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Investigation of Major Storage Fungal Pathogens Associated with Seeds of Some Crops

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Abstract: The storage fungi damage the grains in several ways; they reduce the germination capacity, produce undesirable odor and kernel discoloration, decrease the food value, and also produce toxins that are injurious to the health of consumers. Therefore, this study was designed to investigate the presence, and determine the identity, and incidences of major fungal pathogens associated with crop seeds. Totally fifty-eight seed samples of nine crops were used to investigate the presence and incidence of fungi associated with them in Potato Dextrose Agar (PDA) media. Results of the study revealed that a total of 9 fungi belonging to 8 genera viz. *Penicillium* sp., *Aspergillus flavus*, *Aspergillus niger*, *Bipolaris* sp., *Botrytis* sp., *Alternaria* sp., *Ascochyta* sp., *Fusarium oxysporum*, and *Rhizopus* sp. were isolated from samples. The infection percentage varied from 0-100% in samples of seed multiplication store. Most varieties of crops showed 100% infection followed by 97.5% (HB1307 of barley and Alidoro of wheat), 95% (Kingbird of wheat and RIB13/14 of nug), 90% (Kuncho of teff), 50% (Holetta-1 11/12 of gomenzer), 20% (Ginchi-1 11/12 of nug and Yellow Dodola15/16 of gomenzer), 10% (Shambu 17/18 of oat), and 5% (Shambu 11/12 of oat, S-67 17/18 of gomenzer and Fogera 10/11 of nug) except linseed samples 0%. In general, seed-borne fungi were present in most seed samples of cereals, oils, and legume crops. Some of the identified fungi are potential producers of mycotoxins, thus their presence is important in terms of reduced food safety for humans and animals. In addition, some seed-borne fungi were also the causal agents of diseases of the roots, stems, and leaves of crops. Fungal incidence of seed was highly associated with storage conditions of the independent variables, such as temperature and relative humidity of storage. So, it is suggested that the management of fungal growth, mycotoxin production, and fungal contamination incidence of seed should be investigated and confirmed with additional studies.

Keywords: Crops; Fungal Pathogens; Incidence; Seeds, Seed Borne.

RESEARCH PAPER

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INTRODUCTION

Seeds are the root and foundation for crop production and breeding; also imperatively the strategic wealth for the survival and development of humans. Seed is important for yield gain and quality, moreover, it determine the yield. If the seed is healthy it has been considered an attribute of high quality and one of the most important premises for safe storage [1]. Moreover, seed health plays an important role in the successful cultivation and yield exploitation of crop species. Even though seeds are very important for human being, seed borne pathogens are one of most challenge for seed health. Seed-borne fungal, bacterial, and viral pathogens have some deleterious effects on seeds, such as reducing seed viability, vigor, germination ability, shortening the longevity of conservation, and causing physiological changes. Furthermore, some seed-borne pathogens are also seed-transmitted, which can cause severe diseases in the field after seed movement at a long distance [2]. Not only do sowing contaminated or diseased seeds spread infections, but it can also dramatically lower yields by 15–90% [3].

Some of these fungal pathogens move into the field through the seeds due to their seed-borne nature. Seed-borne diseases caused by fungi are relatively difficult to control as the fungal hyphae get established and become dormant. A seed-associated pathogen present externally, internally, or associated with the seed as a contaminant, may cause abortion, seed rot, seed necrosis, reduction or elimination of germination capacity as well as seedling damage resulting in the

development of disease at later stages of plant growth by systemic or local infection [4, 5].

Seed-borne infections of fungal pathogens are important for contaminate the soil by establishing its inocula permanently [6]. The storage fungi damage the grains in several ways; they reduce the germination capacity, produce undesirable odor and kernel discoloration, decrease the food value, and also produce toxins that are injurious to the health of consumers [7].

A healthy crop can only be grown from healthy seeds. One of the basic strategies to produce certified and non-infected seeds is the identification of seed-borne fungal pathogenic agents in growing fields. For the purpose of checking the health of seeds, it is crucial to identify any fungi, bacteria, or viruses that may cause seed-borne diseases [3]. If infested grain is used as seed, not only would the seed-borne diseases reduce crop yield but also the seed will be a source of inoculum [8]. They are responsible for both pre and post-emergence death of grains, affect seedling vigor, and thus cause some reduction in germination and also variation in plant morphology [9-11]. Again, the contamination of formerly disease-free areas and the introduction of novel diseases are the consequences of seed-borne infections that are most harmful [3].

