicrobial activity of the essential oil as a complex phytochemical mixture rather than isolated individual constituents. Essential oils are known to exert biological effects through synergistic or antagonistic interactions among their components; therefore, testing single compounds was beyond the scope of the present study.

2. 5. Cell culture conditions

MDA-MB-231 (triple-negative breast cancer) and *MCF-10A* (non-tumorigenic epithelial) cell lines were obtained from ATCC. *MDA-MB-231* cells were cultured in RPMI 1640 medium supplemented with 10% fetal bovine serum and gentamicin. *MCF-10A* cells were maintained in DMEM/F12 medium containing 5% horse serum, 20 ng/mL EGF, 10 µg/mL insulin, 0.5 mg/mL hydrocortisone, 100 ng/mL cholera toxin, and antibiotics. All cultures were incubated at 37 °C in a humidified 5% CO_2 atmosphere.[20]

2. 6. Cell viability (XTT) assay

Cells were seeded in 96-well plates at a density of 8×10^3 cells per well and allowed to adhere overnight. Upon reaching 50–60% confluence, cells were treated with extract and oil samples for 72 hours. Cell viability was assessed using the XTT assay according to the manufacturer's protocol. Absorbance was recorded at 550 nm using a microplate reader (BioTek, USA), and results were expressed as percent viability relative to untreated controls.[21] Extract and essential oil samples were dissolved in DMSO, and the final concentration of DMSO in the culture medium was maintained at 0.01% (v/v), which is within the non-cytotoxic range reported for cell culture applications.[22] Cells treated with 0.01% DMSO alone served as vehicle controls.

2. 7. Molecular docking, dynamics, and ADME analysis

The three-dimensional structures of the proteins were obtained from the RCSB PDB protein database in pdb file format.[23] (https://www.rcsb.org/). The proteins to be used in molecular docking analysis are selected from antiapoptotic proteins and the PDB codes of the proteins are given in the Table 7. The three-dimensional structures of metabolites, identified through QTOF-LC/MS analysis, were retrieved from the PubChem database (https://pubchem.ncbi.nlm.nih.gov/) in pdb file format.[24] Molecular docking calculations were performed using Autodock Vina. The interactions between the molecules and the hydrogen (H)-bonds were visualized using the Seamdock online tool.

The molecular dynamics analyses of the protein and protein–ligand complex were performed using the WebGro platform. The stabilities of the protein in both their unbound and ligand-bound states were graphically presented over a 50 ns (nanosecond) simulation period.[25–31]

ADME/T analysis was conducted to determine whether α-cedrol has drug-like properties. As part of this process, the PDB files of the molecules were uploaded to the SwissADME program (http://www.swissadme.ch), and radar graphs were presented.

3. Results

3. 1 Essential oil extraction and GC-MS analysis of *J. chinensis* L. seeds

Gas chromatography mass spectrometry (GC-MS) analysis of *J. chinensis* L. seed essential oil, derived from samples collected in Afyonkarahisar, Türkiye, revealed a total of 25 volatile constituents accounting for 99.78% of the overall oil composition. Among these, α-pinene was the most dominant compound, comprising 79.63% of the oil. This high prevalence is consistent with prior studies highlighting α-pinene as a major constituent across various *Juniperus* species.[32] Known for its pronounced antimicrobial, antioxidant, and anti-inflammatory properties, the abundance of α-pinene may largely explain the bioactivity of the essential oil.

In addition to α-pinene, notable compounds included β-myrcene (4.62 ± 0.20%), β-pinene (2.84 ± 0.12%), and DL-limonene (1.99 ± 0.08%). β-Myrcene is recognized for its anti-inflammatory and analgesic functions and is frequently linked to the ethnomedicinal applications of *Juniperus* oils for musculoskeletal disorders.[33] Similarly, β-pinene structurally analogous to α-pinene has demonstrated notable antibacterial efficacy, particularly against Gram-positive bacteria.[34] DL-Limonene, another major component, is widely reported for its cytotoxic and chemopreventive properties, making it a valuable compound in the context of cancer research.[35]

Although present in smaller quantities, several minor constituents such as γ-terpinene (1.78 ± 0.07%), isobornyl acetate (1.43 ± 0.06%), and α-cedrol (1.08 ± 0.04%) also contribute to the oil's bioactivity. γ-Terpinene is especially known for its robust antioxidant capacity and may act synergistically with other monoterpenes to enhance radical-scavenging potential.[36] Isobornyl acetate is important for both its antimicrobial characteristics and fragrance profile. Of particular interest, α-cedrol despite its lower abundance has been widely studied for its sedative and antibacterial actions. Furthermore, it exhibited the most favorable interaction in molecular docking and simulation analyses, particularly with the AKT-1 protein.[37]

The complex phytochemical composition of *J. chinensis* L. seed oil offers a plausible explanation for its broad pharmacological properties, echoing its traditional medicinal uses and supporting contemporary therapeutic interest. The high α-pinene content may partially contribute to the antimicrobial activity observed; however, the overall effect is more plausibly related to synergistic interactions among multiple terpenoid components[38,39]

In summary, the GC-MS findings highlight the significance of key bioactive constituents, especially α-pinene and α-cedrol, and offer a scientific basis for the potential application of this essential oil in antimicrobial and anticancer formulations.

Furthermore, it is worth emphasizing that essential oils consist of complex mixtures where individual components may act synergistically or antagonistically, thereby influencing the net biological effect of the oil. Consequently, the observed pharmacological actions of *J. chinensis* L. seed essential oil are likely the result of collective interactions among its constituents, rather than the action of a single dominant compound. Such interactions may amplify effects such as antimicrobial, antioxidant, and anti-inflammatory activities, thus meriting additional mechanistic studies.[40]

It is also recognized that the chemical composition of essential oils is subject to variation based on factors such as the geographical location of the plant, seasonal differences, and the extraction technique employed. The current study utilized plant material collected from Afyonkarahis-

Table 1. Chemical Composition of *J. chinensis* L. Seed Essential Oil Analyzed by GC-MS

No	Retention time (min)	Compound name	Peak area (%)	Compound class
1	5.49	α-Pinene	79.63 ± 0.45	Monoterpene
2	5.76	α-Fenchene	0.19 ± 0.02	Monoterpene
3	5.90	Camphene	0.73 ± 0.05	Monoterpene
4	6.73	β-Pinene	2.84 ± 0.12	Monoterpene
5	7.66	Δ-3-Carene	0.19 ± 0.01	Monoterpene
6	8.06	β-Myrcene	4.62 ± 0.20	Monoterpene
7	8.12	α-Phellandrene	0.08 ± 0.01	Monoterpene
8	9.14	DL-Limonene	1.99 ± 0.08	Monoterpene
9	10.75	γ-Terpinene	1.78 ± 0.07	Monoterpene
10	11.51	Cymene	0.27 ± 0.02	Aromatic Monoterpene
11	12.19	α-Terpinolene	1.71 ± 0.05	Monoterpene
12	16.91	D-Fenchone	0.23 ± 0.01	Monoterpenoid Ketone
13	20.78	α-Fenchylacetate	0.13 ± 0.01	Monoterpene Ester
14	22.78	Camphor	0.08 ± 0.01	Monoterpenoid Ketone
15	26.69	Isobornyl acetate	1.43 ± 0.06	Monoterpene Ester
16	26.79	D-Fenchylalcohol	0.29 ± 0.02	Monoterpenoid Alcohol
17	27.38	exo-Methyl-camphenilol	0.08 ± 0.01	Monoterpenoid Alcohol
18	27.78	3-Carene	0.06 ± 0.01	Monoterpene
19	27.91	trans-Caryophyllene	0.14 ± 0.01	Sesquiterpene
20	29.13	α-Farnesene	0.09 ± 0.01	Sesquiterpene
21	30.32	trans-Pinocarveol	0.17 ± 0.02	Monoterpenoid Alcohol
22	31.67	trans-β-Ocimene	0.12 ± 0.01	Monoterpene
23	32.90	Borneol	0.54 ± 0.03	Monoterpenoid Alcohol
24	33.87	γ-Cadinene	1.32 ± 0.05	Sesquiterpene
25	53.54	α-Cedrol	1.08 ± 0.04	Sesquiterpenoid Alcohol

