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Differential Physiological and Biochemical Responses of *Matricaria chamomilla* and *Anthemis nobilis* Seeds to Specific Ultraviolet Radiation Wavelengths

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ABSTRACT

Ultraviolet (UV) radiation, depending on its wavelength, exerts a strong influence on plant metabolic systems by inducing oxidative stress and disturbing protein integrity. Given the increasing environmental relevance of enhanced UV-B radiation and the limited comparative information on medicinal species, this study aimed to clarify species-specific responses to defined UV spectral bands. Seeds of *Matricaria chamomilla* and *Anthemis nobilis* were exposed to controlled UV-C (220–280 nm), UV-B (280–320 nm), and UV-A (320–400 nm) radiation at graded doses under a completely randomized design with appropriate non-irradiated controls and replicated treatments. Seeds were irradiated for different time intervals and then incubated at 25°C for 8 days. Parameters such as germination percentage, seedling vigor (fresh weight, root–shoot ratio), and stress markers, including lipid peroxidation (MDA level), peroxidase, and protease activities, were analyzed. Data were statistically evaluated using analysis of variance (ANOVA) followed by mean comparison tests at $P<0.05$. The results indicated that increasing UV dose, especially below 300 nm, significantly suppressed seed germination and early growth rate in both species. However, *M. chamomilla* exhibited higher antioxidant enzyme activity and lower MDA accumulation compared to *A. nobilis*, suggesting stronger intrinsic tolerance to UV-induced oxidative stress. A moderate UV-B dose induced enzymatic antioxidant activity in *M. chamomilla* without severe membrane damage, indicating a threshold-dependent adaptive response, whereas higher doses resulted in pronounced lipid peroxidation in both species. Overall, UV-B radiation was identified as the most detrimental spectral band for germination stability. The proposed optimal exposure range for *M. chamomilla* appears to be lower and more narrowly defined than for *A. nobilis*, reflecting interspecific variation in oxidative defense capacity. These findings highlight fundamental differences in the adaptive responses of chamomile species under ultraviolet stress and imply potential implications for seed storage and agricultural practice under enhanced UV exposure.

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1. Introduction

Ultraviolet (UV) radiation, as an environmental stressor, profoundly influences plant physiology and metabolism, effects that are particularly significant in valuable medicinal species such as German chamomile (*Matricaria chamomilla*) and Roman chamomile (*Anthemis nobilis*). While the impact of UV radiation on mature plants is increasingly documented, its specific effects on seed germination and early seedling development, especially concerning distinct UV spectral bands (UV-C, UV-B, UV-A), are less understood. This knowledge gap is critical given the documented role of UV radiation in modulating plant defense mechanisms and secondary metabolite production. Research has demonstrated that specific UV wavelengths, notably UV-C and UV-B, can stimulate the biosynthetic pathways of phenolic and flavonoid compounds in plants. These wavelengths were chosen for this study to represent a range from the highly damaging UV-C, often associated with artificial sources, often accompanied by elevated levels of reactive oxygen species and the subsequent activation

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of enzymes like phenylalanine ammonia-lyase (PAL), interpreted as a defensive mechanism aimed at safeguarding cellular structures against UV-induced oxidative stress. However, the intensity and extent of these responses can be modulated by factors including plant genotype, ploidy level, and the physical characteristics of the seed, such as its photoblastic nature (Petruľová *et al.*, 2014; Zhuk *et al.*, 2021). These biochemical shifts, often accompanied by elevated levels of reactive oxygen species (ROS) and the subsequent activation of enzymes like phenylalanine ammonia-lyase (PAL), are interpreted as a defensive mechanism aimed at safeguarding cellular structures against UV-induced oxidative stress.

Despite extensive research into the effects of UV radiation on mature chamomile plants, our understanding of the physiological and biochemical responses of seeds from these two related genera (Matricaria and Anthemis) to specific UV wavelengths during the critical germination phase remains remarkably limited. This study specifically addresses this gap by comparing the responses of *M. chamomilla* and *A. nobilis* seeds, which exhibit differing photoblastic behaviors and genetic backgrounds, to controlled UV treatments. On one hand, German chamomile seeds, being positively photoblastic, are highly responsive to light quality within the visible spectrum. On one hand, German chamomile seeds, being positively photoblastic, are highly responsive to light quality within the visible spectrum. On the other hand, while the stimulatory effects of ionizing radiation on antioxidant content have been explored in German chamomile seedlings, a comparative knowledge gap persists regarding how different UV wavelengths influence germination indices, the induction of antioxidant enzymes, and the accumulation of secondary metabolites in the seeds of these two species (Bączek-Kwinta and Michałek, 2025; Baghalian *et al.*, 2011). The ongoing depletion of the stratospheric ozone layer has resulted in an increased influx of solar ultraviolet (UV) radiation reaching the Earth's surface, particularly in the biologically active UV-B range (280–320 nm) (Rozema *et al.*, 2005; Ven Vanitha Jenishree *et al.*, 2024). This heightened radiation poses a significant threat to terrestrial ecosystems, as UV energy can directly interact with and damage vital biomolecules, especially proteins and nucleic acids. Exposure to elevated UV levels—whether natural or artificial—is known to induce oxidative stress in plants by causing an overproduction of reactive oxygen species (ROS), which negatively affects growth, morphogenesis, and reproductive success (Kataria *et al.*, 2014; Mackerness *et al.*, 1999). Understanding how medicinal plant seeds, crucial for propagation and germplasm conservation, respond to these altered UV conditions is therefore essential for predicting their ecological fate and optimizing agricultural practices.

