



FUNGAL DIVERSITY AND DISTRIBUTION PATTERNS IN *ROSA* SPP. FLOWERS: INFLUENCE OF LOCATION AND DEVELOPMENTAL STAGES

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Abstract:

This study investigated the occurrence and distribution of fungal communities on *Rosa* spp. flowers across ten distinct geographic regions and four stages of floral development. A total of 39 fungal taxa were identified, predominantly belonging to the genera *Alternaria*, *Aspergillus*, *Cladosporium*, *Curvularia*, *Fusarium*, *Penicillium*, *Microphomina*, and *Rhizopus*. Spatial analysis indicated a widespread prevalence of *Aspergillus niger*, *A. flavus*, *A. terreus*, *Penicillium expansum*, *P. corylophilum*, *P. maximae*, and *Cladosporium oxysporum* across most locations, suggesting high dispersal capacity and dominant ecological roles. In contrast, *Lasiodiplodia theobromae* and *Rhizopus stolonifer* exhibited restricted distributions, likely influenced by specific microclimatic requirements. Stage-wise analysis demonstrated a significant correlation between floral maturity and fungal colonization. Microbial infection was minimal during the semi-bud stage, progressed moderately at the open-bud stage, and reached maximum levels during the bloom and senescent phases. The highest incidence of *Penicillium* and *Aspergillus* species was recorded in senescent flowers. This susceptibility is attributed to physiological changes such as tissue softening, increased nutrient exudation, and the degradation of host defence compounds during the ageing process. These findings highlight that *Rosa* spp. flowers serve as critical substrates for diverse fungal species, influenced by both environmental variables and host maturity. This data is pivotal for advancing floral fungal ecology, optimising post-harvest management, and formulating effective disease-control strategies for the ornamental flower industry.

Keywords: *Rosa* spp., *Aspergillus* spp., floral waste, senescent flowers, *Penicillium*.

INTRODUCTION

Flowers are highly dynamic biological systems that experience rapid physiological changes during development, creating microhabitats that support diverse microorganisms, especially fungi. Their colonisation by fungi depends on floral physiology, environmental factors, pollinator activity, and nutrients released during senescence (Nguyen et al., 2020). *Rosa* spp., among the most cultivated ornamental flowers, offers a nutrient-rich substrate with sugars, amino acids, volatile compounds, pigments, phenolics, and senescence-associated metabolites. These biochemical traits make rose petals suitable for saprophytic and opportunistic pathogenic fungi (González-Aguilar et al., 2004). Fungi on flowers serve various ecological roles: saprophytic species promote decomposition, while pathogenic fungi like *Alternaria*, *Aspergillus*, *Fusarium*, and *Penicillium* may cause spoilage before and after harvest, reducing flower quality, vase life, and aesthetic appeal (Pitt & Hocking, 2009). Several *Aspergillus* species, including *A. niger*, *A. flavus*, *A. terreus*, and *A. fumigatus*, are airborne contaminants often found on floral surfaces due to their high sporulation and environmental resilience (Samson et al., 2014). Similarly, *Penicillium* spp., such as *P. expansum* and *P. corylophilum*, commonly colonise senescent plant tissues, where nutrient leakage and weakened cell walls facilitate rapid invasion (Bensch et al., 2012). Flower development influences fungal succession: young floral tissues often contain higher levels of antimicrobial phenolics and structural defences that inhibit fungal growth (González-Aguilar et al., 2004). As flowers age, cellular metabolism decreases, membranes become compromised, and reactive oxygen species accumulate, increasing vulnerability to fungal colonisation (Nguyen et al., 2020). Blooming and senescent flowers often have high humidity, nectar residues, and pollen deposits, creating ideal conditions for fungal growth. Despite the ecological and economic importance of fungal colonisation, systematic studies on its incidence, distribution, and development-related succession in *Rosa* spp. are limited, especially under Indian climatic conditions. Most prior research has focused on foliar pathogens or post-harvest decay, with less attention to the floral mycobiome (Mukadam et al., 2006; Gilman, 2001). Understanding fungal incidence across different environments helps identify influencing factors such as humidity, temperature, dispersal, and human activities. Identifying the floral stage most prone to fungal attack is essential for developing disease prevention strategies for ornamental flowers, rose farms, and the perfume industry. This study aims to document fungal diversity and distribution in *Rosa* spp. across ten locations, assess stage-wise (semi-bud, open bud, bloom, senescent) fungal incidence, and compare ecological patterns based on spatial and developmental variables. The findings will contribute valuable insights into the floral mycobiome of *Rosa* spp. and support future research on biodegradation, post-harvest management, and fungal ecology.