Total identified constituents represent 99.78% of the essential oil composition.

ar, Türkiye, which may represent a distinct chemotype of *J. chinensis* L., potentially differing in both qualitative and quantitative phytochemical profiles from samples reported in other regions. These regional disparities underscore the need for geographically targeted studies to better elucidate chemical variability and its biological implications.[41]

In terms of potential applications, the compounds identified in the essential oil of *J. chinensis* L. seeds exhibit significant promise across multiple industrial sectors. Notably, α-pinene and β-pinene are frequently used as natural preservatives and antimicrobial agents in cosmetic and food industries, while limonene is prized for its aromatic qualities and emerging anticancer properties. These versatile bioactivities align well with traditional medicinal uses of Juniperus species and highlight the potential of these oils as natural alternatives to synthetic additives.[42]

When evaluating the chemical makeup of *J. chinensis* L. in comparison with other members of the Juniperus genus, a notable overlap is observed in major monoterpenes such as α-pinene and β-pinene. However, differences in concentration levels between species suggest the influence of species-specific metabolic pathways and environmental pressures. These interspecies variations may affect the strength and scope of biological effects, which should be taken into account when assessing therapeutic applicability.[43]

It is also important to acknowledge that GC-MS primarily detects volatile compounds, whereas non-volatile phytochemicals which may also play crucial pharmacological roles are not evaluated in the current analysis. Thus, further research incorporating non-volatile profiling and bioactivity-guided fractionation is necessary to achieve a comprehensive understanding of the bioactive constituents and to unlock the full therapeutic potential of this plant.

Importantly, the GC-MS findings were further supported by molecular docking analyses, which indicated that α-cedrol and *trans*-caryophyllene are capable of interacting with key antiapoptotic proteins, including AKT-1. These results suggest that these compounds may contribute to the observed antimicrobial and anticancer activities of *J. chinensis* L. seed essential oil as part of a complex phytochemical mixture, potentially through additive or synergistic interactions with other constituents, rather than acting as sole bioactive agents.

3. 1 Antimicrobial activity of *J. chinensis* L. seed extract and essential oil

J. chinensis L. seed oil is a plant-based product that has been used in traditional medicine for centuries and has recently attracted interest in modern pharmacological research. Historically, it has been applied in the treatment of respiratory conditions, dermatological disorders, and gastrointestinal ailments.[44] Furthermore, various Juniperus species have been reported to exhibit a wide range of pharmacological activities, including analgesic, hepatoprotective, antihyperlipidemic, antimicrobial, anti-inflammatory, diuretic, antioxidant, antihypercholesterolemic, antiepileptic, and neuroprotective effects.[45,46] One of the most prominent attributes of *Juniperus* seed oil is its antimicrobial, antioxidant, and anti-inflammatory properties.[47] The essential oil of *Juniperus communis*, a closely related species, contains volatile compounds such as α-pinene, limonene, and sabinene molecules that have been extensively studied for their antimicrobial potential.[48]

In the present study, the antibacterial activity of *J. chinensis* L. seed extract and essential oil was assessed using the agar well diffusion method. Among the tested bacterial strains, the aqueous extract showed the strongest activity against *Staphylococcus aureus* with a mean inhibition zone of 11 mm, followed by *Escherichia coli* (6 mm) and *Streptococcus mutans* (4 mm) (Table 2, Fig. 1). The essential oil exhibited antimicrobial activity only against *S. mutans* (4 mm), suggesting a narrower antibacterial spectrum under the test conditions.

Table 2. Inhibition zone diameters (mm) of *J. chinensis* L. seed extract and essential oil against bacterial and yeast strains.

Microorganism	Seed extract (mm)	Seed oil (mm)
Staphylococcus aureus	11	–
Streptococcus mutans	4	4
Escherichia coli	6	nd
Pseudomonas aeruginosa	nd	–
Listeria monocytogenes	–	–
Candida sp.	2	–

nd: not detected, –: no activity)

To better contextualize the inhibition zone diameters obtained in this study, the results were compared with previously reported data for plant-derived essential oils. In the literature, inhibition zones of commonly used antibiotics against *Staphylococcus aureus* and *Escherichia coli* are generally reported to exceed 15–20 mm under similar assay conditions, indicating that the activity observed for *J. chinensis* seed extract can be considered moderate. Likewise, essential oils from other *Juniperus* species have been reported to produce inhibition zones ranging between 8 and 18 mm, depending on oil composition and test conditions. Accordingly, the antimicrobial activity observed in the present study is comparable to that of other plant-based essential oils, although lower than standard antibiotics, which is typical for crude extracts and essential oils evaluated by agar diffusion methods.

The GC-MS analysis identified α-pinene as the major constituent of the seed essential oil, accounting for 79.63 ± 0.45% of its total composition. It was reported that α-pinene exhibits antimicrobial activity by targeting the DnaKJE-σ32 chaperone complex, thereby disrupting

