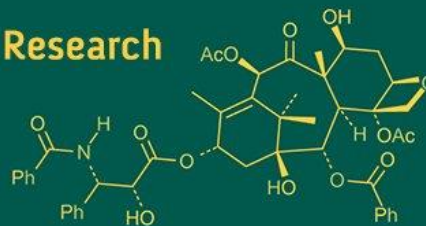


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Comparative biochemical analysis of healthy and *Sclerotinia sclerotiorum*-infected tissues of field pea (*Pisum sativum* L.)

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Abstract

Sclerotinia sclerotiorum (Lib.) de Bary stem rot is one of the most damaging fungal diseases of field pea (*Pisum sativum* L.) crops and can cause serious yield loss of the crops worldwide. Biochemical and photosynthetic responses of healthy and infected plant tissues (leaf, pod and stem) were evaluated by analysis of total phenolic content, tannin content, flavonoid content, protein concentration, chlorophyll pigments and carotenoids. The greatest total phenolic content was detected in infected stems, followed by healthy stems (1076.52 and 970.73 µg/g GAE, respectively) in all plant sections, showing an increased production of phenolic compounds as a defensive strategy. The greatest tannin content was reported in infected leaves (425.47 µg/g GAE) than in healthy leaves (337.57 µg/g GAE). The maximum value of absorbance (0.848) was for total flavonoid concentration in infected leaves, and the minimum (0.178) was for healthy stems. The protein contents in infected pods (9.67 mg/g) and infected leaves (6.33 mg/g) were considerably higher than respective healthy tissues, indicating the activation of stress-associated proteins during infection. Studies of photosynthetic pigments revealed a drastic drop in chlorophyll content in damaged leaves. The amounts of chlorophyll a (5.64), chlorophyll b (4.21) and total chlorophyll (9.85) were significantly higher in healthy leaves compared to diseased leaves (2.09, 3.55 and 5.64, respectively). Carotenoid content was totally absent in the diseased tissues of the plants. The maximum concentration (1.39) of carotenoid was observed in healthy leaves. The breakdown of pigments under pathogenic stress was evident. The observations demonstrated that infection promotes oxidative and physiological stress, resulting in increased accumulation of defensive secondary metabolites and proteins, while at the same time reducing photosynthetic pigments. These molecular markers could act as potential indicators of plant defense and disease development.

Keywords: Biochemical changes, total phenols, flavonoids, tannins, pigments and chlorophyll

1. Introduction

Field pea (*Pisum sativum* L.), also known as pea, is an important pulse crop. It is indigenous to Southern Europe and Western Asia (mainly the Mediterranean region). It is cultivated as a global winter season crop. It is a major, high-yielding pulse crop which can be eaten as a vegetable when dried and green seeds are used for dal or boiled to make snacks. The remaining part is used to feed the cattle. It is a cool-season grain legume crop grown at higher elevations at 7-30°C, which is self-pollinating" (Seepal *et al.*, 2025) [27]. It is a native of the Fabaceae family, which is considered to be the most significant group of flowering plants with 450 genera and 1200 species (Luitel *et al.*, 2021) [17]. It ranks third in global legume production and is one of the oldest food crops still cultivated (Azam *et al.*, 2024) [4]. It is considered one of the most successful, highly nutritious legume crops with great promise to alleviate protein malnutrition at the global level (Pandey *et al.*, 2021) [25]. Traditionally, the two types of peas farmed around the world are field peas and garden peas. It is very sensitive to waterlogging, but likes well-drained loamy soils with a pH of 6.0-7.5. Field peas are very nutritious and contain a lot of protein (23%), essential vitamins such as B1 (thiamine) and B5 (pantothenic acid), 2.2% minerals, 4.5% fibre, 56.5% carbohydrates and 1.1% fat (Anand *et al.*, 2024) [3]. *Sclerotinia sclerotiorum* (Lib.) de Bary, causing stem rot or white mould, is a serious global disease of peas that causes a significant reduction in production (O'Sullivan *et al.*, 2021) [22].