Materials and Methods

Collection of Samples

Rosa spp. flowers were collected from various sites and at different growth stages. Sampling locations included decoration venues, community centres, wedding halls, cultural events, markets, and decorative sites where roses are frequently utilised. All samples were transported to the laboratory in sterile paper bags. In the lab, the floral waste was classified into four physiological stages: S1, Semi-opened bud; S2, opened bud; S3, fully bloomed flower; and S4, Senescence stage.

Isolation of Fungi

Isolation of fungi from *Rosa* spp. floral waste was performed on media such as Potato Dextrose Agar (PDA) and Czapek Dox Agar (CZA). Appropriate antibiotic concentrations were added to prevent bacterial contamination. Samples from each developmental stage (S1, S4) were inoculated onto the media using standard techniques. The plates were incubated at 30°C. After seven days, all observed fungal colonies were recorded, and fungal incidence was calculated using the following formula.

$$\% \text{ Incidence} = \frac{\text{Total number of colonies} - \text{Number of replicates}}{\text{Total number of colonies}}$$

To obtain pure cultures, each fungal colony was transferred to fresh, sterile CZA plates.

Identification and Characterisation of Fungi

Fungal identification was conducted based on morphological and microscopic features. Observations included colony characteristics such as growth pattern, texture, pigmentation, mycelial structure, spore morphology, and sporophore arrangement. Identification utilised standard manuals including Gilman (2001), Ellis (1971), and Mukadam et al. (2006). For confirmation, selected isolates were referred to the Agharkar Research Institute (ARI), Pune. Pure cultures of all identified fungi were maintained on CZA medium for further studies.

Table I: Incidence of fungi on *Rosa* spp. at different locations

Sr. No.	Name of fungi	Locations									
		L1	L2	L3	L4	L5	L6	L7	L8	L9	L10
1	<i>Alternaria cheiranthi</i>	-	-	-	-	+	+	+	+	-	-
2	<i>Alternaria dianthicola</i>	+	+	+	+	-	-	-	-	+	-
3	<i>Alternaria dianthi</i>	-	-	-	-	-	-	-	-	-	+
4	<i>Alternaria limaciformis</i>	-	-	-	-	-	+	+	+	+	+
5	<i>Alternaria longipes</i>	+	+	+	+	-	-	-	-	-	-
6	<i>Alternaria raphani</i>	-	-	-	-	-	-	+	+	+	+
7	<i>Alternaria tenuissima</i>	+	-	+	-	+	+	-	-	-	-
8	<i>Aspergillus aculeatus</i>	-	+	-	+	-	+	-	+	+	-
9	<i>Aspergillus carbonarius</i>	+	-	-	+	-	-	+	-	-	+
10	<i>Aspergillus eucalypticola</i>	-	+	+	-	+	+	-	-	-	-
11	<i>Aspergillus flavus</i>	-	-	-	+	-	-	+	+	+	+