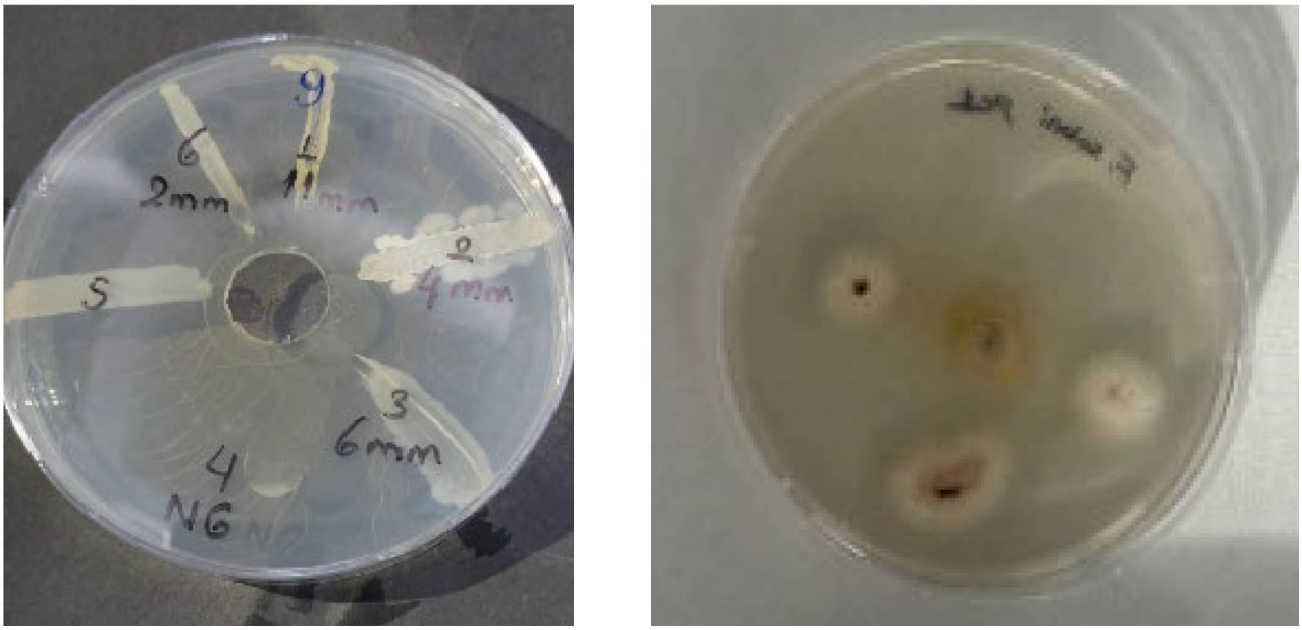

Figure 1. Antibacterial activity of *J. chinensis* L. seed extract and essential oil against selected bacteria using the agar well diffusion method.

protein folding and cellular stress mechanisms in bacterial species including *Escherichia coli*, *Salmonella enterica*, and *Staphylococcus aureus*.[49]

Antifungal assays revealed that the aqueous extract of *J. chinensis* L. inhibited the mycelial growth of *Fusarium solani* NRRL13414 and *Aspergillus niger* NRRL1094 by 56.25% and 33.33%, respectively. The essential oil displayed the strongest inhibitory effect against *A. niger* (56.25%), followed by *A. flavus* NRRL980 (27.77%) and *F. solani* (25.00%) (Table 3).

Table 3. Percent inhibition of fungal mycelial growth by seed extract and essential oil of *J. chinensis* L.

Fungal strain	Seed extract (%)	Seed oil (%)
Penicillium citrinum NRRL174127	10.00	9.09
Aspergillus flavus NRRL980	–	27.77
Fusarium solani NRRL13414	56.25	25.00
Aspergillus niger NRRL1094	33.33	56.25

These findings are consistent with previous reports suggesting that essential oils of *Juniperus* species possess potent antifungal properties.[50] The antifungal mechanism is thought to involve disruption of the fungal cell membrane, leading to leakage of intracellular components and eventual cell death.[51]

Moreover, *Juniperus* seed oils have shown promising activity against multidrug-resistant bacterial strains, highlighting their potential as alternative antimicrobial agents in an era of increasing antibiotic resistance.[52] The high antioxidant potential of *J. communis* essential oil has also been associated with protection against oxidative stress and skin aging,[43] further supporting its therapeutic relevance.

Taken together, the results of this study indicate that *J. chinensis* L. seed extract and essential oil exhibit selective antimicrobial and antifungal activities, likely due to their rich phytochemical composition. These findings support the potential use of *J. chinensis* L. in the development of natural antimicrobial formulations.

The present study contributes novel insights into the antimicrobial and antifungal potential of *J. chinensis* L. seeds, particularly from specimens collected in Turkey a geographical region underrepresented in current literature. The observed activity may be influenced not only by the major volatile component α-pinene but also by the synergistic action of other terpenoids. Furthermore, the relatively higher efficacy of the aqueous extract may suggest the presence of potent polar bioactives, such as flavonoids or phenolic acids, which warrant further phytochemical profiling. Given the rising concern over antibiotic-resistant pathogens, the ability of essential oils to disrupt microbial membranes offers a compelling alternative therapeutic strategy. Nonetheless, additional studies involving MIC determination, broader pathogen spectra, and *in vivo* models are essential to confirm the pharmaceutical relevance of these findings.

3. 3 Cytotoxic effects on MDA-MB-231 breast cancer cells

The antiproliferative potential of *J. chinensis* L. seed extract and essential oil was evaluated on triple-negative MDA-MB-231 breast cancer cells using an XTT-based viability assay. After 72 hours of treatment, the water extract and oil exhibited IC_{50} values of 45 μg/mL and 38 μg/mL,

respectively. Importantly, neither sample displayed cytotoxicity on the normal breast epithelial cell line MCF-10A at concentrations up to 100 μg/mL, suggesting a degree of selective toxicity toward cancer cells (Table 4, Fig.2).

Previous studies have reported anticancer-related activities for α-cedrol and α-cedrol–containing essential oils; however, given its relatively low abundance in the present oil, its contribution should be interpreted as supportive rather than determinant. Although α-cedrol has been reported to exhibit anticancer-related biological activities, its relatively low abundance in the essential oil (approximately 1–2%) suggests that it is unlikely to be the sole determinant of the observed cytotoxic effects. The antiproliferative activity observed in this study is more plausibly attributed to the combined and potentially synergistic effects of multiple constituents present in the essential oil. For instance, significant antiproliferative effects have been reported for α-Cedrol-containing essential oils in various cancer cell models.[53] Likewise, cedarwood oil rich in α-cedrene, β-cedrene, and cedrol was reported to exhibit cytotoxicity against leukemia cells.[54] α-Cedrol has also demonstrated apoptosis-inducing effects in various tumor models through mitochondrial membrane potential disruption and enhanced ROS generation.[55]

These results reinforce the therapeutic potential of *J. chinensis* L., particularly its essential oil, in developing cancer-selective agents. However, further mechanistic and in vivo validation will be essential to confirm its translational applicability. Since cytotoxicity assays were conducted at a limited concentration range, the reported IC_{50} values should be interpreted with caution. Future studies employing a broader concentration range are necessary to more accurately determine dose–response relationships and selective toxicity. It should be noted that the observed cytotoxic effects cannot be attributed to a single compound, and the contribution of minor constituents, as well as potential synergistic interactions, requires further investigation.

The AKT-1 protein is a major regulator of the PI3K/AKT/mTOR signaling pathway, which governs key biological processes including cell survival, proliferation, metabolism, and apoptosis inhibition. Dysregulation of this pathway is frequently observed in solid tumors, particularly breast cancer, and is associated with tumor progression, metastasis, and therapy resistance.[56,57] In triple-negative breast cancer (TNBC), the absence of hormone receptors and HER2 expression limits targeted treatment options, while hyperactivation of AKT signaling correlates with aggressive disease behavior and poor prognosis.[58]

Table 4. Cytotoxic effects (IC_{50}) of *J. chinensis* L. extract and oil on MDA-MB-231 and MCF-10A cell

Sample	MCF-10A (normal epithelial cell line)	MDA-MB-231 (breast cancer cell line)
J. chinensis L. water extract	298.7 μg/mL	45 μg/mL *
J. chinensis L. essential oil	280.3 μg/mL	38 μg/mL **

$p < 0.05$ compared to untreated control group

Based on the observed selective cytotoxicity of *J. chinensis* L. seed essential oil against MDA-MB-231 cells, AKT-1 was selected as a molecular target to link experimental anticancer activity with potential molecular mechanisms. Notably, α-cedrol, a bioactive constituent of the essential oil, has been reported to inhibit AKT signaling and promote apoptosis in tumor cells,[54] supporting the biological relevance of the molecular docking and molecular dynamics analyses performed in this study.[59,60]

3. 4 Molecular docking, dynamics and ADME analyses

α-Cedrol ($C_{15}H_{26}O$) is a sesquiterpenoid alcohol naturally found in essential oils of plants belonging to the cypress and cedar families. Due to its woody and earthy aroma, it is widely utilized in the fragrance and flavor industries. However, recent studies have revealed its potential antitumor and anti-inflammatory activities, making it an attractive candidate for further pharmacological evaluation.