Seed germination and early seedling development are particularly sensitive stages in the plant life cycle, making them critical indicators for assessing radiation stress tolerance (Mahpara *et al.*, 2022; Yang *et al.*, 2024b). Numerous studies have shown that pre-sowing irradiation of seeds with UV light can severely reduce germination rates and seedling vigor, as measured by root and shoot length and biomass, across various species (Semenov *et al.*, 2020). The molecular responses to this stress often involve changes in the activity of key enzymatic scavengers, such as peroxidase (POD) and protease, which are essential for detoxifying ROS and recycling cellular components (Das and Roychoudhury, 2014; Zandi and Schnug, 2022). Lipid peroxidation, indicated by malondialdehyde (MDA) content, serves as a universal marker of oxidative damage to cellular membranes (Mohideen *et al.*, 2023).

While the harmful effects of high-dose UV irradiation are well-documented, understanding the differential sensitivity among closely related species or varieties is a crucial area of research (Robson *et al.*, 2019). Previous studies on certain Thymus species have demonstrated a clear dose-dependent relationship, where higher UV exposure correlates with reduced growth parameters and increased stress enzyme activity (Kordrostami *et al.*, 2024). Investigating these inherent differences in tolerance mechanisms is vital for predicting agricultural outcomes under changing environmental conditions.

The genus Matricaria (Chamomile) is economically significant due to its medicinal compounds, making its resilience to environmental stress particularly relevant. This study focuses on two distinct yet related species within this genus: *M. chamomilla* and *A. nobilis*. Unlike previous research that concentrated solely on one genus or specific UV bands, this study aims to provide a comparative assessment of the immediate effects of a broad range of UV irradiation doses (220–

400 nm) on the initial stages of these two chamomile species (Lal *et al.*, 2019; Yang *et al.*, 2024a). To achieve this, seeds of both species were subjected to a factorial experimental design involving three UV spectral bands (UV-C, UV-B, UV-A) across five distinct dose levels, alongside a non-irradiated control group. Each treatment combination was replicated four times to ensure statistical robustness.

The present study, focusing on the effects of specific wavelengths of UV radiation on seed germination of two chamomile species (*M. chamomilla* and *A. nobilis*), presents a novel approach to seed physiology and biochemistry. This study seeks to discover the specific mechanisms of response of these two species to UV stress by separately examining different UV wavelengths (such as UV-A, UV-B, and UV-C). Such research is innovative because so far, few studies have compared these two important medicinal species under the influence of different levels of UV radiation with wavelength accuracy (Alyas *et al.*, 2023; Kamel *et al.*, 2022; Manukyan, 2013).

The main hypothesis of this study is that different wavelengths of UV radiation will have different effects on physiological (such as germination percentage and rate) and biochemical (such as Proline content, antioxidant enzyme activities such as catalase and POD, and accumulation of secondary compounds) indices in the seeds of the two chamomile species. It is expected that the *A. nobilis* species will show different resistance responses compared to *M. chamomilla* due to differences in genetic and metabolic structure (Etminani *et al.*, 2024; Fazeli-Nasab *et al.*, 2021; Fazeli-Nasab *et al.*, 2025; Lichtenthaler, 1996). All collected data were subjected to a two-way Analysis of Variance (ANOVA) to assess the main effects of UV type, UV dose, and their interaction, as well as the differences between the two species. Post-hoc comparisons were performed using Tukey's HSD test at a significance level of $P<0.05$ to identify specific treatment effects. Statistical analyses were conducted using R statistical software (Version 4.2.1).

The main questions of this research are designed in three axes: first, how specific wavelengths of UV radiation (such as UV-A, UV-B, and UV-C) affect physiological germination indices, including germination percentage and rate in seeds of the two species *M. chamomilla* and *A. nobilis*; second, examining differences in biochemical responses of these two species, including changes in antioxidant enzyme activity (catalase and POD), accumulation of proline, and phenolic compounds under different wavelength treatments; and third, determining the effective wavelength or wavelengths in inducing effective adaptation responses and potentially increasing medicinal metabolites in each species (Cun *et al.*, 2024; Stefanello *et al.*, 2023; Tevini, 2023).

