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Exploring the role of L-tartaric acid in ovarian cancer: Pyroptosis and inflammation as key targets

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Ovarian cancer is one of the most lethal gynecological malignancies, and treatment options for it are limited. L-tartaric acid, an organic compound from natural resources, especially grapes, has shown potential anticancer properties but remains underexplored in ovarian carcinoma. The present study was designed to investigate its effects on A2780 ovarian cancer cells, with a focus on cell cycle control, pyroptosis, autophagy, and inflammation. Cells were treated with different concentrations of L-tartaric acid, and viability was assessed using MTT assays. Expressions of *CCND1*, *CCNE1*, *GSDMD*, *GSDME*, *MAP1LC3B*, *ATG5*, *IL1B*, and *IL6* were determined by RT-qPCR, while IL-1β and IL-6 protein levels were measured using ELISA. L-tartaric acid significantly reduced cell viability ($P< 0.05$) and downregulated *CCND1* and *CCNE1*, indicating G1 phase arrest. *GSDMD* and *GSDME* expression, as well as IL-1β and IL-6 secretion, were also decreased, whereas autophagy-related genes (*MAP1LC3B*, *ATG5*) remained unchanged. These findings raise the possibility that L-tartaric acid may exhibit cytostatic and anti-inflammatory activities against ovarian carcinoma cells, likely by inhibition of pyroptosis-involved inflammatory pathways. The findings support further investigation of L-tartaric acid as a candidate compound for ovarian cancer therapy.

Keywords: L-Tartaric acid, Ovarian cancer, Pyroptosis, Cell cycle arrest, Inflammation

Ovarian cancer remains one of the leading causes of gynecological cancer mortality, with approximately 314,000 new cases diagnosed annually and high fatality rates largely due to late-stage detection and limited therapeutic options[1]. Despite advances in surgery and platinum-based chemotherapy, recurrence and chemoresistance continue to impede durable control[2], underscoring the need for agents that selectively target ovarian cancer cells while minimising systemic toxicity[2]. Naturally derived compounds have attracted considerable attention for anticancer development owing to their biochemical diversity and favourable safety profiles[3]. Among these, L-tartaric acid, a dicarboxylic acid abundant in grapes and other tart fruits, has long been used in food and pharmaceutical applications for its antioxidant, chelating, and acidifying properties[4,5]. Although its biological effects are recognised, direct anticancer evidence remains limited; preliminary reports suggest that L-tartaric acid and related derivatives can influence oxidative stress and apoptosis-linked pathways, but their mechanistic roles in ovarian carcinoma are not well defined[4,5].

Cell death pathways in cancer cells are diverse and highly regulated, encompassing apoptosis, necrosis, autophagy, and more recently elucidated forms such as pyroptosis and ferroptosis. Pyroptosis, a pro-inflammatory form of programmed cell death, is mediated by pore-forming proteins of the gasdermin family, notably gasdermin D (*GSDMD*) and gasdermin E (*GSDME*). Its activation involves caspase-dependent cleavage, such as by caspase-1, -3, or -8, leading to membrane pore formation, cell rupture, and the release of pro-inflammatory cytokines like IL-1β and IL-18[4]. While chronic inflammation within the tumor microenvironment (TME) can promote tumorigenesis by fostering an immunosuppressive niche[6], controlled induction of pyroptosis in cancer cells has shown potential to enhance anti-tumor immunity by releasing danger-associated molecular patterns (DAMPs) and activating immune effector cells, thereby overcoming

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immune evasion[7]. For instance, *GSDME*-mediated pyroptosis has been linked to improved immune responses in various cancers, including melanoma and colorectal cancer, by shifting the TME from "cold" to "hot" states[7,8,9]. Consequently, pharmacological agents that modulate the pyroptotic pathway, such as chemotherapy drugs triggering caspase-3/*GSDME* activation or novel GSDMD-targeting compounds, have attracted significant interest as potential cancer therapies, with recent studies exploring their synergy with radiotherapy and immunotherapy[10,11].

Autophagy, another key cellular process, exhibits a dual role in cancer development and progression. Under nutrient stress or therapeutic pressure, autophagy promotes cell survival by recycling nutrients and clearing damaged organelles, thus supporting tumor growth and chemoresistance[12]. Conversely, excessive or dysregulated autophagy can trigger cell death or sensitise tumour cells to chemotherapeutic agents by disrupting cellular homeostasis, a phenomenon exploited in cancers such as ovarian carcinoma, where autophagy inhibitors enhance treatment efficacy[13]. Therefore, identifying agents that selectively modulate autophagic flux, either to suppress survival mechanisms or amplify death pathways, offers a promising strategy to reduce cancer cell viability. The specific effects of L-tartaric acid on autophagy remain underexplored, particularly in ovarian carcinoma cells. Preliminary evidence suggests that tartaric acid derivatives may influence oxidative stress and apoptosis-related pathways[4], but a comprehensive assessment of L-tartaric acid's ability to regulate autophagic processes in this context has yet to be conducted, presenting an opportunity for further investigation given its established bioactive properties[45].