Molecular docking analysis was performed between antiapoptotic proteins and bioactive molecules identified in *J. chinensis* L. (see Supporting Information, Table S1 and Table S2). Among the tested compounds, α-cedrol and *trans*-caryophyllene exhibited the lowest binding energy scores, suggesting strong potential interactions with target proteins. Notably, α-cedrol formed hydrogen bonds specifically with the AKT-1 protein, prompting further investigation via molecular dynamics simulation (see Supporting Information, Fig. S1,S2).

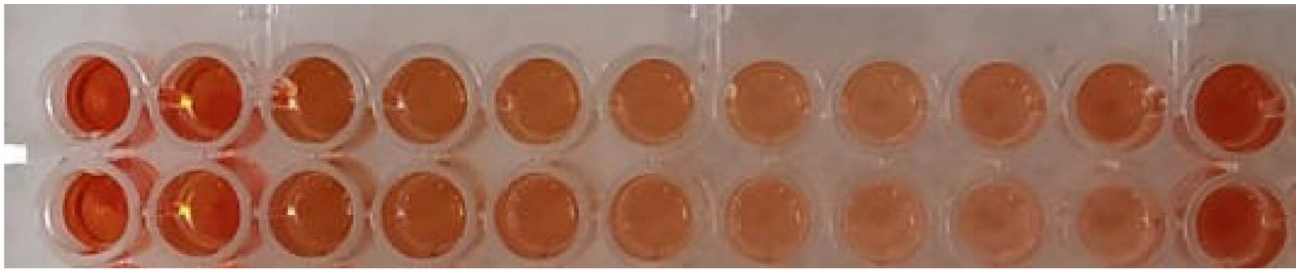

Figure 2. Cell viability of MDA-MB-231 cells after 72 h treatment with *J. chinensis* L. seed extract and essential oil evaluated by XTT assay.

The AKT-1 protein, regulated by the PI3K gene, is a serine/threonine kinase integral to the signaling pathways involved in cancer progression. It orchestrates critical cellular functions including proliferation, survival, metabolism, and motility.[61,62] As a key component of the phosphatidylinositol 3-kinase (PI3K) pathway, AKT also termed protein kinase B (PKB) exists in three isoforms: AKT-1, AKT-2, and AKT-3. Among these, AKT-1 is commonly activated by phosphatidylinositol-3,4,5-triphosphate (PIP3) at the cell membrane.

Once activated, AKT-1 facilitates cellular survival mechanisms by stimulating anti-apoptotic proteins such as Bcl-2 protein and concurrently inhibiting pro-apoptotic factors. Aberrant activation of AKT-1 has been frequently observed in various malignancies, contributing to enhanced cell proliferation, metastasis, and resistance to chemotherapeutics. Somatic mutations in the AKT-1 gene, particularly the E17K substitution, have been identified in multiple cancer types, including lung, colorectal, and ovarian carcinomas.[63] These mutations tend to arise in tissue-specific regions and are associated with distinct pathological and clinical outcomes.[64]

Due to its pivotal role in oncogenic signaling, AKT-1 is considered a significant molecular target for anticancer therapies. Notably, inhibitors targeting AKT have demonstrated therapeutic potential across a range of cancers. The E17K mutation in AKT-1 has been detected in approximately 1.4–8% of breast cancer cases, highlighting its relevance in breast tumorigenesis.[65] Investigating such mutations provides valuable insights into targeted strategies for suppressing tumor cell proliferation. Mutations in AKT-1 have been emphasized as promising therapeutic targets.[66] Similarly, early inhibition of AKT-1 activity has been proposed as a viable approach to limiting carcinogenesis at initial disease stages.[67]

The lowest binding energy (–7.5 kcal/mol) was found to be between α-cedrol and AKT1 protein, while the second binding energy was found to be between α-cedrol and Bcl-2 protein protein with –7.0 kcal/mol (Table 5, Figure 3). These binding energies represent *in silico* predictions derived from molecular docking simulations and do not correspond to experimentally measured binding affinities.

In particular, hydrogen bonding analysis revealed interactions between α-cedrol and amino acid residues Glu191 and Thr195 of AKT-1, as shown in Table 6.

To evaluate the drug-likeness of α-cedrol, its ADME properties were predicted using the Swiss ADME tool. According to Lipinski's and Weber's rules, α-cedrol complied with key pharmacokinetic parameters, indicating favorable absorption, distribution, metabolism, and excretion characteristics.

Doxorubicin served as the control medication, and molecular docking investigations were conducted with AKT-1 and BCL-2 proteins. The docking data indicated

Table 5. Predicted binding energies (kcal/mol) of selected compounds obtained from molecular docking simulations with the target proteins.

	AKT1 (PDB ID: 6BUU)	BAX (PDB ID: 1F16	BCL2 (PDB ID: 8SM5)	BCL2A1 (PDB ID: 6MBB)	BCL2L1 (PDB ID: 6DCO)	BCL2L10 (PDB ID: 4B4S	BIRC3 (PDB ID: 2UVL)	BIRC5 (PDB ID: 1XOX)
α-pinene	–5.3	–5.3	–5.9	–5.4	–5.4	–4.1	–5.0	–4.3
α-fenchene	–5.3	–5.3	–5.9	–5.2	–5.4	–3.9	–5.0	–5.4
Camphene	–5.3	–5.2	–5.8	–5.2	–5.4	–4.1	–4.7	–5.6
β-pinene	–5.3	–5.2	–5.7	–5.3	–5.1	–4.0	–4.9	–4.3
Δ-3-carene	–5.6	–5.3	–5.9	–4.6	–5.0	–4.5	–5.2	–4.6
β-myrcene	–5.2	–5.2	–5.6	–4.9	–5.1	–3.8	–4.5	–4.4
α-phallandrene	–5.9	–4.9	–6.0	–5.0	–5.4	–5.6	–5.0	–6.4
D limonene	–5.8	–5.6	–5.9	–5.1	–5.3	–5.3	–5.0	–6.2
γ-terpinene	–5.9	–5.3	–6.3	–5.2	–4.8	–4.5	–5.0	–4.7
Cymene	–5.9	–5.2	–6.3	–5.2	–5.6	–5.8	–5.0	–4.9
α-terpinelene	–6.3	–5.1	–6.1	–5.2	–5.9	–5.0	–5.2	–5.7
D fenchone	–5.8	–5.7	–6.3	–5.1	–5.2	–4.7	–4.5	–4.6
α-fenchylacetate	–5.6	–6.0	–5.9	–5.9	–5.6	–4.8	–5.4	–4.8
Camphor	–5.7	–5.1	–5.9	–5.6	–5.5	–4.1	–4.9	–4.0
Isobornylacetate	–6.1	–5.6	–6.0	–5.7	–5.7	–4.7	–4.6	–5.8
D fenchylalcohol	–5.8	–5.4	–6.0	–5.6	–5.1	–4.2	–5.4	–4.9
Exomethylcamphenilol	–5.1	–4.6	–5.1	–5.1	–4.7	–3.9	–4.1	–5.5
3-carene	–5.5	–5.1	–5.9	–5.7	–5.6	–4.3	–5.1	–5.1
Trans caryophllene	–7.2	–6.1	–7.9	–6.2	–6.6	–5.7	–5.3	–5.6
Trans pinocarveol	–5.9	–5.3	–6.1	–4.6	–5.3	–4.0	–5.0	–4.3
Trans beta ocimene	–5.3	–4.7	–5.7	–4.8	–4.1	–4.9	–4.5	–4.2
Berneol	–5.9	–5.2	–5.6	–4.8	–4.9	–4.1	–4.7	–4.8
γ-cadinene	–6.8	–6.2	–6.9	–6.3	–6.6	–6.8	–5.5	–5.7
α-cedrol	–7.5	–6.4	–7.0	–5.6	–5.6	–5.1	–5.3	–5.6