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The disease occurs on all above-ground parts of the plant: stems, leaves, flowers, and pods. The distinguishing features of the disease are the prominent black sclerotia in the mycelium and in the fissures of diseased tissue (Rahman *et al.*, 2020) [26]. Ordóñez *et al.* (2015) [23] have divided the later stages of sclerotia formation into four stages: condensation, enlargement, consolidation and pigmentation. There are three distinct phases of sclerotia production, which are initiation, development and maturation. These developmental stages include biochemical, metabolic, physiological and morphological alterations (Liang *et al.*, 2018) [13] and are determined by toxic metals, microbial competitors, temperature, UV radiation and other internal and external factors. The germination of sclerotia and the production of ascospores can be explained by some parameters like temperature, humidity and wet conditions during incubation (Shahoveisi *et al.*, 2020) [30].

Plants face the challenge of pathogenic organisms by turning on a cascade of biochemical and physiological defense responses (Agrios, 2005) [1]. These include accumulation of phenolic compounds, flavonoids, tannins and pathogenesis-related (PR) proteins which act in concert to limit pathogen invasion and spread (Nicholson and Hammerschmidt, 1992; Dixon and Paiva, 1995) [21, 8]. Phenolic compounds are the products of the phenylpropanoid pathway and are precursors for the synthesis of lignin, which reinforces cell walls against mechanical invasion by pathogens (Lamb and Dixon, 1997) [11]. Flavonoids are a diverse group of secondary metabolites that have broad-spectrum antimicrobial properties and are involved in key roles in plant immunity (Treutter, 2006) [33]. The total protein content, including that of PR proteins such as chitinases and glucanases, increases in infected tissues as a measure of the hypersensitive response and systemic acquired resistance (Van Loon *et al.*, 2006) [34]. On the other hand, chlorophyll degradation is a typical symptom of senescence and chloroplast disorganisation induced by disease (Agrios, 2005) [1].

The present study, therefore, aimed to evaluate the biochemical alterations in infected versus healthy plant parts (leaves, stems, pods) of field pea in response to *S. sclerotiorum* infection.

2. Materials and Methods

A research investigation named “Biochemical Evaluation of Healthy and Diseased Plant Parts of Field Pea (*Pisum sativum* L.) Infected by *Sclerotinia sclerotiorum*” was conducted at the plant pathology lab of the School of Agriculture at Uttaranchal University in Dehradun during the year 2025-2026. The materials, methods, and experimental procedures employed in this study are described below.

2.1 Collection of Plant Material

Healthy field pea plant parts and diseased field pea plants showing characteristic stem rot symptoms, viz., white cottony mycelial growth, water-soaked lesions and wilting were collected from the field in polythene bags. These samples were brought to the Plant Pathology laboratory of the School of Agriculture, Uttaranchal University.

2.2 Biochemical Analysis of Plant Parts

Healthy and infected parts of the field pea, like leaves, pods and stems, were collected from the field in a polythene bag.

The collected samples were kept in a refrigerator for biochemical analysis.

2.2.1 Preparation of Extract

Leaf samples (0.5 g) were homogenised in 5000 µl of ice cold 95% methanol with the help of an ice-cold mortar and pestle. The samples were incubated in the dark at 25°C for 48 hours. The samples were then spun at 5000 rpm for 5 min at room temperature.

2.2.2 Total Phenolic Content (TPC)

TPC was estimated using the Folin-Ciocalteu (F-C) reagent and micro colourimetric method (Ainsworth *et al.* 2007) [2]. TPC was measured by discarding the supernatant. The supernatant (100 µl) was vortexed well with 100 µl of 10% (v/v) F-C reagent, then 800 µl of 700 mM Na₂CO₃ was added. Thereafter, samples were maintained at room temperature for 1 hour. Blank absorbance was recorded using a UV-VIS spectrophotometer at 765 nm, and the result was expressed as mg GAE/g. Different amounts of gallic acid were used to draw a standard curve, and a linear regression equation was obtained. The phenolic content of the samples was determined by means of the linear regression equation.