In this study, we explored the anticancer efficacy of L-tartaric acid in the human ovarian carcinoma cell line A2780, focusing on cell viability, cell cycle arrest, and cell death pathways, including pyroptosis and autophagy. Given the inflammatory nature of pyroptosis, we further examined the impact of L-tartaric acid on pro-inflammatory cytokines IL-1β and IL-6, which often contribute to tumor progression and chemotherapy resistance. By dissecting these mechanisms, we aim to elucidate the potential of L-tartaric acid as a novel therapeutic strategy against ovarian cancer, ultimately laying a foundation for future preclinical investigations and potential clinical translation.

Materials and Methods

Ethics approval

All experiments were performed following institutional biosafety and ethical regulations. This study has been approved by the Medical Ethics Committee of the Xuzhou Central Hospital (xzzx2024R-45).

Structural characteristics of L-tartaric acid

L-tartaric acid (IUPAC name: (2R,3R)-2,3-dihydroxybutanedioic acid) is a naturally occurring dicarboxylic acid with the empirical formula COOH(CHOH)\₂COOH (Fig. 1). It contains two chiral centers at carbons 2 and 3, which impart unique stereochemical properties. The molecule-s hydroxyl and carboxyl groups enable potent chelating and antioxidant capabilities, allowing L-tartaric acid to form stable complexes with various metal ions and to quench reactive oxygen species. These features are considered critical to its bioactivity in diverse physiological and pathological contexts, including cancer and inflammatory disorders.

Cell culture and reagents

Human ovarian carcinoma A2780 cells were maintained in Dulbecco's Modified Eagle Medium (DMEM) supplemented with 10% fetal bovine serum and 1% penicillin-streptomycin. Cultures were incubated at 37°C in a humidified atmosphere with 5% CO_2. L-tartaric acid of analytical grade was acquired from a commercial supplier and dissolved in sterile phosphate-buffered saline (PBS) prior to all

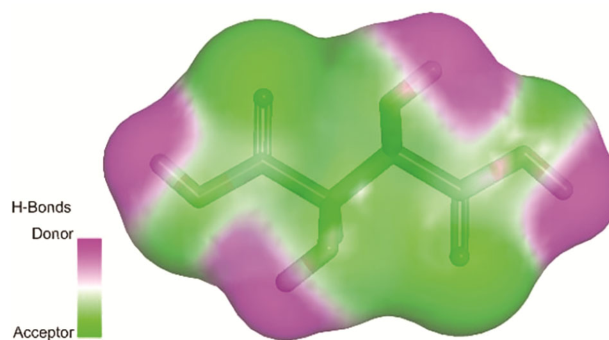

Fig. 1 — 2D representation of L-tartaric acid, highlighting the dicarboxylic and hydroxyl functionalities that underlie its reactivity. Hydrogen bond donors are indicated in pink, and hydrogen bond acceptors appear in green, illustrating the molecule's capacity for extensive hydrogen bonding. Through these interactions, L-tartaric acid can influence redox balance, mitigate oxidative stress, and potentially confer cytoprotective effects. Such structural attributes provide a mechanistic basis for investigating its therapeutic potential, particularly in oncological and inflammatory disease models.

experiments. Concentrations used for treatment were prepared fresh to maintain stability and minimise degradation.

Assessment of cell viability

Cell viability was determined using a colourimetric MTT assay. A2780 cells were seeded into 96-well plates at a density of approximately $5×10^3$ cells per well. Following overnight attachment, cells were exposed to increasing concentrations of L-tartaric acid or vehicle control. After the specified incubation period (24 hours), MTT solution was added to each well and plates were returned to the incubator for an additional 3 hours. The resulting formazan crystals were dissolved in dimethyl sulfoxide (DMSO), and absorbance at 570 nm was measured using a microplate reader. Cell viability was expressed as a percentage relative to untreated controls.

RNA extraction and quantitative Real-Time PCR

Total RNA from A2780 cells was extracted with TRIzol reagent (Invitrogen, USA) according to the manufacturer′s instructions and assessed for quality based on A_{260}/A_{280} ratio > 1.9. RevertAid First-Strand cDNA Synthesis Kit (Thermo Fisher Scientific, USA) was used for the synthesis of cDNA from 1 µg total RNA. For quantitative PCR, SYBR Green PCR Master Mix (Applied Biosystems) was used in the QuantStudio 5 Real-Time PCR System. The thermocycling conditions included an initial heat-denaturing step at 95 °C for 10 minutes and then cycling (40) through programmed temperature shifts at 95 °C for 15 s and 60 °C for 60 s. Primer efficiency was between the range of 95-105 %. The relative gene expression levels were determined by $2^{-\Delta\Delta Ct}$ method after normalisation with GAPDH as a reference gene. Each assay was conducted with 10 biological replicates and 3 technical replications.