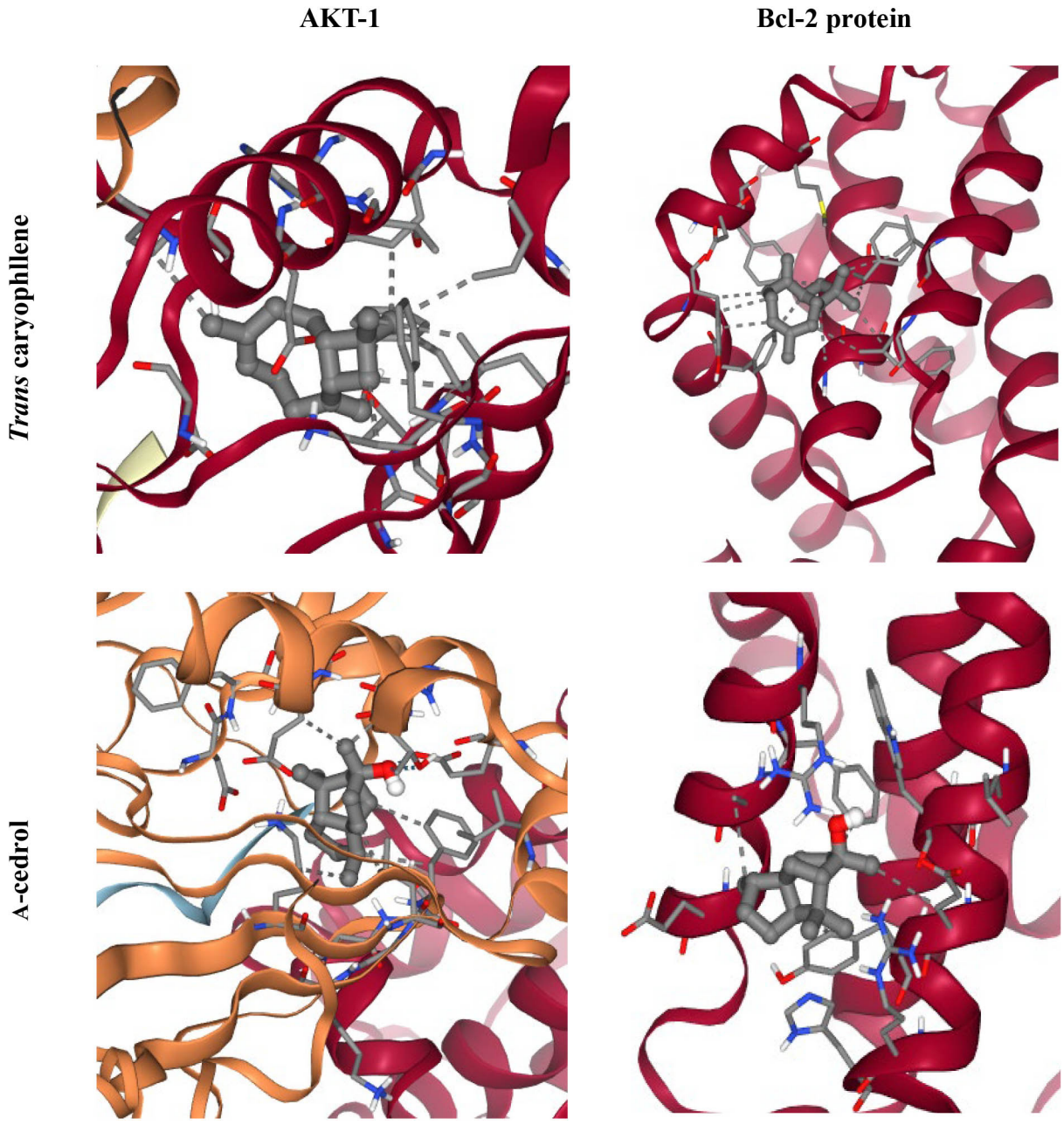

Figure 3. Representation of interaction between AKT-1 and Bcl-2 protein with *trans*-caryophllene and α-cedrol

Table 6. Hydrogen bond interactions between α-cedrol and AKT-1 protein residues.

Interaction type	Ligand atom	Receptor residue (chain)	Atom type (receptor)
Hydrogen bond	O1	Glu191 (B)	OE2
Hydrogen bond	O1	Thr195 (B)	OG1
Hydrogen bond	O1	Thr195 (B)	OG1

that the binding energy of doxorubicin with the AKT-1 protein was −9.8 kcal/mol, with one hydrogen bond identified in this interaction. The docking analysis of the BCL-2 protein revealed a binding energy of −8.0 kcal/mol and the establishment of six hydrogen bonds.

Nevertheless, the *in silico* ADME predictions should be interpreted cautiously, as α-cedrol is a highly lipophilic compound with limited aqueous solubility, which may affect its bioavailability under physiological conditions.

To further confirm the interaction between α-cedrol and AKT-1, molecular dynamics (MD) simulation was conducted using the GROMOS96 43A1 force field. The root mean square deviation (RMSD) trajectories of both the free protein and the protein-ligand complex were monitored over a 50 ns simulation (Figure 4, Figure 5)

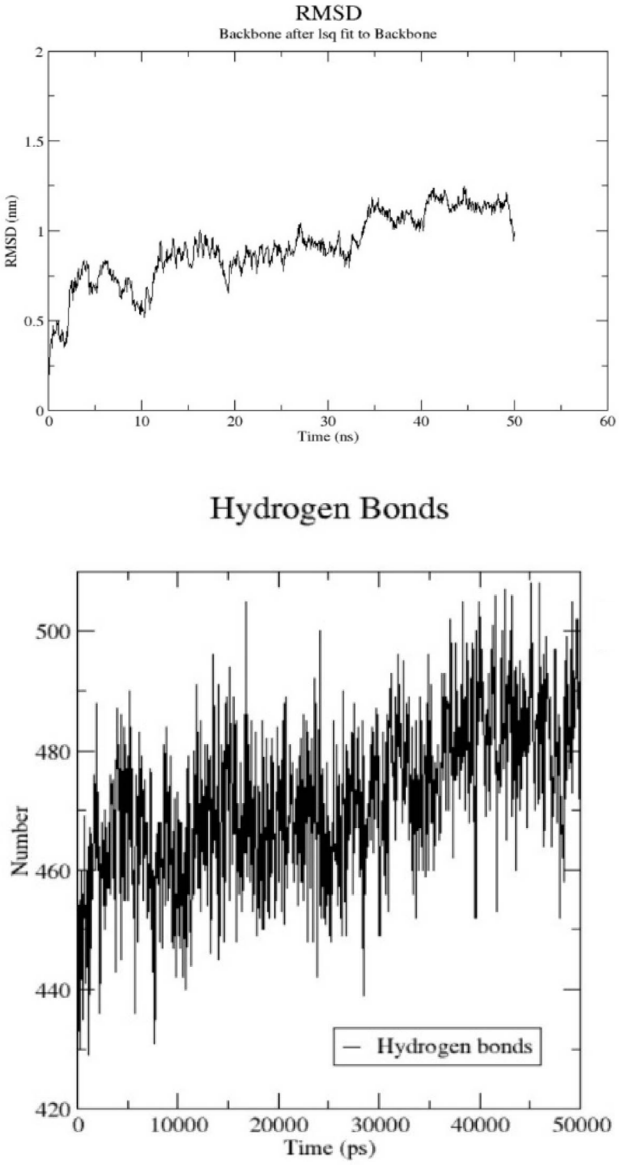

Figure 4. RMSD trajectory of AKT-1 protein during 50 ns MD simulation.