In Ethiopia, there are limitations of testing the status of seed health. In this study, the technique of seed health testing was applied to monitor and analyze the fungi that infect wheat (*Triticum aestivum*), barley (*Hodeum vulgare*), teff *(Eragrostis tef (Zucc.)* Trotter), oat *(Avena sativa*), faba bean (*Vicia faba*), field pea (*Pisum sativum*), linseed (*Lens culinaris*), gomenzer (*Brassica carinata*) and nug (*Guizotia abyssinica* L.) seeds stored in the seed multiplication store of Holetta Agricultural Research Center. And Potato Dextrose Agar (PDA) used for the experiment test, which is common microbiological growth media from potato infusion and dextrose. Potato Dextrose Agar (PDA) is the most widely used media for growing fungi and bacteria which attack living plants or decaying dead plant matter. Therefore, this study was designed to investigate the presence, and determine the identity, and incidences of major fungal pathogens associated with crop seeds.

MATERIALS AND METHODS

The study was designed to investigate the presence, determine the identity, and incidences of major fungal pathogens associated with some crop seeds, in Holetta Agricultural Research Center seed multiplication at the plant quarantine laboratory of the center in 2022.

The Crop Seeds of Collected Samples

Seeds of different seed classes (a total of 58 samples) were obtained from the seed multiplication store at Holetta Agricultural Research Centre (HARC), Ethiopian Institute of Agricultural Research (EIAR). These samples belonging to seven, eleven, three, one, twelve, six, ten, two, and six varieties of (*Triticum aestivum*), barley (*Hodeum vulgare*), teff (*Eragrostis tef (Zucc.)* Trotter), oat (*Avena sativa*), faba bean (*Vicia faba*), field pea (*Pisum sativum*), linseed (*Lens culinaris*), gomenzer (*Brassica carinata*) and nug (*Guizotia abyssinica* L.) respectively grown in 2021 main season were used in this experiment after six months of storage.

Isolation of Fungi Associated with Sample Crops

Fifty seeds per sample were surface sterilized with 10% Chlorox solution to remove saprophytes for 3 min, followed by three times rinse in sterile distilled water for one minute each. Five surface sterilized seeds were then placed on each Potato Dextrose Agar (PDA-semi-selective) media plate for the growth of most fungi (general purpose media) and incubated for seven days at 25°C. Finally, after eight days of incubation, the seeds on each petri dish were examined under a stereo microscope for the observation of the presence of associated fungi, mycelia growth, and fungal isolation. And pure cultures of different out-growing fungi were obtained by transferring fungal colonies to new PDA plates using a sterile loop and incubating the plates for seven days at 25°C. The pure culture of each isolate was then stored at 4°C in vials containing 2.5 ml of sterile distilled water for further use [12]. The number of infected seeds was counted and expressed in percentage and the proportion of samples that yielded isolates was determined as follows [12]:

$$\textbf{Frequency of occurrence (IN \%)} = \frac{\text{Number of seeds on which fungal species occurs}}{\text{Total number of seeds plated}} \text{ X } 100$$

$$\textbf{Isolation Frequency (IF \%)} = \frac{\text{Number of samples of occurrence of fungi species}}{\text{Total number of samples}} \text{ X } 100$$

Identification and Characterization of Fungal Species

From the isolates, pure cultures were obtained after repeated sub-culturing of fungi appearing on seeds on Potato Dextrose Agar (PDA) plates. The fungi were identified based on spore morphology and colony characteristics using a stereoscopic microscope. A list of morphological characters of taxonomic importance such as spore size, shape, septation, color, and their arrangement on the conidiophores, characters of the mycelium were compiled for each fungus. Identification of the fungus was performed using all characteristics observed and identification reference manuals [13, 14].

Data Analysis

Data on frequency and incidence of seed infection by fungal species for samples collected from HARC storage was subjected to simple descriptive analysis and data were expressed by using the percentage.