The present study was designed with the following primary objectives: to quantitatively assess the impact of varying UV irradiation doses on the germination percentage and early seedling vigor (fresh weight, root/shoot ratio) of *M. chamomilla* and *A. nobilis* seeds; to compare the differential activation of key biochemical defense mechanisms—specifically protease and POD activities, alongside lipid peroxidation (MDA content)—in response to UV stress across the two species; and to elucidate the species-specific radio-sensitivity threshold based on observed physiological and biochemical parameters, providing insights into their relative adaptation capacities under UV exposure.

2. Materials and methods

2.1. Plant material and experimental design

Seeds from *M. chamomilla* and *A. nobilis* genotypes were exposed to five different doses of UV radiation, ranging from 220 nm to 400 nm, using a UV source calibrated according to the experimental design. A UV source emitting wavelengths between 220 nm and 400 nm was employed. The specific doses of UV radiation applied were selected based on preliminary range-finding experiments and literature review concerning UV effects on seed germination, ensuring a comprehensive spectrum of potential biological impacts. The selected treatment groups encompassed five distinct UV doses (e.g., D1, D2, D3, D4, D5) applied across the specified wavelength range, alongside a non-irradiated control group.

After irradiation, germination assays were conducted. Thirty seeds from each treatment group were sown in separate pots filled with autoclaved fine sand, with untreated seeds serving as the control group. The experiment was designed as a completely randomized trial with three biological replicates per treatment. All pots were kept in an incubator at a constant temperature of 25°C. Daily records of germination indicators were maintained over six days

to facilitate the determination of essential parameters, namely Final Germination Percentage (FGP), Mean Germination Time (MGT), and the duration required to reach 50% germination (T50). At seven days post-sowing, the seedlings were meticulously collected to assess various morphological characteristics, encompassing the lengths of roots and shoots (measured in centimeters), the proportional ratio between root and shoot lengths, as well as the fresh biomass of the seedlings. All data collected were subjected to statistical analysis, including a two-way Analysis of Variance (ANOVA), to evaluate the effects of UV treatment (wavelength and dose) and species, as well as their interactions. Post-hoc tests were performed where significant differences were detected.

2.2. Biochemical assays

For biochemical assays, fresh seedling tissues (primarily leaves, unless otherwise specified for each assay) were immediately homogenized in a pre-cooled mortar and pestle with 50 mM potassium phosphate buffer (pH 7.0) containing appropriate protective conditions to minimize enzyme degradation. Leaf tissue specimens were pulverized promptly in a pre-cooled mortar and pestle with 50 mM potassium phosphate buffer (maintained at pH 7.0). The resulting homogenate was subsequently centrifuged at 14,000 revolutions per minute for a duration of 10 minutes under refrigerated conditions (0°C). The resulting supernatant was then isolated to enable the quantitative assessment of enzymatic activities and the extent of lipid peroxidation.

2.2.1. Protease activity

Proteolytic (Protease) activity was determined by means of a caseinolytic assay, following modifications to conventional spectrophotometric methodologies as previously described (Plett *et al.*, 2022). Enzyme functionality was quantified in terms of units, with a single unit defined as the quantity of protease required to catalyze the release of acid-soluble peptides resulting in an increment of 0.001 in absorbance at 280 nm per minute, under controlled conditions of 37 °C and pH 7.8.

2.2.2. POD activity

POD activity was assessed using established methods with guaiacol as the substrate (Faria *et al.*, 2023). The reaction mixture (3 mL) contained 50 mM potassium phosphate buffer (pH 7.8), 20 mM guaiacol, 40 mM hydrogen peroxide (H_2O_2), and 100 µL of the prepared enzyme extract. The reaction rate was monitored by measuring the change in absorbance at 470 nm every 20 seconds. One unit of POD activity was defined as an increase in absorbance of 0.01 units per minute.

2.2.3. MDA content (lipid peroxidation)

Lipid peroxidation levels, assessed through MDA accumulation, were evaluated employing the standard thiobarbituric acid reactive substances (TBARS) protocol, as outlined in previous studies (Mohideen *et al.*, 2023). For each sample, 2 mL of enzyme extract was mixed with 1 mL of a reagent containing 20% (v/v) trichloroacetic acid (TCA) and 0.5% (v/v) thiobarbituric acid (TBA). The mixture was incubated in a boiling water bath at 95°C for 30 min and then cooled to room temperature before centrifugation at 14,000 rpm for 10 min. An aliquot of 2 mL from the enzymatic extract was combined with 1 mL of a solution containing 20% (v/v) trichloroacetic acid (TCA) and 0.5% (v/v) thiobarbituric acid (TBA). The resulting mixture was subjected to heating in a water bath maintained at 95°C for a duration of 30 minutes, subsequently allowed to return to ambient temperature, and finally centrifuged at 14,000 revolutions per minute for 10 minutes. Absorbance readings of the clarified supernatant were recorded at a wavelength of 532 nm, with corrections applied for background absorbance measured at 600 nm. Quantification of MDA was performed utilizing the molar extinction coefficient of 155 $mM^{-1}cm^{-1}$ (Kong *et al.*, 2016).