2.2.3 Tannin Content

To the above assay (TPC), 0.1g of PVP was added and vortexed to mix thoroughly. The sample was centrifuged at 5000 rpm for 10 min. Absorbance was determined at 765 nm (Shamshad *et al.*, 2024) [31]. The results are presented as mg gallic acid equivalents (GAE) per gram of fresh weight (mg GAE/g FW).

2.2.4 Total Flavonoid Content (TFC)

Total flavonoids were measured by the aluminium chloride colourimetric method (Lin *et al.* 2007) [15]. The sample (400 µl + 1600 µl dH₂O) was mixed with 0.1 ml of 10% aluminium chloride hexahydrate, 0.1 ml of 1M Potassium acetate and 2.8 ml of deionised water. The reaction mixture was incubated at room temperature for 40 minutes, and then the absorbance was measured at 415 nm using a UV-VIS spectrophotometer.

2.2.5 Total Protein Content

Total soluble protein was measured using the Lowry technique (Lowry *et al.*, 1951) [16]. Absorbance was determined at 660 nm using bovine serum albumin (BSA) as a standard. The results are presented in mg protein/g fresh weight (mg/g FW).

2.2.6 Chlorophyll Content

Dissolve chlorophyll in 80% acetone and filter with a suction flask. Put the filtrate into a volumetric flask and make up to the 50ml mark. Place the sample in the spectrophotometer to determine the optical density. Pigment concentrations (lycopene, chlorophyll a, chlorophyll b, total chlorophyll, carotenoids) in leaves were determined using the technique of Lichtenthaler *et al.* (1983). Absorbance was measured at 663, 645, 505, 453 and 470 nm using a UV-VIS spectrophotometer (U-2800). Chlorophyll a, Chlorophyll b, Total Chlorophyll and Carotenoids were determined by the following formula and given as mg/g FW.

Chlorophyll a = $12.7 A_{663} - 2.69 A_{645}$

Chlorophyll b = $22.9 A_{645} - 4.68 A_{663}$

Total Chlorophyll = Chlorophyll a + Chlorophyll b

$$\text{Carotenoids} = \frac{1000A_{470} - 1.82(\text{Chl a}) - 85.02(\text{Chl b})}{198}$$

3. Results and Discussion

3.1 Biochemical Changes in Infected vs. Healthy Plant Parts

3.1.1 Total Phenolic Content (TPC)

The infected stem had the highest level of phenolics (1076.52 µg/g GAE; absorbance 2.232) compared with the healthy stem (970.73 µg/g GAE; absorbance 2.031) of all the tested samples. The infected leaf had slightly higher phenolic content (690.21 µg/g GAE) than the healthy leaf (653.36 µg/g GAE) in leaves. Likewise, infected pods had higher phenol levels (684.42 µg/g GAE) than healthy pods (587.57 µg/g GAE), as shown in Table 1.

In all studied parts (leaves, stems, and pods), total phenolic content was significantly higher in infected plant tissues compared to healthy tissues. The rise in TPC in infected tissues was consistent with the known role of phenolics in plant defense against pathogens. The highest total phenolic content was in infected stems, followed by infected leaves and pods. Physical and chemical barriers are afforded by phenolic compounds against the invasion of pathogens by lignification, which strengthens the cell wall, and by having direct adverse effects on the enzymes and membranes of the pathogen (Nicholson and Hammerschmidt, 1992) [21]. In response to pathogen infection, phenylpropanoid pathway enzymes such as phenylalanine ammonia lyase (PAL) are activated, leading to increased synthesis of phenolic metabolites (Dixon and Paiva, 1995) [8]. Similar increases in total phenolic content (TPC) have been reported in *Fusarium oxysporum* - infected chickpea (Sharma and Chaure, 2017) [32] and in *S. sclerotiorum* - infected sunflowers (Seiler *et al.*, 2012) [28], supporting the hypothesis that phenolic accumulation is a general plant response to necrotrophic diseases.