12	<i>Aspergillus fumigatus</i>	+	+	+	-	-	+	-	-	-	-
13	<i>Aspergillus ibericus</i>	-	-	-	-	+	-	-	+	+	+
14	<i>Aspergillus nidulance</i>	-	+	+	+	-	-	+	-	-	-
15	<i>Aspergillus niger</i>	+	-	-	+	+	+	+	+	+	+
16	<i>Aspergillus phoenicus</i>	-	+	+	-	-	-	-	-	-	-
17	<i>Aspergillus sydowii</i>	-	-	-	+	+	+	-	-	+	+
18	<i>Aspergillus terreus</i>	+	+	+	-	+	-	+	+	+	-
19	<i>Aspergillus tubengensis</i>	-	-	-	+	-	+	+	-	-	+
20	<i>Aspergillus ustus</i>	-	-	-	+	-	+	-	+	-	+
21	<i>Aspergillus versicolor</i>	+	+	+	-	+	-	-	-	+	-
22	<i>Cladosporium chlorocephalum</i>	-	-	-	-	-	-	+	+	-	-
23	<i>Cladosporium cladosporioids</i>	+	+	+	+	-	+	+	-	-	+
24	<i>Cladosporium oxysporum</i>	-	-	-	-	+	-	-	+	+	+
25	<i>Curvularia lunata</i>	+	+	+	+	-	+	+	+	+	-
26	<i>Curvularia ovoidea</i>	-	-	-	-	+	-	-	-	-	+
27	<i>Fusarium fujikuroi</i>	+	+	+	+	-	+	+	+	+	+
28	<i>Fusarium oxysporum</i>	+	-	-	-	+	-	+	+	-	-
29	<i>Fusarium poae</i>	-	+	+	+	-	-	-	-	-	-
30	<i>Lasiodiplodia theobromae</i>	+	+	+	-	+	+	+	+	+	+
31	<i>Microphomina phaseolina</i>	-	-	-	+	-	-	-	+	+	+
32	<i>Nigrospora oryzae</i>	+	+	+	+	+	+	+	+	-	-
33	<i>Penicillium echinulatum</i>	+	+	+	+	+	+	+	+	+	-
34	<i>Penicillium expansum</i>	+	-	-	-	-	+	+	+	-	-
35	<i>Penicillium crysogenum</i>	+	-	-	-	+	-	+	+	+	+
36	<i>Penicillium corylophilum</i>	-	+	+	+	-	-	-	-	-	-
37	<i>Penicillium lilacinum</i>	-	+	+	+	+	+	+	+	+	+
38	<i>Penicillium maximae</i>	-	+	+	+	+	-	-	-	-	-
39	<i>Rhizopus stolonifer</i>	+	-	+	+	+	+	+	+	+	+

- = No fungal occurrence, + = occurrence of fungi

Table II: Incidence of fungi on *Rosa* spp. at a different stage

Sr. No	Name of fungi	Semi bud	Open bud	Bloom flower	Senescent flower
		(s1)	(s2)	(s3)	(s4)
1	<i>Alternaria cheiranthi</i>	-	-	30%	45%
2	<i>Alternaria dianthicola</i>	-	-	48%	50%
3	<i>Alternaria dianthi</i>	-	-	35%	55%
4	<i>Alternaria limaciformis</i>	-	-	40%	50%
5	<i>Alternaria longipes</i>	-	-	35%	49%
6	<i>Alternaria raphani</i>	2%	5%	38%	46%
7	<i>Alternaria tenuissima</i>	-	-	30%	40%
8	<i>Aspergillus aculeatus</i>	-	-	30%	50%
9	<i>Aspergillus carbonarius</i>	-	-	43%	46%
10	<i>Aspergillus eucalypticola</i>	-	-	40%	40%
11	<i>Aspergillus flavus</i>	-	-	35%	51%
12	<i>Aspergillus fumigatus</i>	-	-	30%	43%
13	<i>Aspergillus ibericus</i>	-	-	38%	40%
14	<i>Aspergillus nidulance</i>	-	-	40%	47%
15	<i>Aspergillus niger</i>	2%	5%	68%	80%
16	<i>Aspergillus phoenicus</i>	-	-	20%	23%
17	<i>Aspergillus sydowii</i>	-	-	40%	50%
18	<i>Aspergillus terreus</i>	2%	5%	60%	78%
19	<i>Aspergillus tubengensis</i>	-	-	29%	46%
20	<i>Aspergillus ustus</i>	-	-	31%	45%
21	<i>Aspergillus versicolor</i>	-	-	30%	52%
22	<i>Cladosporium chlorocephalum</i>	-	-	20%	21%
23	<i>Cladosporium cladosporioids</i>	2%	5%	59%	75%
24	<i>Cladosporium oxysporum</i>	-	-	40%	40%
25	<i>Curvularia lunata</i>	1%	3%	65%	79%
26	<i>Curvularia ovoidea</i>	-	-	20%	25%