2.2.4. Total soluble protein content

Total soluble protein content in the extracts was determined spectrophotometrically using Bradford's method (Bradford, 1976).

2.3. Statistical analysis

All experimental procedures, including germination studies and biochemical analyses, were replicated three times, analyzing 90 seedlings for germination and 30 seedlings/pooled samples for biochemical assays per replication. Descriptive statistics were used for data organization. The homogeneity of variances among samples was assessed using the F-test. For all measured

variables, the statistical significance of differences observed between the means of the irradiated treatment groups and the non-irradiated controls was assessed via a two-tailed Student's t-test. All statistical computations and data handling were performed using Microsoft Excel software (Version 2019).

3. Results and discussion

3.1. Germination and early growth

The germination response of *M. chamomilla* and *A. nobilis* seeds was significantly affected by exposure to UV radiation ranging from 220 to 400 nm. A general trend of increasing mean germination time (MGT) with decreasing UV wavelength was observed for both species. The delay in germination was more pronounced in *A. nobilis* compared to *M. chamomilla* (Fig. 1).

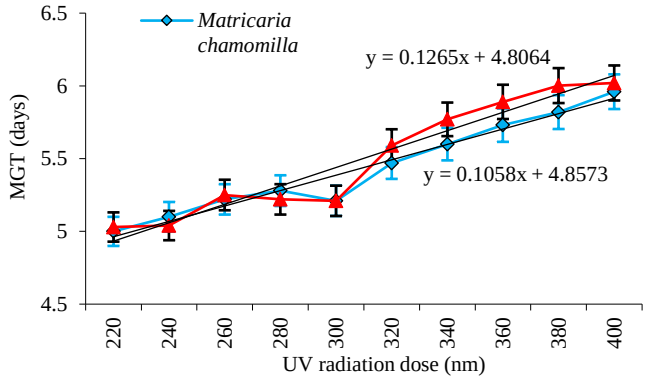


Figure 1. Effect of UV radiation dose (nm) on the percentage of MGT in *M. chamomilla* and *A. nobilis*.

The final germination percentage (FGP) of *M. chamomilla* showed no significant differences across all irradiation treatments. In contrast, *A. nobilis* experienced a notable decrease in germination percentage at lower UV doses, especially between 220 nm and 300 nm. The most significant decline was observed with exposure around 240 nm (Fig. 2).

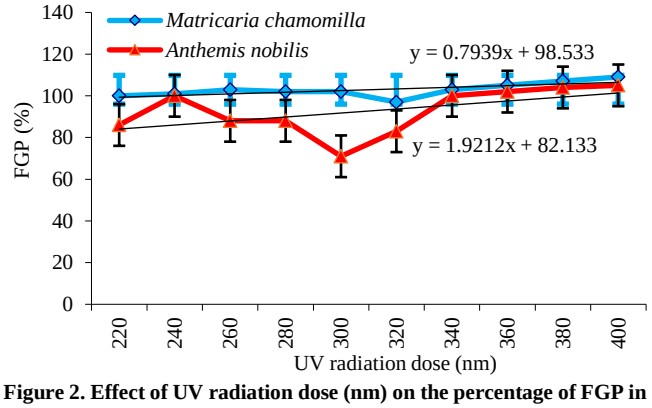


Figure 2. Effect of UV radiation dose (nm) on the percentage of FGP in *M. chamomilla* and *A. nobilis*.

3.2. Seedling growth parameters

UV irradiation generally suppressed seedling growth in both species compared to the non-irradiated controls, shoot length demonstrated a progressive decrease as the UV wavelength decreased. The most significant reduction in shoot length was observed within the 220–260 nm range for both *M. chamomilla* and *A. nobilis*. Shoot length decreased progressively as the UV wavelength decreased, with the most significant reduction occurring in the 220–260 nm range for both chamomile species (Fig. 3).

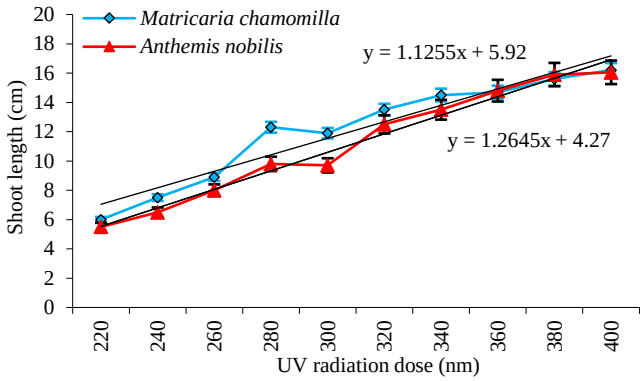


Figure 3. Effect of UV radiation dose (nm) on the Shoot Length in *M. chamomilla* and *A. nobilis*.