3.1.2 Tannin Content

The results revealed that the concentration of tannins was quite different between healthy and diseased plant tissues. Absorbance value of the infected leaf was 0.995, and the greatest concentration of tannin observed was 425.47 µg/g GAE in all the examined samples. The second and third most polluted were the infected pod (367.05 µg/g GAE) and infected stem (388.10 µg/g GAE), respectively. Healthy plant tissues were found to contain comparatively less tannin. Healthy leaf contains 337.57 µg / mL GAE and healthy pod 331.26 µg / mL GAE. The healthy stem showed the lowest tannin concentration of 135.47 µg/g GAE, with the value of 0.444 absorbance as shown in Table 2.

Tannin concentration was substantially higher in infected plant sections than in healthy ones, with the maximum rise observed in leaves. Tannins are polyphenolic chemicals that precipitate proteins, block cell wall-degrading enzymes produced by pathogens and create complexes with metal ions required for pathogen enzyme activity (Mayer *et al.*, 2001) [20]. Increased accumulation in infected tissues suggests activation of defence-related secondary metabolism. Increased tannins have been related to resistance responses in several host-pathogen interactions, including pea infected with *Fusarium* species (Kraft and Pfleger, 2001) [10]. In the present study, the increased tannin

levels in all types of infected tissues are evidence of systemic biochemical response to *S. sclerotiorum* infection.

3.1.3 Total Flavonoid Content (TFC)

The infected leaf showed the highest absorbance value (0.848) among all the samples studied, followed by the healthy leaf (0.787). The absorbance values of the infected stem and infected pod were 0.449 and 0.347, respectively. The absorption values were lower in the healthy stem (0.178) and the healthy pod (0.217), as shown in Table 3. Infected plant tissues exhibited higher absorbance values, indicating higher flavonoid accumulation than healthy ones. The rise of flavonoids in diseased tissues could be ascribed to the activation of defensive systems in plants during pathogen invasion. Flavonoids are key secondary metabolites with antioxidant, antibacterial and stress-protecting characteristics that enhance a plant's resilience to disease.

Flavonoids are a structurally varied group of phenylpropanoid derivatives, as antibacterial phytoalexins, antioxidants and signalling molecules in plant defense (Treutter, 2006) [33]. Zhao *et al.* (2005) proposed that salicylate- and jasmonate-dependent signalling pathways are involved in their activation upon pathogen invasion. The increase in flavonoids in affected tissue might be a sign that the host was trying to prevent the development of the disease by producing an environment that is biochemically less conducive. It was well known that the infection with the fungus increases flavonoid production in legumes. Padmavathi *et al.* (2013) showed that the total flavonoid content in lentil and pea tissues was dramatically increased upon exposure to necrotrophic fungi. Isoflavones, a subclass of flavonoids in leguminous plants, have been reported to be phytoalexins against *Sclerotinia* infections (Lygin *et al.*, 2013) [18].

3.1.4 Total Protein Content

The lowest protein concentration was found in a healthy pod (8.53 mg/g, absorbance 2.656), while the highest protein content was found in an infected pod (9.67mg/g, absorbance 3.000). The protein concentration of the infected leaf was 6.33 mg/g (absorbance 1.988), and the protein content of the healthy leaf was 1.39 mg/g (absorbance 0.494). The lowest protein concentration was found in the uninfected stem (1.35 mg/g; absorbance 0.481), while the highest protein concentration was found in the infected stem (3.59 mg/g; absorbance 1.159), as shown in Table 4. Protein concentration was higher in infected plant tissues than in healthy tissues. The elevated protein levels in infected samples might be due to the synthesis of defense and stress-related proteins in response to infection by the pathogen. The primary effects of infection are usually the induction of the defense and metabolic processes in plants, and typically an increase in protein synthesis.