Enzyme-Linked Immunosorbent Assay (ELISA)

Cell-culture supernatants were collected after 24 hours treatment with L-tartaric acid. Levels of IL-1β and IL-6 were quantified using human ELISA kits (R&D Systems, USA) according to the manufacturer′s instructions. Absorbance was read at 450 nm with a reference wavelength of 570 nm on a SpectraMax iD3 microplate reader (Molecular Devices). Cytokine concentrations were interpolated from standard curves generated from recombinant standards. All samples were assayed in duplicate from three independent experiments.

Evaluation of cell cycle-related proteins and pyroptosis markers

Cyclin D1 and cyclin E mRNA levels were analysed by measuring transcript levels through RT-qPCR, as outlined above, to assess the potential of L-tartaric acid to induce G_1 phase arrest. Pyroptosis was evaluated by quantifying *GSDMD* and *GSDME* mRNA expression. Cells were treated for defined durations to capture relevant changes in these markers, and time points were selected based on preliminary optimisation experiments.

Measurement of autophagy

Autophagy modulation by L-tartaric acid was examined by assessing *LC3* and *ATG5* gene expression through RT-qPCR. Parallel experiments involved morphological inspection of cells using phase-contrast microscopy to detect any notable cytoplasmic vacuolisation suggestive of autophagosomes. In all experiments, untreated cells served as negative controls.

Correlation analysis

Correlation analysis was performed to elucidate the relationships among gene expression levels of cell cycle regulators (cyclin D1, cyclin E), pyroptosis-associated markers (*GSDMD*, *GSDME*), autophagy indicators (*LC3*, *ATG5*), and inflammatory cytokines (*IL-1β*, *IL-6*). All correlation coefficients were computed using Pearson's method on replicate-level data, yielding a square correlation matrix in which the row and column labels denote each variable–concentration pair (e.g., CyclinE_Control, CyclinE_250, CyclinE_500, etc.). For interpretation, correlation coefficients above +0.7 or below −0.7 were considered strong positive or negative correlations, respectively.

Statistical analysis

All experiments were performed with 10 biological and 3 technical replicates. Results are expressed as mean ± standard deviation (SD). Analyses were conducted using GraphPad Prism 9.0 (GraphPad Software, San Diego, CA, USA). Shapiro–Wilk tests were used to verify normal distribution and Levene's tests to assess homogeneity of variances. When assumptions were met, one-way ANOVA followed by Tukey's multiple-comparison post hoc test was applied. Pearson correlation coefficients (ρ) were computed to evaluate associations between variables in the correlation matrix. Differences were considered statistically significant at $P < 0.05$.

Results

MTT assay

The cytotoxic effects of L-tartaric acid on A2780 human ovarian carcinoma cells were assessed using the MTT assay. Cells were treated with increasing concentrations of L-tartaric acid (50, 100, 250, 500, and 1000 µg/mL) for 24 hours, and cell viability was measured relative to the untreated control. The results demonstrated a dose-dependent decrease in cell viability. At lower concentrations (50 and 100 µg/mL), cell viability remained above 80%, indicating minimal cytotoxic effects. However, significant reductions in cell viability were observed at higher concentrations. Treatment with 250 µg/mL L-tartaric acid resulted in approximately 55% cell viability, while 500 µg/mL led to a further decrease to around 30%. The highest concentration tested, 1000 µg/mL, exhibited the most pronounced cytotoxic effect, reducing cell viability to approximately 10% ($P < 0.05$ compared to control). Based on these findings, 250 µg/mL and 500 µg/mL were selected for further mechanistic studies to elucidate the underlying pathways of L-tartaric acid-induced cytotoxicity in A2780 cells (Supplementary Fig. 1).

L-tartaric acid downregulates cyclin D1 and cyclin E expression

Gene expression levels for cyclin D1 and cyclin E in A2780 ovarian cancer cells were quantified following treatment with 250 or 500 µg/mL L-tartaric acid (Fig. 2A & B). Although no statistically significant difference was observed in cyclin D1 expression between the control and 250 µg/mL L-tartaric acid groups ($P = 0.32$), a marked reduction in cyclin D1 was detected at 500 µg/mL ($P = 0.01$). Similarly, cyclin E remained unchanged after exposure to 250 µg/mL L-tartaric acid ($P = 0.3$) but exhibited a significant decrease at 500 µg/mL relative to the control ($P = 0.03$). These data indicate that higher concentrations of L-tartaric acid effectively attenuate the expression of key cell cycle regulators.