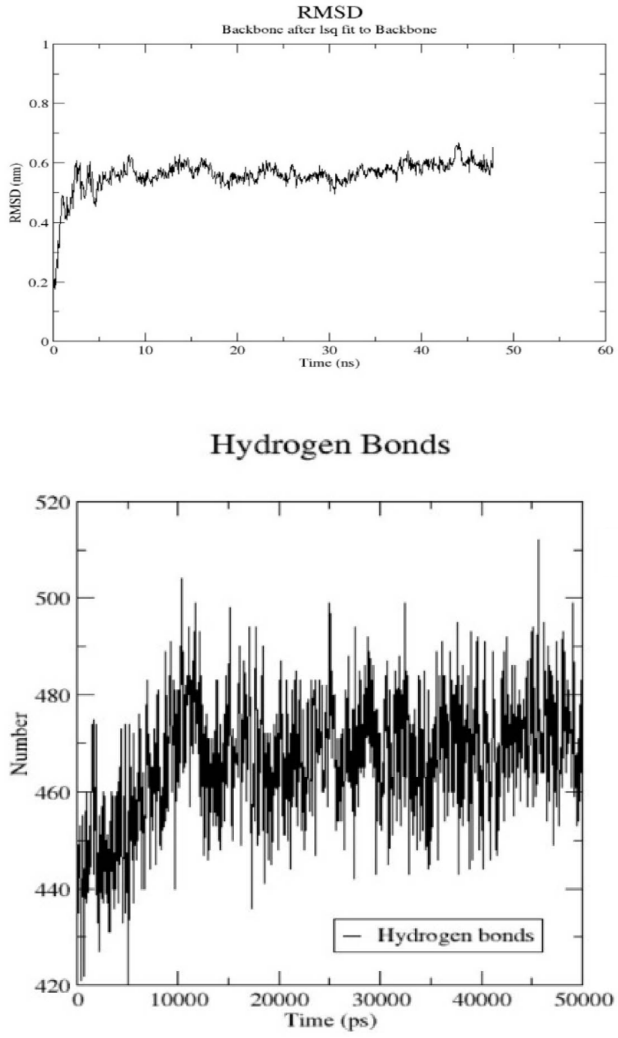

Figure 5. RMSD trajectory of the AKT-1– α-cedrol complex during 50 ns MD simulation.

The RMSD values showed slight fluctuations that stabilized after approximately 40 ns, indicating that the protein-ligand complex achieved conformational stability, supporting the binding affinity observed in docking results. Based on *in silico* ADME predictions, α-cedrol may be considered a potential lead compound for further drug development studies; however, these predictions remain theoretical and require experimental validation, particularly considering its lipophilicity and solubility limitations.

4. Conclusion

Breast cancer continues to be a predominant cause of cancer-related deaths among women worldwide, with triple-negative breast cancer (TNBC) presenting distinct therapeutic difficulties due to its aggressive behavior and limited treatment modalities. This study aimed to evaluate the therapeutic potential of *J. chinensis* L. seed essential oil and aqueous extract through a combination of *in vitro* assays assessing cytotoxic, antimicrobial, and antifungal activities, alongside *in silico* molecular docking, molecular dynamics simulations, and ADME profiling.

GC-MS analysis identified α-pinene as the principal constituent of the essential oil, comprising 79.63% of its composition, supplemented by other bioactive terpenoids including β-myrcene, DL-limonene, γ-terpinene, isobornyl acetate, and α-cedrol. These compounds have been extensively documented for their antimicrobial, antioxidant, and anticancer properties, which correspond with the empirical findings of this investigation. The aqueous extract demonstrated pronounced antibacterial efficacy against *Staphylococcus aureus*, whereas the essential oil exhibited moderate inhibitory effects on *Streptococcus mutans*. Ad-

ditionally, both preparations showed antifungal activity, notably against *Fusarium solani* and *Aspergillus niger*.

Cytotoxicity assays revealed that the aqueous extract and essential oil selectively suppressed the growth of MDA-MB-231 TNBC cells, with IC_{50} values of 45 μg/mL and 38 μg/mL, respectively, while showing no cytotoxicity toward normal breast epithelial MCF-10A cells. Molecular docking studies indicated strong binding affinities of α-cedrol and *trans*-caryophyllene toward anti-apoptotic targets such as AKT1, BCL-2, and BIRC5. Notably, α-cedrol exhibited the lowest binding energy with AKT1 (–7.5 kcal/mol), which was corroborated by stable hydrogen bond interactions and consistent RMSD patterns observed in molecular dynamics simulations. *In silico* ADME analysis indicated that α-cedrol meets several drug-likeness criteria; however, these findings remain predictive and do not account for formulation or bioavailability constraints.

Collectively, these results underscore the multiple *in silico*-supported biological activities of *J. chinensis* L. seed-derived compounds, particularly α-cedrol encompassing antimicrobial, antifungal, antioxidant, and cytotoxic effects. Although molecular docking and molecular dynamics simulations provide valuable hypotheses regarding ligand–protein interactions, these findings remain predictive in nature and require further experimental validation through biochemical binding assays and mechanistic studies. Overall, this study provides preliminary experimental and computational evidence supporting the biological potential of *J. chinensis* L. seed-derived products, while highlighting the necessity for further validation to substantiate their pharmacological relevance.