27	<i>Fusarium fujikuroi</i>	2%	3%	60%	81%
28	<i>Fusarium oxysporum</i>	-	-	40%	45%
29	<i>Fusarium poae</i>	-	-	20%	30%
30	<i>Lasiodiplodia theobromae</i>	2%	5%	70%	85%
31	<i>Microphomina phaseolina</i>	-	-	35%	40%
32	<i>Nigrospora oryzae</i>	1%	5%	56%	70%
33	<i>Penicillium echinulatum</i>	3%	10%	35%	88%
34	<i>Penicillium expansum</i>	-	-	30%	37%
35	<i>Penicillium crysogenum</i>	-	-	48%	60%
36	<i>Penicillium corylophilum</i>	-	-	30%	38%
37	<i>Penicillium lilacinum</i>	2%	3%	65%	85%
38	<i>Penicillium maximae</i>	-	-	28%	39%
39	<i>Rhizopus stolonifer</i>	-	-	60%	66%

- Absent (0%), + =Minimum (15%), ++ =Moderate (25-50%), +++ =Maximum (50-75%), +++++(>75%)

Result:

Incidence of Fungal Taxa Across Different Geographic Areas. The survey across 10 sites (L1-L10) revealed diverse mycobiota associated with *Rosa* spp., including 39 fungal species, with notable variation in their distribution. ubiquitous Species: *Aspergillus niger* and *Cladosporium cladosporioides* were found in all locations, suggesting high adaptability and effective spore dispersal. Commonly Found Species: species like *Aspergillus flavus*, *A. terreus*, *Fusarium oxysporum*, and *Penicillium corylophilum* appeared in most sites. Restricted Distribution: Some species, such as *Curvularia ovoides* (found only in L5 and L10) and *Aspergillus phoenicis* (found in L2, L3, L5, and L9), showed limited distribution, probably due to specific microclimatic or soil preferences. Stage-wise Fungal Succession During Flower Development. As the flower developed from semi-bud to senescence, an increase in fungal colonisation was observed. Initial Stages (S1 & S2): at the semi-bud (S1) and open-bud (S2) stages, fungal presence was minimal, with species such as *Alternaria raphani* (2-5%), *Aspergillus niger* (2-5%), and *Penicillium echinulatum* (3-10%) establishing early. This low incidence results from natural antifungal compounds and structural protection of floral tissues. Peak Colonisation (S3 & S4): During Bloom (S3) and Senescent (S4) stages, fungal diversity and prevalence increased significantly. The highest infection rates in S4 were observed for *Penicillium echinulatum* (88%), *Lasiodiplodia theobromae* (85%), and *Fusarium fujikuroi* (81%). Other fungi involved in decay during this stage were *Aspergillus niger* (80%), *Aspergillus terreus* (78%), and *Curvularia lunata* (79%).

Discussion

The transition from bud to senescence involves complex physiological changes that favour fungal growth. As the flower ages, there is a natural decline in host defence mechanisms and an increase in tissue permeability. The leakage of nutrients such as sugars and amino acids onto the floral surface provides an ideal substrate for saprophytic and opportunistic pathogenic fungi. The high prevalence of *Aspergillus* and *Penicillium* across both locations and stages suggests that they play a primary role as decomposers in the floral ecosystem. The presence of *Lasiodiplodia theobromae* specifically in the later stages (reaching 85% in S4) highlights its role as a potent post-harvest pathogen that accelerates floral wilting. These findings emphasise the need for stage-specific disease management, particularly focusing on the bloom stage to prevent heavy colonisation during senescence.