The overall content of soluble proteins was substantially greater in infected tissues than in healthy ones. The increase was mainly due to the production of pathogenesis-related (PR) proteins, a heterogeneous group of enzymes including chitinases, glucanases, thaumatin-like proteins and peroxidases, which are induced upon pathogen infection (Van Loon *et al.*, 2006) [34]. PR proteins are involved in the direct degradation of fungal cell wall components (chitin and glucan) and in signalling systemic acquired resistance (SAR) (Sels *et al.*, 2008) [29]. The increase in the protein

accumulation in infected stems and leaves was in agreement with the studies in soybean challenged with *S. sclerotiorum*, where activation of PR protein genes was identified (Calla *et al.*, 2009) [6]. In addition, the proteinaceous reactive oxygen species (ROS)-scavenging enzymes superoxide dismutase (SOD), catalase (CAT) and peroxidase (POX) are also significantly upregulated during oxidative bursts induced by pathogen recognition (Bolwell and Wojtaszek, 1997) [5], which might also contribute to the increase in total protein in infected plant parts.

3.1.5 Chlorophyll Content

The healthy leaf had the highest concentration of chlorophyll a of 5.64, chlorophyll b of 4.21 and total chlorophyll of 9.85 among all the chlorophyll samples. Conversely, the infected leaf showed a significantly reduced pigment level, 2.09 for chlorophyll a, 3.55 for chlorophyll b and 5.64 for total chlorophyll. This reduction suggests that the infection had an adverse effect on the photosynthetic efficiency of leaf tissue. Chlorophyll a and total chlorophyll concentration in pods were somewhat higher in the healthy pod (1.54 and 3.95, respectively) than in the infected pod (1.47 and 3.93, respectively). Similarly, healthy stem tissues showed a slightly higher content of pigment than infected stems. The levels of chlorophyll a, chlorophyll b and total chlorophyll in the healthy stem were 1.37, 1.93 and 3.29, respectively, but the infected stem had levels of 1.23, 1.98 and 3.21, respectively. The carotenoid content was found only in healthy parts of the plant, while in diseased tissues, there was no carotenoid at all. The highest concentration of carotenoids was recorded in healthy leaves (1.39), followed

by healthy pods (0.08) and healthy stems (0.05), as shown in Table 5.

Healthy tissue had considerably more chlorophyll than infected tissue, as opposed to the biochemicals involved in defense. Degradation of chlorophyll, an important indicator of illness development, is caused by pathogen-driven structural and functional changes of chloroplasts (Agrios, 2005) [1]. Necrotrophic infections such as *S. sclerotiorum* produce rapid necrosis of tissues and breakdown of chlorophyll by secretion of oxalic acid and cell wall-dissolving enzymes (Godoy *et al.* 1990; Williams *et al.* 2011) [9, 36]. During pathogen-induced senescence, chlorophyllase hydrolyses chlorophyll, creating phytol and chlorophyllide (Matile *et al.*, 1999) [19]. Chlorophyll concentration decline was an indicator of tissue damage and reduced photosynthetic potential, hence reduced plant yields. The current results are supported by similar reductions in the chlorophyll content due to Sclerotinia infection in sunflower (Davar *et al.*, 2012) and rapeseed (Li *et al.*, 2015) [12].

Table 1: Total Phenolic Content of Healthy and Infected Plant Parts Expressed as Gallic Acid Equivalents (GAE)

Plant Parts	Absorbance at 765nm	Total Phenolic Content (µg/g GAE)
Infected Leaf	1.498	690.21
Healthy Leaf	1.428	653.36
Infected Pod	1.487	684.42
Healthy Pod	1.303	587.57
Infected Stem	2.232	1076.52
Healthy Stem	2.031	970.73