Pyroptosis-related genes respond differentially to L-tartaric acid

The expression of pyroptotic markers *GSDMD* and *GSDME* was assessed to determine whether L-tartaric acid modulates pyroptosis in A2780 cells (Fig 2C & D). *GSDMD* showed no significant alteration at 250 µg/mL ($P = 0.09$) but was significantly decreased at 500 µg/mL compared with control ($P = 0.002$). Conversely, *GSDME* was reduced at both tested concentrations: 250 µg/mL ($P= 0.01$) and 500 µg/mL ($P= 0.001$). Although the difference between 250 and 500 µg/mL for *GSDME* did not reach significance ($P= 0.67$), the consistent downregulation of *GSDME* at both doses highlights its sensitivity to L-tartaric acid treatment. These results suggest that higher concentrations may be required to achieve robust inhibition of *GSDMD*, whereas *GSDME* responds to a broader dose range.

Autophagy markers remain unchanged following L-tartaric acid exposure

To evaluate the potential effect of L-tartaric acid on autophagy, *LC3* and *ATG5* mRNA levels were measured (Fig. 2E & F). Neither 250 nor 500 µg/mL L-tartaric acid significantly influenced *LC3* expression compared with the control ($P= 0.86$ and $P= 0.69$, respectively). Similarly, *ATG5* expression was not affected by either concentration ($P= 0.67$ and $P= 0.5$, respectively). The lack of significant changes in these two key autophagy-related genes indicates that, under the tested conditions, L-tartaric acid does not modulate autophagic pathways to a degree that is detectable at the transcriptional level.

L-tartaric acid suppresses pro-inflammatory cytokine production

IL-1β RT-qPCR results showed a significant alteration at 250 µg/mL ($P = 0.01$) and 500 µg/mL compared with control ($P = 0.0004$). (Fig. 2G & H)IL-6 expression was reduced at only 500 µg/mL ($P = 0.01$). ELISA was performed to examine the secretion of two *p*ro-inflammatory cytokines, IL-1β and IL-6, as these factors can be elevated during pyroptosis-mediated cell death and contribute to tumor-promoting inflammation. A concentration-dependent suppression of IL-1β was observed (Fig. 3A), with significant reductions at both 250 µg/mL ($P = 0.028$) and 500 µg/mL ($P = 0.0001$) compared with untreated controls. IL-6 levels were diminished at 500 µg/mL ($P = 0.003$) and 250 µg/mL ($P = 0.03$) (Fig. 3B). Collectively, these findings reinforce the involvement of a pyroptosis-like mechanism and underscore the potential anti-inflammatory influence of L-tartaric acid in ovarian cancer cells.

Correlation analysis

A comprehensive correlation matrix was generated to examine how cell cycle, pyroptosis, autophagy, and inflammatory markers responded to varying concentrations of L-tartaric acid. Several notable pairwise associations emerged (Fig. 4):