Similarly, root length declined significantly across all UV treatments in both *M. chamomilla* and *A. nobilis*. The most pronounced reduction was observed at 220 nm and 240 nm in *M. chamomilla* and at 240 nm in *A. nobilis* (Fig. 4).

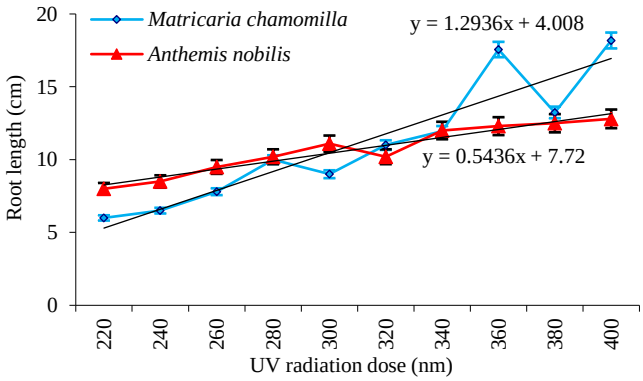


Figure 4. Effect of UV radiation dose (nm) on the Root Length in *M. chamomilla* and *A. nobilis*.

The *root-to-shoot ratio (R/S)* increased at intermediate UV doses, reaching its highest point at approximately 280 nm for *M. chamomilla* and 300 nm for *A. nobilis*. This suggests that UV radiation has a relatively stronger inhibitory effect on shoot elongation than on root growth at these specific wavelengths (Fig. 5).

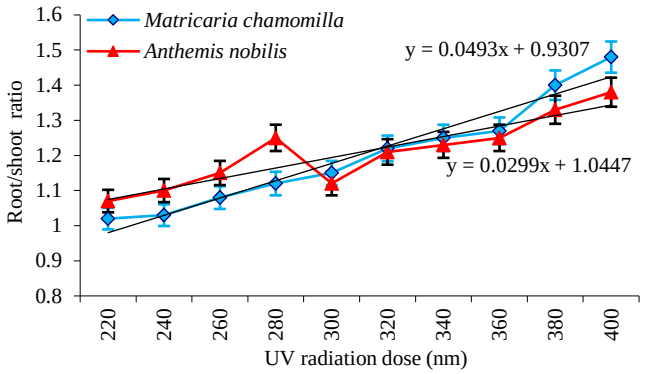


Figure 5. Effect of UV radiation dose (nm) on the Root/Shoot ratio in *M. chamomilla* and *A. nobilis*.

In both *M. chamomilla* and *A. nobilis*, exposure to nearly all applied radiation doses resulted in an elevation of seedling fresh biomass relative to the non-irradiated controls. The lowest recorded values for this parameter were consistently observed in the untreated control groups for both species (Fig. 6).

Across all UV dosages applied, seedling dry matter accumulation in *A. nobilis* exhibited an increase relative to the untreated control group. Nevertheless, while seed irradiation had a statistically significant impact on this parameter, the observed augmentation in dry weight was only marginal following specific treatment doses when compared to the control (Fig. 7).

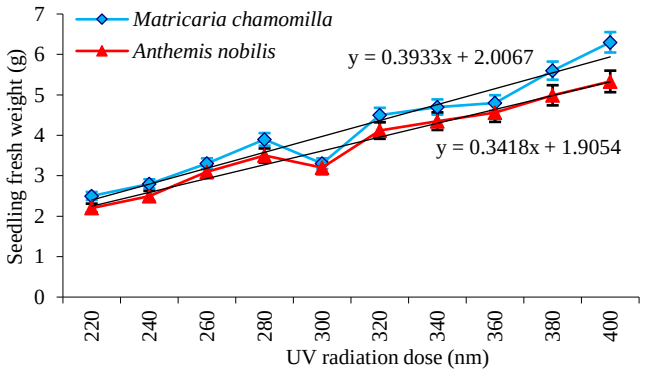


Figure 6. Effect of UV radiation dose (nm) on seedling fresh weight (g) in *M. chamomilla* and *A. nobilis*.

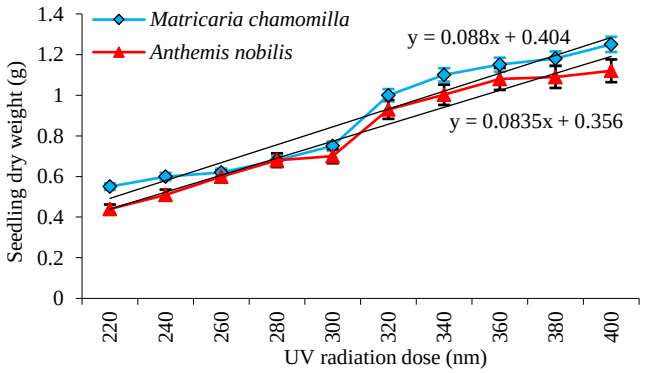


Figure 7. Effect of UV radiation dose (nm) on dry weight (g) in *M. chamomilla* and *A. nobilis*.