RESULTS AND DISCUSSION

Fungi Contamination Frequency and Association with the Sample Crops

From this study, five fungi were isolated from both wheat and barley seeds. Fungi isolated from both wheat and barley seeds are presented (Table 1). *Alternaria* sp., *Aspergillus flavus*, *Aspergillus niger*, *Fusarium oxysporum*, and *Bipolaris* sp. were found in wheat and barley seeds. Four fungal species such as *Alternaria* sp., *Aspergillus flavus*, *Aspergillus niger*, and *Bipolaris* sp were found to be associated with teff seeds. *Aspergillus flavus*, *Aspergillus niger*, *Alternaria* sp., and *Fusarium oxysporum* were also from oat crops. *Botrytis* sp., *Penicillium* sp., *Ascochyta* sp., and *Rhizopus* sp. were isolated from faba bean, whereas, *Alternaria* sp., *Aspergillus flavus*, *Botrytis* sp., *Penicillium* sp., *Ascochyta* sp., *Fusarium oxysporum* and *Rhizopus* sp., from field pea crops. Four fungus species such as *Aspergillus flavus*, *Alternaria* sp., *Penicillium* sp., and *Fusarium oxysporum* were isolated from nug, and *Aspergillus flavus*, *Alternaria* sp., and *Fusarium oxysporum* were isolated from gomenzer. None of the fungi were isolated from the linseed sample (Table 1).

The result revealed the contamination of crop seeds by different fungal species with different frequencies. The most predominant fungus isolated was *Aspergillus flavus* (62.07%) followed by *Alternaria* sp. (37.93%), *Botrytis* sp., and *Ascochyta* sp. were equally dominant (31.04%), *Aspergillus niger*, *Fusarium oxysporum*. *Rhizopus* sp. *Bipolaris* sp., and *Penicillium* sp. (25.86%, 17.24%, 12.07%, 8.62%, and 5.17%), were found, respectively (Table 2).

To establish an effective control and management system, identifying the disease-causing agents is a preliminary necessity [15]. To identify soil borne diseases different characteristics of the soil borne pathogens have been suggested. Different scholars suggested that the colonies of *Aspergillus flavus* is characterized by yellow to dark yellowish-green pigments, consisting of a dense felt of conidiophores or mature vesicles bearing phialides over their entire surface; whereas, colonies of other species of *Aspergillus* are orange green in color surrounded by a clear white zone; growth is rapid covering the entire plate within 120 hours of incubation [16-18], The current result (Figure 1) is the same with previous studies [19-22] suggested that *A. flavus* colonies are being initially yellow, turning to yellow-green or olive green with age and appearing dark green with a smooth shape and having rapid growth. In this study, *Aspergillus flavus* was one of the dominant species isolated from the collected samples. The result agrees with a previous study by Zafar *et al*., [23] reported that the most predominant fungi isolated were *A. flavus* (20%) followed by *Penicillium* spp. (18%), *Aspergillus niger* (13%), *Alternaria alternata* (11%), and *Rhizopus* sp. (7%).

Alternaria sp. is characterized by a dark grey colony but may also be white, olive green, brown, or almost black, and conidiophores are dark to olive brown and smooth, arising singly or unbranched. Its distinctive character is light brown, tapered to a beak, with conidia with transverse and longitudinal septa [22, 24]. The current study also confirmed the production of light brown, tapered-to-beak, conidia with transverse and longitudinal septa and having quick growth (Figure 1). *Alternaria* sp. and *Botrytis* sp. were other dominant species of fungi isolated from the samples of crop seeds

Similar results were reported in a previous study while testing the wheat germplasm conserved in the gene bank. The predominant fungi isolated were *Alternaria*, *Rhizopus*, *Penicillium*, *Aspergillus*, *Bipolaris*, *Cladosporium*, *Fusarium*, *Cladosporium*, and *Trichothecium* [1, 22].

Agreed with the presence of *Fusarium moniliforme*, *Alternaria* sp., *Bipolaris* sp., *Fusarium oxysporum*, *Aspergillus niger*, *Aspergillus flavus*, *Alternaria* sp., *Penicillium* sp., and *Trichoderma* sp. associated with most crop seeds both in storage and in the field have been reported earlier [22, 23, 25].

The current result revealed that most of the samples were infected by several species of fungi in the crop seed varieties tested except linseed samples. Some fungi such as *Alternaria*, *Aspergillus*, *Bipolaris*, and *Fusarium* produced different fungal toxins, which could make changes in the chemical ingredients inside the seeds, reduce the nutritive value and viability of seeds, and even cause seed death. Several fungi isolated in the present study are known to produce mycotoxins which are harmful to human health. Mycotoxins can cause severe damage to the liver, kidney, and nervous system of man even in low dosages [26]. *Fusarium* and *Aspergillus* species are common fungal contaminants of seeds and also produce mycotoxins [27, 28]. *Aspergillus flavus* produces aflatoxin B1, B2, G1, and G2 which are carcinogenic and produce liver cancer [29, 30]. *F. oxysporum* produces Zeralenone α and β causing haemorrhage and necrosis in bone marrow [31]. And that renders the seed unacceptable due to high toxicity for human or animal consumption [32].