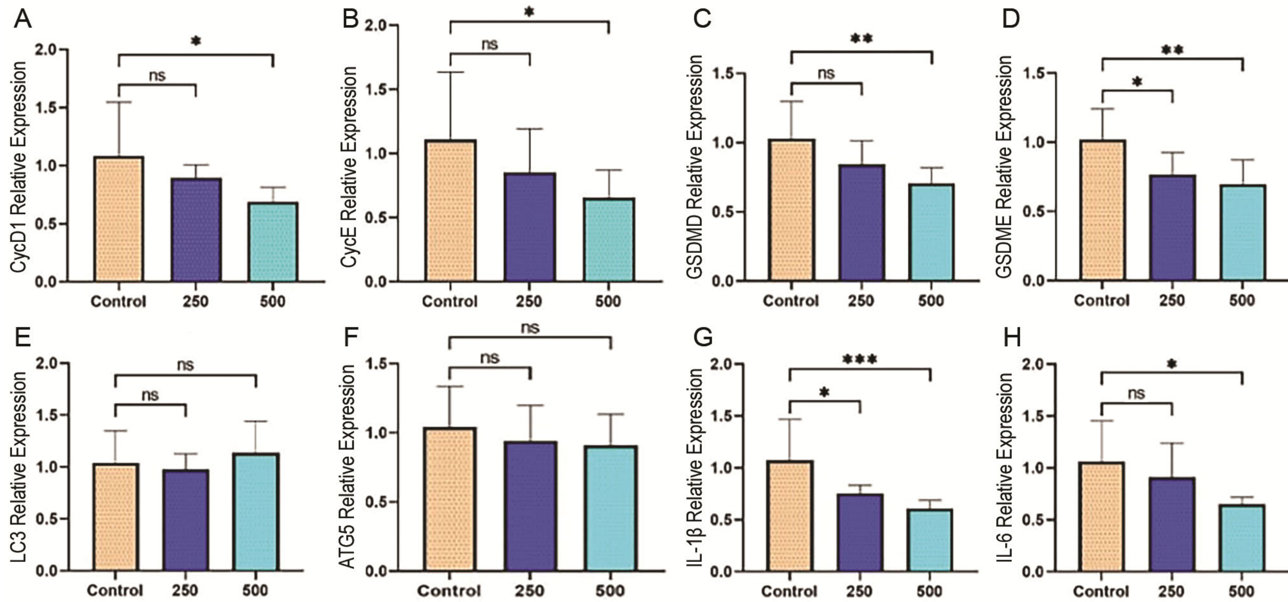

Fig. 2 — L-tartaric acid–induced changes in key regulators of cell cycle, pyroptosis, and autophagy in A2780 ovarian carcinoma cells. (A) *CCND1*, (B) *CCNE1*, (C) *GSDMD*, (D) *GSDME*, (E) *MAP1LC3B*, and (F) *ATG5* (G) *IL-1β* (H) *IL-6* gene expression were analysed by RT-qPCR following treatment with 250 or 500 µg/mL L-tartaric acid for 24 h. [Data are presented as mean ± SD. All experiments were performed with 10 biological and 3 technical replicates. Statistical analysis was performed using one-way ANOVA followed by Tukey's post hoc test. Significance levels: $P< 0.05$ (*),$P< 0.01$ (**), $P< 0.001$ (***) versus control]

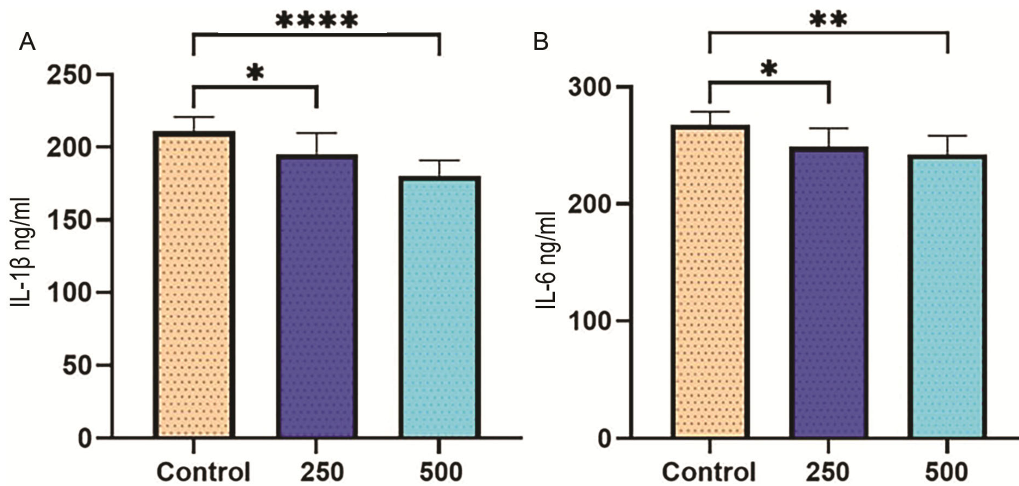

Fig. 3 — Effect of L-tartaric acid on pro-inflammatory cytokine secretion in A2780 cells. (A) IL-1β and (B) IL-6 concentrations (ng/mL) were measured by ELISA in cell culture supernatants after 24 h of exposure to 250 or 500 µg/mL L-tartaric acid. [Values represent mean ± SD. All experiments were performed with 10 biological and 3 technical replicates. One-way ANOVA with Tukey's multiple comparison test was applied; significance levels: $P< 0.05$ (*),$P< 0.01$ (**),$P< 0.001$ (***),$P< 0.0001$ (****) compared with untreated control]

Strong negative correlation between IL-1β _control and cyclinE_250

A coefficient of −0.93 suggests an inverse relationship between baseline IL-1β expression and cyclin E levels under moderate-dose (250 µg/mL) L-tartaric acid. This finding raises the possibility that inflammatory signaling may be inversely linked to cell cycle regulatory pathways in these cells.