3.3. Total soluble protein contents

Following the exposure of seeds to varying doses of ultraviolet radiation, soluble protein concentrations were evaluated in both *A. nobilis* and *M. chamomilla* (Fig. 8). In the case of *A. nobilis*, the highest foliar protein content was recorded under the 400 nm UV treatment, a trend that was similarly observed in *M. chamomilla* (Fig. 6).

Upon subjecting seeds to various ultraviolet irradiation regimes, a marginal decline in foliar protein content was observed relative to the non-irradiated controls. In the *M. chamomilla* genotype, protein concentrations were diminished prior to exposure within the 220 to 240 nm UV range when contrasted with the untreated group. Furthermore, lower irradiation dosages (spanning 220 to 300 nm UV) induced a suppression of leaf protein content in *M. chamomilla* compared to the control baseline. The most pronounced decrement in protein content, relative to the control, was registered in both *M. chamomilla* and *A. nobilis* genotypes prior to the 240 nm UV dose; however, this reduction was markedly more accentuated in the former species (Fig. 8).

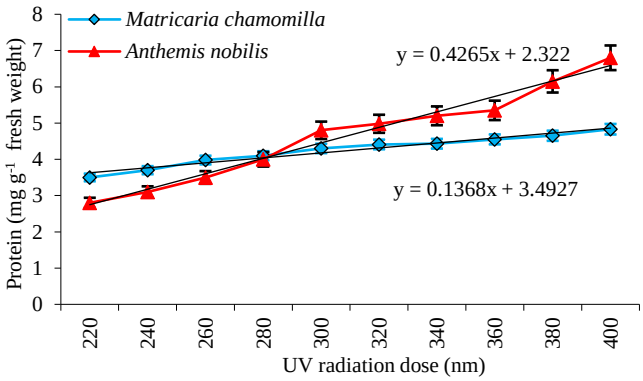


Figure 8. Effect of UV radiation dose (nm) on protein content (mg g^{-1} fresh weight) in *M. chamomilla* and *A. nobilis*.

3.4. POD activity

Seed exposure to ultraviolet radiation elicited distinct modulations in foliar peroxidase (POD) activity, as illustrated in Fig. 9. In *M. chamomilla*, the observed alterations in POD activity followed a dose-dependent pattern. Specifically, enzymatic activity was elevated following irradiation at wavelengths of 300, 340, and 380 nm; conversely, all other applied UV doses resulted in reduced activity relative to the non-irradiated control. By contrast, *A. nobilis* exhibited a general decline in leaf POD activity in response to seed irradiation compared to the control baseline. However,

a transient increase was noted upon exposure to the 260 nm dose, after which activity demonstrated a progressive elevation up to the 400 nm treatment. A particularly sharp enhancement in activity was detected within the interval spanning 280 to 300 nm (Fig. 9).

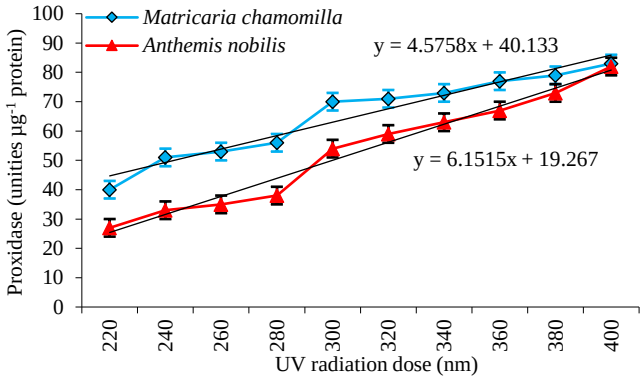


Figure 9. Effect of UV radiation dose (nm) on proxidase content (units μ^{-1} protein) in *M. chamomilla* and *A. nobilis*.

3.5. Protease activity

UV irradiation of seeds influenced leaf protease activity in both *M. chamomilla* and *A. nobilis* (Fig. 10). In *M. chamomilla*, the change in leaf protease activity was dose-dependent. Specifically, leaf protease activity was elevated after exposure to 240, 260, and 280 nm wavelengths, decreased following the 300 nm dose, and then increased again after the 320 nm exposure, compared to the non-irradiated control. Statistically significant differences from the non-irradiated control were observed only after the 400 nm dose (higher) and the 220 nm dose (lower). In *A. nobilis*, leaf protease activity generally decreased following seed irradiation, with the exception of the 300 nm dose, where activity levels were comparable to those of the non-irradiated control. The lowest leaf protease activity was observed at the 220 nm dose, exhibiting a significantly reduced activity compared to the non-irradiated control (Fig. 10).