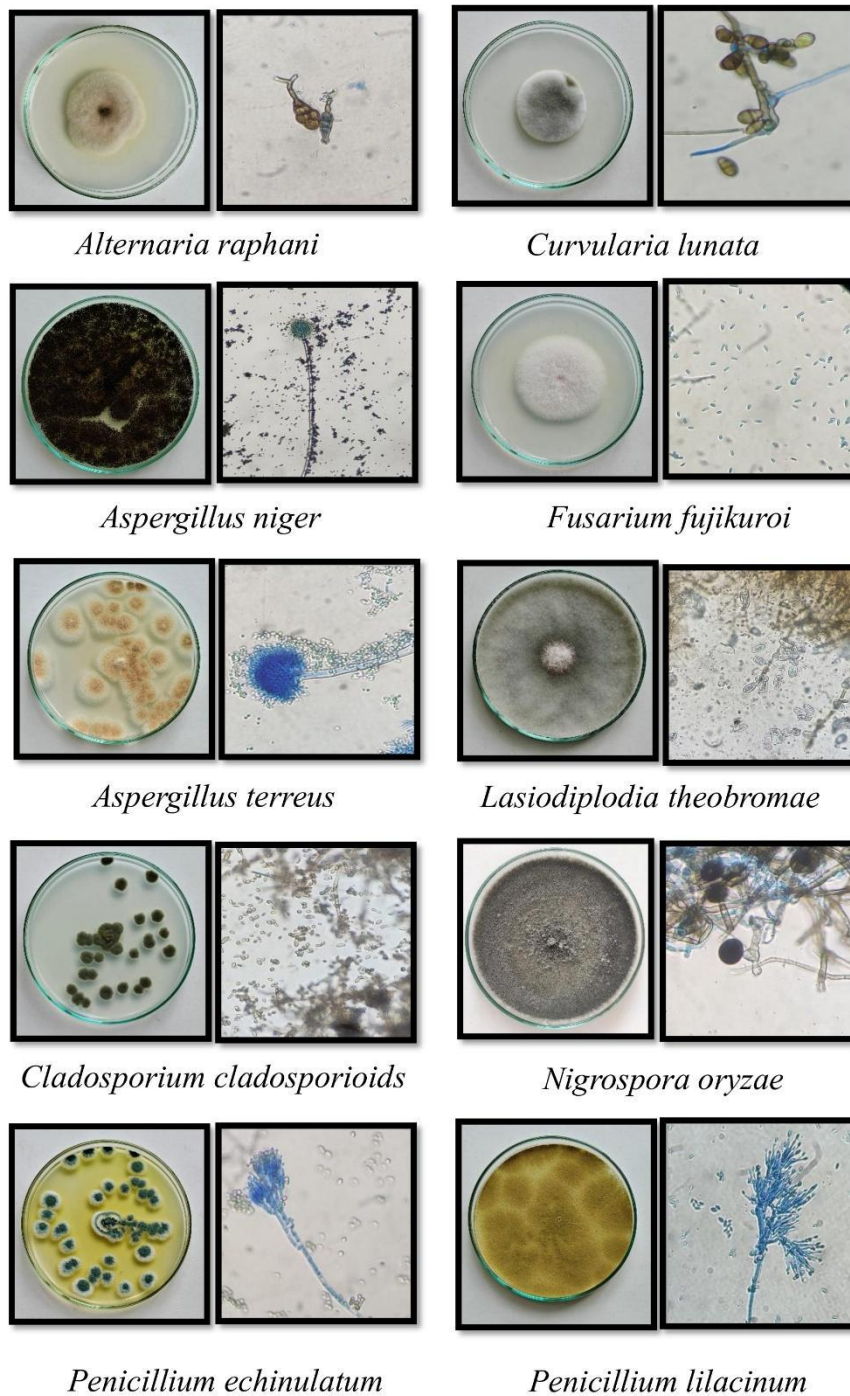


Fig. 1: Pure culture and microphotograph of some fungi

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