Positive association of IL1b_250 with GSDME_250 (P≈0.82)

IL-1β and *GSDME* levels at 250 µg/mL show a pronounced positive correlation, hinting at

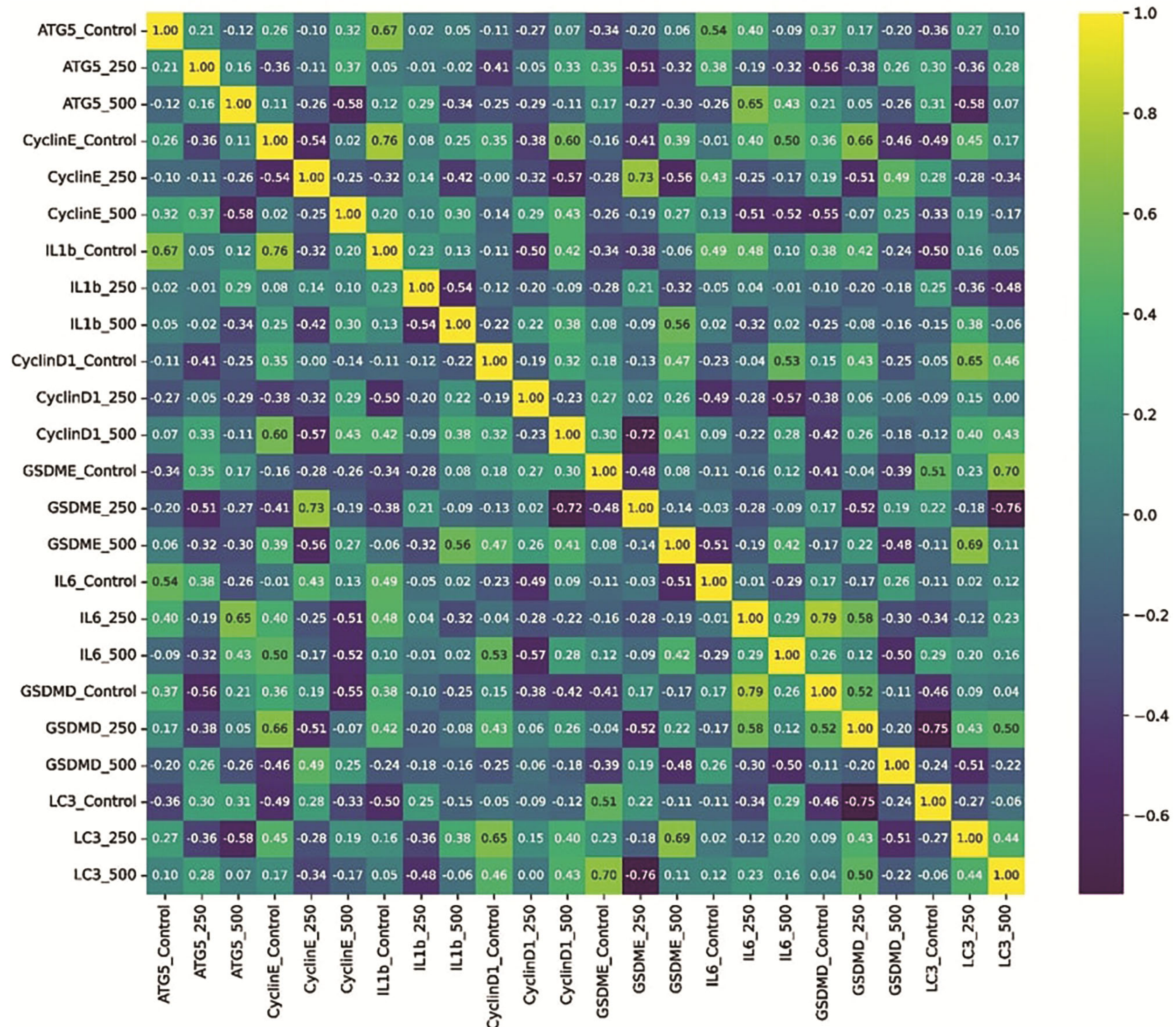

Fig. 4 — Correlation heatmap (Pearson's ρ) among cyclins (cyclin D1, cyclin E), pyroptosis-related markers (*GSDMD*, *GSDME*), autophagy indicators (*LC3*, *ATG5*), and cytokines (IL-1β, IL-6) under control, 250 µg/mL, and 500 µg/mL L-tartaric acid conditions. Colours encode correlation strength (blue = negative; yellow-red = positive). All experiments were performed with 10 biological and 3 technical replicates; keyF relationships discussed in text.

overlapping regulatory or feedback mechanisms in pyroptosis-like cell death and cytokine release at intermediate L-tartaric acid doses.

Dose-dependent shifts in pyroptosis markers

Moderate negative correlations were observed between IL-1β_500 and *GSDMD*_500 (*P*≈−0.53), suggesting that *GSDMD* expression may vary inversely with elevated IL-1β levels under higher L-tartaric acid exposure. These results align with the gene-expression data reported earlier, indicating a complex interplay between gasdermins and cytokines in pyroptosis regulation.