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Conflict of Interest

The authors report that there is no potential conflict of interest to declare

5. References

1. D. J. Lim, J. S. Song, B. H. Lee, Y. K. Son, Y. Kim, *Molecules* **2003**, *28*, 3937. **DOI:**10.3390/molecules28093937
2. A. S. Khamis, L. C. Chai, *Int. J. Anal. Chem.* **2021**, *2021*, 9937522. **DOI:**10.1155/2021/9937522
3. M. F. Taviano, A. Marino, A. Trovato, V. Bellinghieri, T. M. La Barbera, A. Güvenç, N. Miceli, *Pharm. Biol.* **2011**, *49*, 1014–1022. **DOI:**10.3109/13880209.2011.560161
4. R. B. Mansour, H. Wasli, S. Bourgou, S. Khamessi, R. Ksouri, W. Megdiche-Ksouri, S. M. Cardoso, *Molecules* **2023**, *28*, 7547. **DOI:**10.3390/molecules28227547
5. A. Bouchareb, A. Djemel, I. Kadi, A. Djemoui, C. Bensouici, M. Atanassova, A. Zoukel, M. Benmohamed, S. F. Ahmad, S. M. Attia, F. Benaceur, W. Zahnit, M. Messaoudi, *Ital. J. Food Sci.* **2024**, *36*, 370–394. **DOI:**10.15586/ijfs.v36i4.2729
6. N. Tzenios, M. E. Tazanios, M. Chahine, *Medicine* **2024**, *103*, e36831. **DOI:**10.1097/MD.0000000000036831
7. S. Byler, S. Goldgar, S. Heerboth, M. Leary, G. Housman, K. Moulton, S. Sarkar, *Anticancer Res.* **2014**, *34*, 1071–1077.
8. E. I. Obeagu, G. U. Obeagu, *Medicine* **2024**, *103*, e36905. **DOI:**10.1097/MD.0000000000036905
9. A. G. Waks, E. P. Winer, *JAMA* **2019**, *321*, 288. **DOI:**10.1001/jama.2018.19323
10. S. K. Mishra, Y. S. Bae, Y. M. Lee, J. S. Kim, S. H. Oh, H. M. Kim, *Front. Cell Dev. Biol.* **2021**, *8*, 571676. **DOI:**10.3389/fcell.2020.571676
11. M. A. Thalappil, P. Singh, A. Carcereri de Prati, S. K. Sahoo, S. Mariotto, E. Butturini, *Phytother. Res.* **2024**, *38*, 556–591. **DOI:**10.1002/ptr.8054
12. R. H. Liu, *J. Nutr.* **2004**, *134*, 3479S–3485S. **DOI:**10.1093/jn/134.12.3479S
13. B. d. S. Feitosa, O. O. Ferreira, C. d. J. P. Franco, H. Karakoti, R. Kumar, M. M. Cascaes, R. D. Jawarkar, S. N. Mali, J. N. Cruz, I. C. de Menezes, M. S. de Oliveira, E. H. de Aguiar Andrade, *Molecules* **2024**, *29*, 947. **DOI:**10.3390/molecules29050947
14. S. Singh, N. Nabya, *Int. J. Pharm. Sci. Res.* **2023**, *14*, 920–923. **DOI:**10.13040/IJPSR.0975-8232.14(2).920-23
15. K. S. Rodrigo, A. T. Herath, *South Asian Res. J. Nat. Prod.* **2024**, 7, 451–460. **DOI:**10.9734/sarjnp/2024/v7i3176
16. K. O. Fagbemi, D. A. Aina, O. O. Olajuyigbe, *Sci. World J.* **2021**, *2021*, 8. **DOI:**10.1155/2021/5961586
17. R. P. Adams, *Identification of Essential Oil Components by Gas Chromatography/Mass Spectrometry*, Allured Publishing Corporation, Carol Stream, IL, USA, **1995.**
18. M. Galgano, P. Capozza, F. Pellegrini, M. Cordisco, A. Sposato, S. Sblano, M. Camero, G. Lanave, G. Fracchiolla, M. Corrente, F. Cirone, A. Trotta, M. Tempesta, D. Buonavoglia, A. Pratelli, *Antibiotics* **2022**, *11*, 979. **DOI:**10.3390/antibiotics11070979
19. B. Kebede, W. Shibeshi, *Vet. Med. Sci.* **2022**, *8*, 1802–1815. **DOI:**10.1002/vms3.772
20. M. Nikkhah, J. S. Strobl, E. M. Schmelz, P. C. Roberts, H. Zhou, M. Agah, *Biomaterials* **2011**, *32*, 7625–7632. **DOI:**10.1016/j.biomaterials.2011.06.041
21. L. Huyck, C. Ampe, M. Van Troys, *Assay Drug Dev. Technol.* **2012**, *10*, 382–392. **DOI:**10.1089/adt.2011.391
22. M. Gallardo-Villagrán, L. Paulus, D. Y. Leger, B. Therrien, B. Liagre, *Molecules* **2022,** *27*, 4472. **DOI:**10.3390/molecules27144472
23. RCSB PDB, Homepage. https://www.rcsb.org/ (assessed May 21, 2021).
24. PubChem, PubChem database. https://pubchem.ncbi.nlm.nih.gov/ (assessed May 21, 2021).
25. H. Bekker, H. J. C. Berendsen, E. J. Dijkstra, S. Achterop, R. van Drumen, D. van der Spoel, M. K. R. Renardus, *Proc. 4th Int. Conf. Comput. Phys. (PC 92)*, World Scientific, Singapore, **1993**, pp. 252–256.