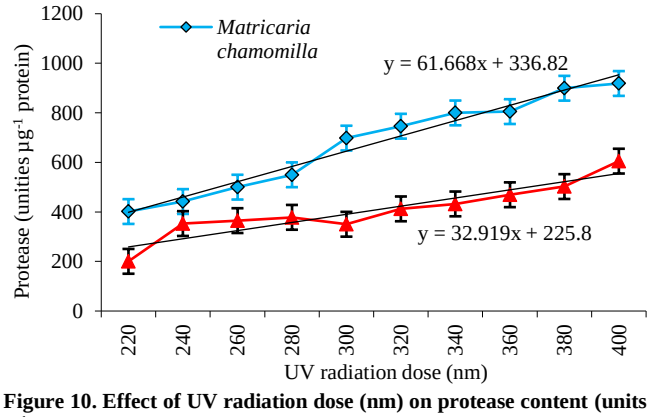


Figure 10. Effect of UV radiation dose (nm) on protease content (units μ^{-1} protein) in *M. chamomilla* and *A. nobilis*.

3.6. Lipid peroxidation (MDA contents)

Leaf MDA content significantly decreased with all seed UV irradiation doses in both genotypes of *M. chamomilla* and *A. nobilis* (Fig. 11). In *M. chamomilla*, MDA levels were several-fold lower between the 220 and 280 nm doses, with a gradual increase in MDA content observed as the irradiation dose increased. In contrast, *A. nobilis* exhibited higher leaf MDA content than *M. chamomilla*, both in the non-irradiated control and after all irradiation doses. Among the irradiated seeds, the highest increase in MDA was recorded after the 300 nm dose in *A. nobilis* and after the 320 nm dose in *M. chamomilla*.

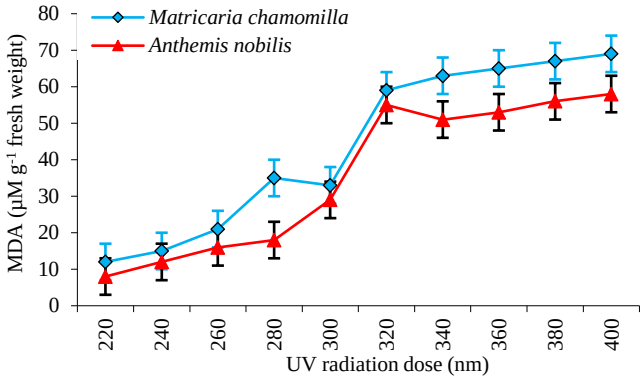


Figure 11. Effect of UV radiation dose (nm) on MDA content (µM g^{-1} fresh weight) in *M. chamomilla* and *A. nobilis*.

Water radiolysis, the primary effect of ionizing radiation on living organisms, generates reactive oxygen species (ROS). Therefore, it can be hypothesized that the enzymes found in plants, bacteria, and animals that protect cells from oxidative stress will respond similarly to ionizing radiation as they do to other stressors (Lal *et al*., 2019). Antioxidants and POD are involved in the compensatory mechanisms for scavenging free radicals formed after seed irradiation (Mailänder *et al*., 2022).

An inverse relationship between growth and POD activity has previously been reported in thyme seedlings exposed to UV and neutron radiation, where seedlings irradiated with UV doses of 320–360 nm showed reduced height but increased POD activity relative to non-irradiated controls (Gorgini Shabankareh *et al*., 2025). Similarly, in this study, leaf POD activity in *M. chamomilla* increased following UV irradiation at doses of 300, 340, and 380 nm. However, unlike the thyme study, shoot length increased in both *M. chamomilla* and *A. nobilis* across all UV treatments, suggesting that seed irradiation

stimulated growth while simultaneously activating antioxidant defenses (Gorgini Shabankareh *et al.*, 2025; Mavandi *et al.*, 2021).

Prolonged UV irradiation of wheat seeds (*Triticum aestivum* L.) for 1 to 6 hours has been reported to increase lipid peroxidation levels in seedlings. A dose-dependent decline in triacylglycerol content was observed, along with a corresponding rise in free fatty acids (Catani *et al.*, 2021; Madadi *et al.*, 2022). In contrast, the present study demonstrated a dose-dependent decrease in MDA content in *M. chamomilla*, indicating that UV seed irradiation did not intensify membrane lipid peroxidation in this genotype. In *A. nobilis*, MDA content was generally higher than in *M. chamomilla* under both control and irradiated conditions, although it also declined after most UV treatments. Additionally, it was previously suggested that nutmeg treatment should be limited to a 300 nm UV dose due to the increase in free fatty acids (Aksoy and Sözbilir, 2012; Salimi *et al.*, 2016).