Cell cycle–inflammation crosstalk

Certain cytokine levels (e.g., IL-1β_500) displayed moderate positive correlations with cyclin D1 under 500 µg/mL conditions (*P*≈0.51), implying that inflammatory factors may track with G1/S transition machinery. Additional experiments are warranted to determine whether this correlation reflects a causal relationship or a secondary effect of overall cell stress.

Discussion

This study provides the first comprehensive evaluation of L-tartaric acid′s impact on ovarian cancer

cells, suggesting its potential to downregulate key regulators of the cell cycle and pro-inflammatory signals without triggering significant autophagic responses. These findings contribute to our understanding of L-tartaric acid′s pharmacological profile and suggest its potential as a targeted anticancer agent.

The reduction in cyclin D1 and cyclin E levels observed at higher concentrations of L-tartaric acid suggests G1 phase arrest and underscores a link between L-tartaric acid treatment and impaired cell cycle progression. Cyclin D1 and cyclin E coordinate the G1/S transition, and their downregulation is frequently associated with decreased proliferation in cancer cells, including those of ovarian origin[14,15]. Intriguingly, while cyclin D1 and cyclin E were suppressed most robustly at 500 μg/mL, no significant changes were noted at 250 μg/mL. This dose-dependent effect implies that adequate cellular accumulation of L-tartaric acid may be critical for eliciting measurable changes in cell cycle regulatory genes. These observations corroborate prior studies highlighting how natural compounds can disrupt cyclin/CDK complexes and induce cytostatic effects. For instance, research has demonstrated that various phytochemicals can modulate the expression of cyclins and CDKs, leading to cell cycle arrest in different cancer cell lines[16,17,18]. Specifically, the concentration-dependent effects of these compounds have been well documented, indicating that higher concentrations are often necessary to achieve significant biological responses[19]. Pyroptosis is driven by gasdermin pore formation, with *GSDMD* cleaved by inflammatory caspases (caspase-1/4/5/11) during canonical inflammasome activation and *GSDME* cleaved by caspase-3 during apoptosis-to-pyroptosis switching. In our model, L-tartaric acid reduced *GSDMD* and *GSDME* transcripts and lowered *IL1B*/*IL6*, a pattern most consistent with attenuation of inflammasome-linked inflammatory death rather than induction of pyroptosis. The simplest explanation is transcriptional down-modulation of upstream NF-κB/STAT3 signaling and/or feedback dampening of gasdermin expression as cytokine output declines, which aligns with the correlation analysis (positive *IL-1β–GSDME* at 250 μg/mL; inverse *IL-1β–GSDMD* at 500 μg/mL). Because pyroptosis is ultimately defined by protein cleavage and pore activity, definitive assignment will require immunoblot detection of cleaved *GSDMD/GSDME* and caspase-1/3 activation in future work. Moreover, assessing caspase-1 and caspase-3 enzymatic activity in response to L-tartaric acid would help confirm whether transcriptional suppression of *GSDMD* and *GSDME* corresponds to decreased cleavage and activation of the pyroptotic machinery. Alternatively, as gasdermins are subject to caspase-mediated cleavage, decreased full-length transcript could coincide with increased formation of cleaved, active gasdermin fragments[20,21]. Future studies employing immunoblot analyses to distinguish cleaved versus full-length gasdermin isoforms will be instrumental in confirming whether pyroptosis is definitively induced or suppressed by L-tartaric acid in ovarian cancer cells[22]. Parallel to changes in gasdermin genes, we observed diminished secretion of pro-inflammatory cytokines IL-1β and IL-6, consistent with the notion that L-tartaric acid may mitigate tumor-promoting inflammation. IL-1β plays a central role in pyroptosis and in shaping a pro-inflammatory tumor microenvironment that fosters immune evasion and metastatic progression[23]. Similarly, IL-6 is known to promote cancer cell proliferation and is linked to chemoresistance in ovarian malignancies[24,25]. The observed attenuation of these cytokines, particularly at the higher dose of L-tartaric acid, points to a broader anti-inflammatory effect. These anti-inflammatory effects may also be partially attributed to the antioxidant and metal-chelating properties of L-tartaric acid, which enable it to neutralise reactive oxygen species (ROS) and stabilise cellular redox balance. Since ROS-mediated signaling increases cytokine production and activates inflammasome components, oxidative stress and inflammation are closely related. L-tartaric acid may indirectly limit the expression of IL-1β and IL-6 by reducing oxidative stress through its hydroxyl and dicarboxylic functional groups, which would explain the observed anti-inflammatory profile. This mechanism is consistent with other findings showing that tartaric acid derivatives inhibit proinflammatory cascades by lowering lipid peroxidation and restoring redox equilibrium in tumor-bearing mice[4,26]. Such an effect may be beneficial when combined with established chemotherapeutic agents or immune therapies, as pro-inflammatory cytokines frequently undermine treatment efficacy by activating survival pathways in cancer cells[27,28]. Nevertheless, it will be necessary to confirm whether the suppression of IL-1β and IL-6 arises from alterations in transcription, reduced post-translational processing, or direct modulation of cytokine release pathways.