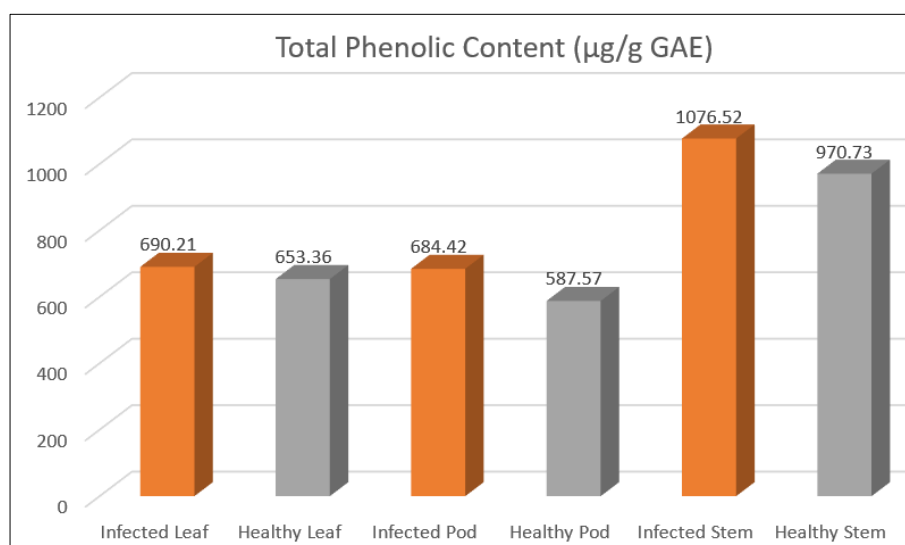


Fig 1: Graphical representation of Total Phenolic Content (TPC)

Table 2: Total Tannin Content of Healthy and Infected Plant Parts Expressed as Gallic Acid Equivalents (GAE)

Plant Parts	Absorbance at 765nm	Total Tannins Content (µg/g GAE)
Infected Leaf	0.995	425.47
Healthy Leaf	0.828	337.57
Infected Pod	0.924	388.10
Healthy Pod	0.816	331.26
Infected Stem	0.884	367.05
Healthy Stem	0.444	135.47

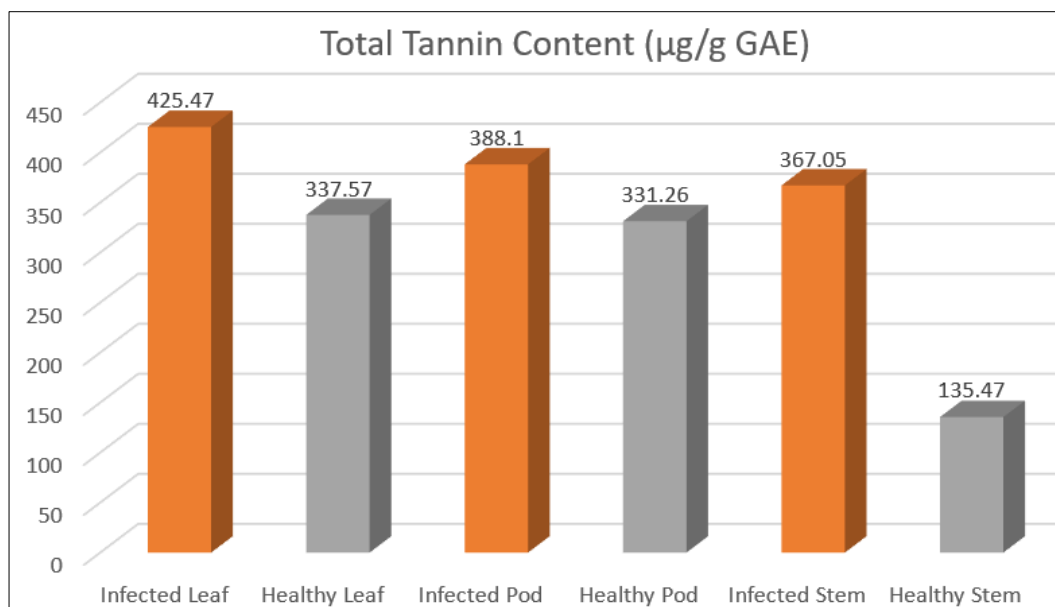


Fig 2: Graphical representation of Total Tannin Content

Table 3: Absorbance Values at 415 nm for Total Flavonoid Content in Healthy and Infected Plant Parts