In addition, some seed-borne fungi are also the causal agents of diseases of the roots, stems, and leaves of crops. The diseases transmitted by seeds increased difficulty in disease control and a decline in yield and quality. The seed-borne pathogenic fungi keep long-term survival in seeds when the seeds are conserved in storage under conditions of low temperature and relative

humidity, which could hurt germplasm viability and genetic integrity and can cause a potential threat to agricultural production when the seed is planted and propagated [1]. Moreover, fungal incidence was highly associated with two of the independent variables, namely, temperature and relative humidity of storage [33]. Therefore, seed health testing is vital for the management of seed-borne pathogens in the preserved seeds. And there is a need for proper storage of seeds to minimize fungal infection and mycotoxin production during storage and provide disease-free seeds for crop production and human consumption.

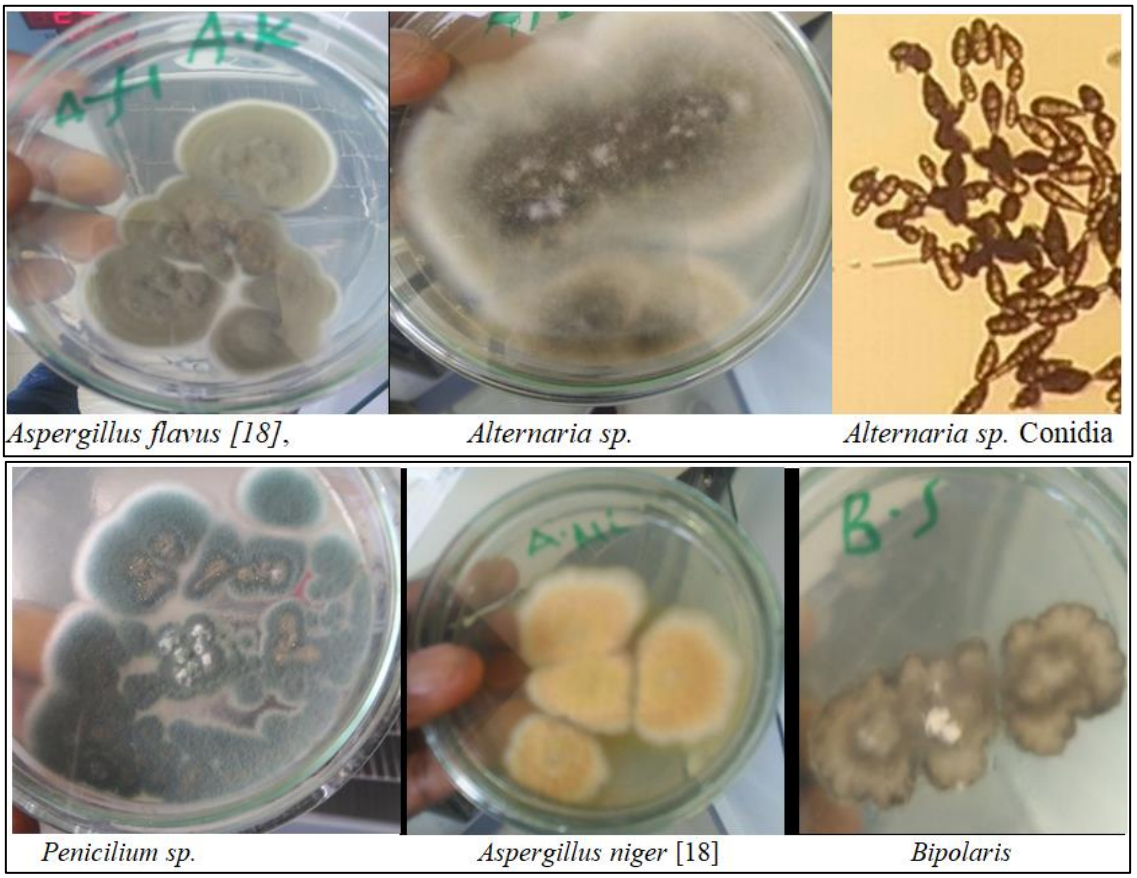

Figure 1: Some of the species of fungi isolated from samples from HARC seed store