In contrast to the significant changes in cyclin and gasdermin transcripts, markers of autophagy, LC3 and ATG5, remained largely unaltered by L-tartaric acid. While some studies of natural compounds have shown that autophagy can be either upregulated or downregulated in a context-specific manner[29,30]. our results imply that, under the conditions tested, L-tartaric acid does not provoke a substantial shift in autophagic flux. It is possible that autophagy-related adaptations occur only at higher doses or beyond the 24-hour time frame investigated here. Indeed, autophagy can function as both a survival mechanism and a form of cell death, especially in the context of ovarian cancer where it has been linked to chemoresistance[31]. Additional studies employing autophagy flux assays (such as LC3-II turnover or p62 degradation) and extended time points could shed light on whether L-tartaric acid exerts more subtle or delayed modulation of autophagy pathways. The dual capacity of L-tartaric acid to modulate cell cycle progression and inflammatory mediators suggests a multifaceted mechanism of action that may hold therapeutic value. Agents that reduce cancer cell viability while concurrently dampening inflammatory mediators often show synergistic effects in combination with cytotoxic drugs and immune checkpoint inhibitors[32,33]. Furthermore, the ability to selectively target cancer cells while preserving normal tissue integrity is paramount in reducing off-target toxicity. Notably, correlation analysis revealed robust associations among inflammatory cytokines, pyroptosis markers, and cell cycle regulators at specific L-tartaric acid concentrations, hinting that these pathways may be closely interconnected. Although our data indicate potent anticancer and anti-inflammatory activities, it remains essential to validate these findings in vivo, where stromal and immune components of the tumor microenvironment may either reinforce or oppose these effects. Using xenograft or syngeneic ovarian cancer models can elucidate the impact of L-tartaric acid on tumor growth, metastatic spread, and therapeutic response.

Limitations

Several limitations should be acknowledged. First, the present study was conducted in a single ovarian cancer cell line (A2780). To enhance generalizability and ensure the robustness of our conclusions, future validation in additional ovarian carcinoma models such as SKOV3 and OVCAR3 is warranted, as these lines differ in genetic background, p53 status, and chemoresistance profiles. Second, the study primarily assessed mRNA expression levels, and protein-level confirmation is essential to establish mechanistic relevance. Future work should incorporate Western blot analyses of *CCND1* and *CCNE1* to verify cell-cycle modulation, as well as detection of full-length and cleaved *GSDMD* and *GSDME* to determine whether L-tartaric acid suppresses or activates pyroptotic signaling. In addition, caspase-1 and caspase-3 activity assays are recommended to clarify the functional link between transcriptional and proteolytic events in pyroptosis regulation. Third, only two concentrations of L-tartaric acid (250 and 500 µg/mL) and a single 24-hour exposure time were tested, limiting insight into concentration- and time-dependent responses. Future studies should employ expanded dose–response (e.g., 50–1000 µg/mL) and time-course analyses (e.g., 12, 24, and 48 hours) to better characterise temporal dynamics and identify optimal treatment conditions. Broader dose–time kinetics, mechanistic protein assays, and validation across multiple cell lines will strengthen the translational potential of L-tartaric acid as an anticancer agent.

Conclusion

The present study provides novel insights into the probable capacity of L-tartaric acid to restrict ovarian cancer cell proliferation, possibly through downregulation of cyclin D1/E expression and modulation of pyroptosis-associated genes and pro-inflammatory cytokines. The lack of an effect on autophagy markers suggests that L-tartaric acid may exert its anticancer activity independently of major shifts in autophagy. Our data underscore the potential utility of L-tartaric acid as a pharmacological agent in the context of ovarian cancer therapy and pave the way for further research into its mechanism of action, optimal dosing strategies, and synergistic use with existing treatment modalities. Future in vivo studies using xenograft or patient-derived models will be essential to validate these cellular effects, determine pharmacokinetic safety, and establish the translational potential of L-tartaric acid as an adjuvant or standalone anticancer compound.

Ethical statement

All experiments were performed following institutional biosafety and ethical regulations. This

study has been approved by the Medical Ethics Committee of the Xuzhou Central Hospital (xzzx2024R-45).

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Conflict of interest

The authors have no conflict of interest to declare.

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