Plant Parts	Absorbance at 415nm
Infected Leaf	0.848
Healthy Leaf	0.787
Infected Pod	0.347
Healthy Pod	0.217
Infected Stem	0.449
Healthy Stem	0.178

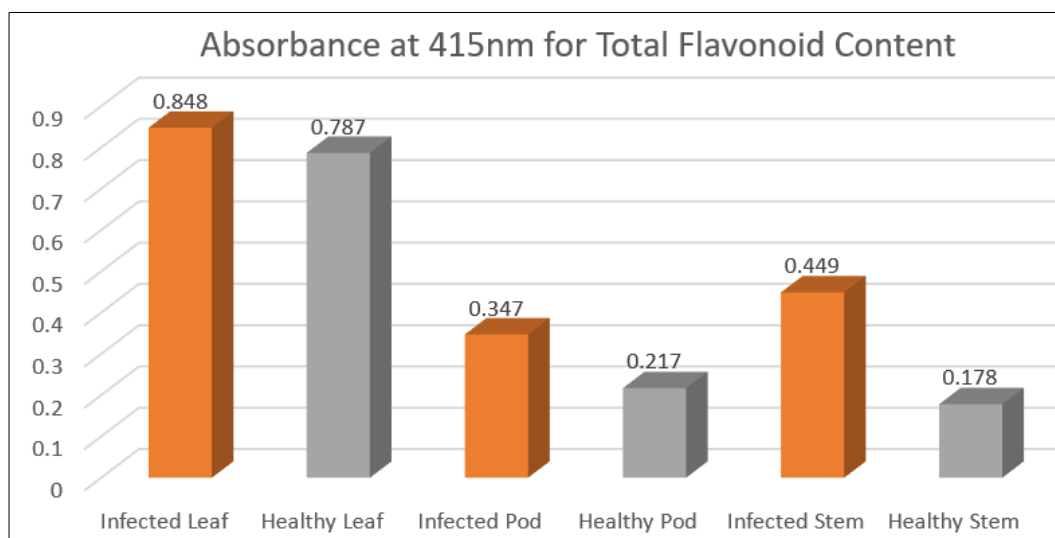


Fig 3: Graphical representation of Total Flavonoid Content

Table 4: Total Protein Content of Healthy and Infected Plant Parts Expressed as mg/g

Plant Parts	Absorbance at 660nm	Total Protein Content (mg/g)
Infected Leaf	1.988	6.33
Healthy Leaf	0.494	1.39
Infected Pod	3	9.67
Healthy Pod	2.656	8.53
Infected Stem	1.159	3.59
Healthy Stem	0.481	1.35