26. C. Oostenbrink, A. Villa, A. E. Mark, W. F. van Gunsteren, *J. Comput. Chem.* **2004**, *25*, 1656–1676. **DOI:**10.1002/jcc.20090
27. P. Bjelkmar, P. Larsson, M. A. Cuendet, B. Hess, E. Lindahl, *J. Chem. Theory Comput.* **2010**, *6*, 459–466. **DOI:**10.1021/ct900549r
28. K. Lindorff-Larsen, S. Piana, K. Palmo, P. Maragakis, J. L. Klepeis, R. O. Dror, D. E. Shaw, *Proteins* **2010**, *78*, 1950–1958. **DOI:**10.1002/prot.22711
29. M. J. Abraham, T. Murtola, R. Schulz, S. Páll, J. C. Smith, B. Hess, E. Lindahl, *SoftwareX* **2015**, *1*, 19–25. **DOI:**10.1016/j.softx.2015.06.001
30. S. Yalçınkaya, S. Y. Azarkan, A. G. K. Çakmakçı, *J. Mol. Struct.* **2022**, *1261*, 132939. **DOI:**10.1016/j.molstruc.2022.132939
31. N. Çankaya, M. H. Kebiroğlu, M. M. Temüz, *Drug Chem. Toxicol.* **2024**, *47*, 1226–1240. **DOI:**10.1080/01480545.2024.2353724
32. K. H. C. Başer, G. Buchbauer, *Handbook of Essential Oils: Science, Technology, and Applications*, CRC Press, Boca Raton, FL, **2020.**
33. A. A. Jojić, S. Liga, D. Uţu, G. Ruse, L. Suciu, A. Motoc, C. M. Şoica, D.-S. Tchiakpe-Antal, *Plants* **2024**, *13*, 3233. **DOI:**10.3390/plants13223233
34. A. C. Rivas da Silva, P. M. Lopes, M. M. Barros de Azevedo, D. C. Costa, C. S. Alviano, D. S. Alviano, *Molecules* **2012**, *17*, 6305–6316. **DOI:**10.3390/molecules17066305
35. P. L. Crowell, *J. Nutr.* **1999**, *129*, 775S–778S. **DOI:**10.1093/jn/129.3.775S
36. G. Ruberto, M. T. Baratta, *Food Chem.* **2000**, *69*, 167–174. **DOI:**10.1016/S0308-8146(99)00247-2
37. J. W. Wang, S. S. Chen, Y. M. Zhang, J. Guan, G. Y. Su, M. Ding, W. Li, Y.-Q. Zhao, *Environ. Toxicol. Pharmacol.* **2019**, *68*, 13–18. **DOI:**10.1016/j.etap.2019.02.005
38. A. Sivropoulou, E. Papanikolaou, C. Nikolaou, S. Kokkini, T. Lanaras, M. Arsenakis, *J. Agric. Food Chem.* **1996**, *44*, 1202–1205. **DOI:**10.1021/jf950540t
39. X. Han, T. L. Parker, *Cogent Med.* **2017**, *4*, 1306200. **DOI:**10.1080/2331205X.2017.1306200
40. F. Bakkali, S. Averbeck, D. Averbeck, M. Idaomar, *Food Chem. Toxicol.* **2008**, *46*, 446–475. **DOI:**10.1016/j.fct.2007.09.106
41. H. Medini, A. Elaissi, F. Farhat, M. L. Khouja, R. Chemli, F. Harzallah-Skhiri, *Chem. Biodivers.* **2009**, *6*, 1378–1387. **DOI:**10.1002/cbdv.200800202
42. S. Burt, *Int. J. Food Microbiol.* **2004**, *94*, 223–253. **DOI:**10.1016/j.ijfoodmicro.2004.03.022
43. D. Kalemba, A. Kunicka, *Curr. Med. Chem.* **2003**, *10*, 813–829. **DOI:**10.2174/0929867033457719
44. M. Hoferl, I. Stoilova, E. Schmidt, J. Wanner, L. Jirovetz, D. Trifonova, L. Krastev, A. Krastanov, *Antioxidants* **2014**, *3*, 81–98. **DOI:**10.3390/antiox3010081
45. İ. Karaman, F. Şahin, M. Güllüce, H. Öğütçü, M. Şengül, A. Adıgüzel, *J. Ethnopharmacol.* **2003**, *85*, 231–235. **DOI:** 10.1016/S0378-8741(03)00006-0
46. S. Bais, N. S. Gill, N. Rana, S. Shandil, *Int. Sch. Res. Notices* **2014**, *2014*, 634723. **DOI:**10.1016/S0378-8741(03)00006-0
47. E. Ehsani, K. A. Noghabi, M. Teimouri, A. Khadem, *Afr. J. Microbiol. Res.* **2012**, *6*, 6704–6710. **DOI:**10.5897/AJMR12.686
48. S. Pepeljnjak, I. Kosalec, Z. Kalodera, N. Blazević, *Acta Pharm.* **2005**, *55*, 417–422.
49. M. F. A. Borges, R. S. Lacerda, J. P. A. Correia, T. R. de Melo, S. B. Ferreira, *Med. Sci. Forum* **2022**, *12*, 11. **DOI:**10.3390/eca2022-12709
50. F. M. Abbas, *J. Clin. Images Med. Case Rep.* **2024**, *2*, 36–45. **DOI:**10.36346/sarjmcr.2023.v04i04.001
51. P. V. Stuckey, F. H. Santiago-Tirado, *Infect. Immun.* **2023**, *91*, e0043422. **DOI:**10.1128/iai.00434-22
52. S. B. Glisic, S. Z. Milojevic, S. I. Dimitrijevic, A. M. Orlovic, D. U. Skala, *J. Serb. Chem. Soc.* **2007**, *72*, 311–320. **DOI:**10.2298/JSC0704311G
53. H. O. Elansary, S. A. M. Abdelgaleil, E. A. Mahmoud, K. Yessoufou, K. Elhindi, S. El-Hendawy, *BMC Complement. Altern. Med.* **2018**, *18*, 1–10. **DOI:**10.1186/s12906-018-2262-1
54. A. M. Saab, R. Gambari, G. Sacchetti, A. Guerrini, I. Lampronti, M. Tacchini, et al., *Nat. Prod. Res.* **2018**, *32*, 1415–1427. **DOI:**10.1080/14786419.2017.1346648
55. K. F. Chang, X. F. Huang, J. T. Chang, Y. C. Huang, W. S. Lo, C. Y. Hsiao, C. Y. Tsai, N. M. Tsai, *J. Nat. Prod.* **2020**, *83*, 3021–3029. **DOI:**10.1021/acs.jnatprod.0c00580
56. D. A. Altomare, J. R. Testa, *Oncogene* **2005**, *24*, 74557464**.** **DOI:**10.1038/sj.onc.1209085
57. B. D. Manning, A. Toker, *Cell* **2017**, *169*, 381405. **DOI:**10.1016/j.cell.2017.04.001
58. B. D. Lehmann, J. A. Bauer, X. Chen, M. E. Sanders, A. B. Chakravarthy, Y. Shyr, J. A. Pietenpol, *J. Clin. Invest.* **2011**, *121*, 2750–2767. **DOI:**10.1172/JCI45014
59. N. Çankaya, S. Yalçın, *Saudi J. Biol. Sci*. **2022**, 29, 101670. **DOI:**10.1016/j.sjbs.2020.04.030
60. E. Tamtürk, S. Yalçın, F. Ercan, A. S. Tuncbilek, *Anti-Cancer Agents Med. Chem.* **2025**, 25, 499–516. **DOI:**10.2174/0118715206340868241018075528
61. A. Bellacosa, C. C. Kumar, A. Di Cristofano, J. R. Testa, *Adv. Cancer Res.* **2005**, *94*, 29–86. **DOI:**10.1016/S0065-230X(05)94002-5
62. G. Hoxhaj, B. D. Manning, *Nat. Rev. Cancer* **2020**, *20*, 74–88. **DOI:**10.1038/s41568-019-0216-7
63. Y. Chen, L. Huang, Y. Dong, C. Tao, R. Zhang, H. Shao, H. Shen, *Front. Cell Dev. Biol.* **2020**, *8*, 996. **DOI:**10.3389/fcell.2020.573599
64. G. Schneider, M. Schmidt-Supprian, R. Rad, D. Saur, *Nat. Rev. Cancer* **2017**, *17*, 239–253. **DOI:**10.1038/nrc.2017.5
65. M. Rashid, S. Karim, B. Ali, S. Khan, M. Ahmad, A. Husain, R. Mishra, *Chin. J. Pharm. Sci.* **2017**, *26*, 621. **DOI:**10.5246/jcps.2017.09.070
66. D. T. Kumar, N. Jain, J. Evangeline, B. Kamaraj, R. Siva, H. Zayed, C. G. P. Doss, *Comput. Biol. Med.* **2019**, *115*, 103513. **DOI:**10.1016/j.compbiomed.2019.103513
67. J. A. Crowell, V. E. Steele, J. R. Fay, *Mol. Cancer Ther.* **2007**, *6*, 2139–2148. **DOI:**10.1158/1535-7163.MCT-07-0120

Povzetek

V tej študiji je bilo eterično olje semen *Juniperus chinensis* L. analizirano z GC-MS, pri čemer je bilo identificiranih 25 spojin, ki so predstavljale 99,78 % olja. Glavna sestavina je bil α-pinen (79,63 ± 0,45 %), sledili so β-mircen, β-pinen in DL-limonen. Olje je pokazalo protimikrobno aktivnost z zaviralnimi conami 11 mm (*S. aureus*), 6 mm (*E. coli*) in 4 mm (*S. mutans*). Protiglivični učinki so bili opaženi proti *Fusarium solani* in *Aspergillus niger*. Testi citotoksičnosti so razkrili selektivne učinke na rakave celice dojke MDA-MB-231 (IC_{50}: 38 μg/mL), brez toksičnosti za normalne celice MCF-10A. Molekulsko sidranje je pokazalo močno vezavno afiniteto α-cedrola do proteina AKT-1 (–7,5 kcal/mol), kar so potrdile analize stabilnosti RMSD in vodikove vezi. Profiliranje ADME je potrdilo ugodne lastnosti α-cedrola glede podobnosti zdravilom. Ti rezultati nakazujejo, da je eterično olje semen *J. chinensis* L., zlasti kot kompleksna fitokemična mešanica, ki vsebuje α-cedrol, obetaven naravni vir protimikrobnih in protirakavih učinkovin.