Recent findings emphasize the complexity of cellular regulation in plants through proteolysis, which plays a crucial role in the maturation, degradation, and reconstruction of proteins in response to various external stimuli, as well as in the removal of abnormal and denatured proteins (Muleya *et al.*, 2022; van Wijk, 2015; Zaka *et al.*, 2002). An increasing body of evidence suggests that proteases are involved in protein turnover during abiotic stress responses (Zaka *et al.*, 2002). The degradation and recycling of proteins, influenced by proteolytic enzyme levels, are essential for a plant's response to environmental stresses (Heidari and Sarani, 2012). In this study, higher proteolytic activity was observed in *M. chamomilla* after exposure to UV doses of 220–300 nm, indicating protein degradation by proteases to eliminate damaged proteins and facilitate rebuilding processes following UV irradiation. The breakdown of denatured and potentially harmful proteins supplies free amino acids necessary for synthesizing new proteins.

Significant differences in biochemical parameters were found between *M. chamomilla* and *A. nobilis*. *M. chamomilla* demonstrated inherently higher protein content, while *A. nobilis* exhibited greater POD and protease activities (by twofold) and elevated MDA levels. In terms of growth parameters, *A. nobilis* had greater root and shoot lengths, as well as higher fresh and dry seedling weights compared to *M. chamomilla*. Consequently, it can be concluded that *A. nobilis* possesses a higher antioxidant capacity (POD activity), whereas *M. chamomilla* has a higher protein content. The biochemical parameters examined in this study indicate that *M. chamomilla* and *A. nobilis* respond differently to UV irradiation. Notably, a significant loss in protein content occurred in *M. chamomilla* before the 300 nm UV dose, while in *A. nobilis*, this was observed at the 280 nm UV dose. Additionally, POD activity increased at 260 and 300 nm doses in *M. chamomilla*, while it decreased after 220 nm doses in *A. nobilis*. The lowest MDA content was recorded after the 220 nm dose in *A. nobilis* and after the 240 nm dose in *M. chamomilla*. Furthermore, MDA levels rose continuously from 300 to 400 nm UV doses in *M. chamomilla*, whereas *A. nobilis* showed a decline in MDA content with increasing doses from 260 to 400 nm. These inherent differences may explain the distinct responses of *M. chamomilla* and *A. nobilis* to UV irradiation (Alharbi *et al.*, 2022; Kiani *et al.*, 2022; Li *et al.*, 2024; Shabir *et al.*, 2022; Yanting *et al.*, 2024).

A set of fundamental radiobiological endpoints, encompassing germination rates, seedling viability, and the sterility of both pollen and ovules, is routinely employed for the preliminary evaluation of mutagenic efficacy following irradiation. The stimulatory effects of ultraviolet treatment on maize have been substantiated through analyses of chlorophyll fluorescence and absorption spectra across various dosage regimens. In alignment with these findings, the present investigation utilized biochemical markers—specifically, protein concentration, MDA content, and the enzymatic activities of protease and peroxidase (POD), to determine genotype-specific optimal doses. For *A. nobilis*, the 400 nm UV treatment proved superior, as it maintained stable protein levels and POD activity while concurrently reducing both MDA accumulation and protease function. Conversely, the 400 nm dose was identified as optimal for *M. chamomilla*, characterized by enhanced POD activity, consistent protein and protease profiles, and diminished MDA content (Chen *et al.*, 2024; Hassan *et al.*, 2025; Li *et al.*, 2025; Ma *et al.*, 2024; Weisany *et al.*, 2023).

4. Conclusion

The combined data on protein content, as well as protease and POD activities, revealed a distinct, species-specific response to UV irradiation. The

optimal irradiation doses suggested for preserving beneficial biochemical markers and minimizing cellular damage (measured by MDA) are 400 nm UV for *M. chamomilla* and 500 nm UV for *A. nobilis*. Notable biochemical differences were observed between the species: protease and POD activities were approximately twofold higher in *A. nobilis* compared to *M. chamomilla*, while total protein content was higher in *M. chamomilla*. This indicates that POD plays a vital role in the mechanisms that inhibit free radicals generated by UV irradiation in seeds. Overall, biochemical parameters, including protein content, protease and POD activities, and lipid peroxidation (MDA content), serve as valuable indicators for assessing the effectiveness of specific irradiation doses for seed treatment.

Conflict of interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Ethics approval and consent to participate

No humans or animals were used in the present research. The authors have adhered to ethical standards, including avoiding plagiarism, data fabrication, and double publication.

Consent for publications

The authors consent to the publication of this work.

Availability of data and material

The datasets generated and/or analyzed during the current study are available from the corresponding author on reasonable request.

Authors' contributions

All authors had an equal role in study design, work, statistical analysis and manuscript writing.

Informed consent

The authors declare not to use any patients in this research.

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Generative AI statement

The author declares that generative AI (artificial intelligence) tools, including Grammarly & QuillBot, were used to enhance the language & clarity of this work. The author takes full responsibility for the accuracy & integrity of the content.

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