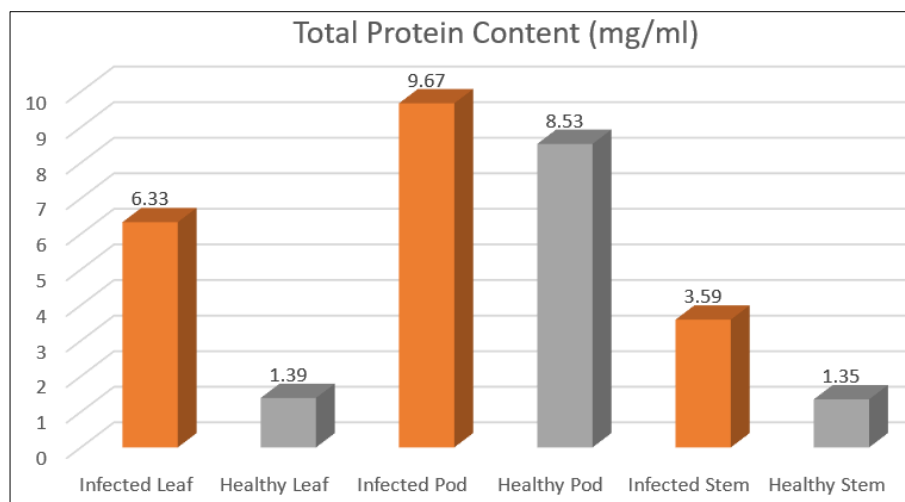


Fig 4: Graphical representation of Total Soluble Protein

Table 5: Chlorophyll and Carotenoid Content in Healthy and Infected Plant Parts

Plant part	Chl a	Chl b	Total Chlorophyll	Carotenoids
Infected leaf	2.09	3.55	5.64	0.00
Healthy leaf	5.64	4.21	9.85	1.39
Infected pod	1.47	2.46	3.93	0.00
Healthy pod	1.54	2.41	3.95	0.08
Infected stem	1.23	1.98	3.21	0.00
Healthy stem	1.37	1.93	3.29	0.05

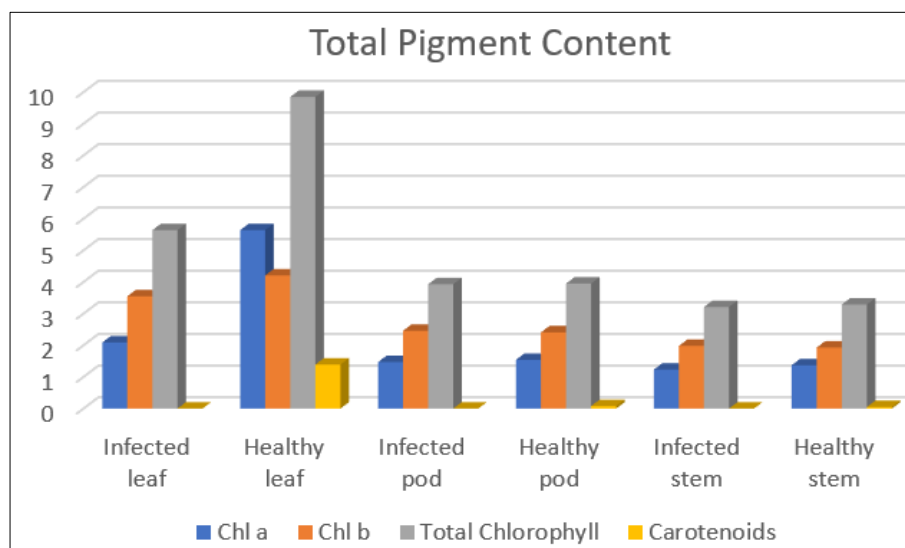


Fig 5: Graphical representation of Total Pigment Content

5. Conclusion

The present study offered extensive evidence that *Sclerotinia sclerotiorum* infection in field pea (*Pisum sativum* L.) significant impact on biochemical and physiological features of several areas of plants. Increased accumulation of phenolics, tannins, flavonoids and proteins in diseased tissues indicated the activation of plant defense mechanisms under stress conditions. The maximum phenolic content was recorded in the infected stem (1076.52 µg/g GAE). The highest tannin (425.47 µg/g GAE) and flavonoid content (0.848 absorbance at 415 nm) were recorded in the infected leaves. Moreover, the protein content was much higher in infected pods (9.67 mg/g), which showed an increase in metabolic and defensive activities during infection.

However, infection has deleterious impacts on

photosynthetic pigments. Healthy leaves showed the highest amounts of chlorophyll a, chlorophyll b and total chlorophyll (5.64, 4.21 and 9.85, respectively), but the pigments were substantially lower in diseased tissues. Carotenoids were absent in the infected tissues but present in healthy tissues, particularly in healthy leaves (1.39), signifying major oxidative injury and reduced photosynthetic efficiency under infection stress.

Overall results indicated that the pathogen infection stimulated biochemical defense systems but damaged the photosynthetic system of the plant. Resistance methods might include increased secondary metabolites and protein synthesis. Whereas, reduced levels of chlorophyll and carotenoid contents are an indication of the impairment of normal physiological processes. The findings give valuable information on plant-pathogen interactions and may be used

in the development of biochemical markers for disease detection and stress tolerance research in plants.

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