Table 1: Isolation frequency of fungi from samples of crops

Isolation Frequency (%)											
Crop	**Variety**	**Seed class**	**Afl**	**Anig**	**Alt**	**Bipo**	**Botr**	**Foxy**	**Peni**	**Rhiz**	**Asc**
Barley	Iboni	breeder	100	100	100	0	0	100	0	0	0
		prebasic	100	100	100	100	0	100	0	0	0
	Holker	breeder	100	100	0	0	0	0	0	0	0
		prebasic	100	100	100	100	0	100	0	0	0
	HB1307	breeder	100	0	100	0	0	0	0	0	0
		prebasic	100	100	100	100	0	0	0	0	0
	HB1966	breeder	100	0	100	0	0	100	0	0	0
	HB1963	breeder	100	100	100	0	0	0	0	0	0
	EH1493	breeder	100	0	100	0	0	0	0	0	0
	EH1847	breeder	100	0	100	0	0	0	0	0	0
	CI4198	breeder	100	0	100	0	0	0	0	0	0
Wheat	Kingbird	breeder	100	100	100	0	0	100	0	0	0
	Alidoro	breeder	100	100	0	0	0	0	0	0	0
		prebasic	100	0	100	100	0	0	0	0	0
	Lemu	breeder	100	100	100	0	0	0	0	0	0
		prebasic	100	100	100	0	0	0	0	0	0
	Tay	prebasic	100	0	100	0	0	0	0	0	0
	Danda'a	basic	100	100	100	0	0	100	0	0	0
Teff	Degem	prebasic	100	100	0	100	0	0	0	0	0

Isolation Frequency (%)											
Crop	**Variety**	**Seed class**	**Afl**	**Anig**	**Alt**	**Bipo**	**Botr**	**Foxy**	**Peni**	**Rhiz**	**Asc**
	Kuncho	prebasic	100	100	0	0	0	0	0	0	0
	Kora	prebasic	100	100	100	0	0	0	0	0	0
fababean	Didia	breeder	0	0	0	0	100	0	0	0	100
	Wolki	breeder	0	0	0	0	100	0	0	0	100
		prebasic	0	0	0	0	100	0	0	0	100
	Dosha	breeder	0	0	0	0	100	0	0	0	100
		prebasic	0	0	0	0	100	0	0	0	100
	Chalew	breeder	0	0	0	0	100	0	0	0	100
	Gebelcho	prebasic	0	0	0	0	100	0	0	100	100
	Tumsa	breeder	0	0	0	0	100	0	0	0	100
	Gora	breeder	0	0	0	0	100	0	0	0	100
	Moti	breeder	0	0	0	0	100	0	100	100	100
	Hachalu	breeder	0	0	0	0	100	0	0	100	100
	Degaga	breeder	0	0	0	0	100	0	0	0	100
fieldpea	Tegegnech	breeder	100	0	0	0	100	0	0	0	100
		prebasic	100	0	100	0	100	0	0	100	100
	Burkitu	breeder	0	0	0	0	100	0	100	100	100
		prebasic	100	0	0	0	100	0	0	100	100
	Jeldu	breeder	100	0	0	0	100	100	0	100	100
	Bursa	prebasic	100	0	0	0	100	0	0	0	100
Oat	CI8237	basic	100	100	100	0	0	100	0	0	0
Nug	Pb0101	prebasic	100	0	100	0	0	0	0	0	0
	Shambu 17/18	breeder	100	0	0	0	0	0	0	0	0
	Shambu 11/12	breeder	100	0	0	0	0	0	0	0	0
	RIB13/14	breeder	100	0	100	0	0	100	100	0	0
	Fogera 10/11	breeder	100	0	0	0	0	0	0	0	0
	Ginchi-1 11/12	breeder	100	0	0	0	0	0	0	0	0
Linseed	Chilalo 16/17	breeder	0	0	0	0	0	0	0	0	0
	Belay-96	breeder	0	0	0	0	0	0	0	0	0
	Berene	breeder	0	0	0	0	0	0	0	0	0
	Tolle 15/16	breeder	0	0	0	0	0	0	0	0	0
	Kulumsa 15/16	breeder	0	0	0	0	0	0	0	0	0
	Kassa-2 13/14	breeder	0	0	0	0	0	0	0	0	0
	Jeldu 14/15	breeder	0	0	0	0	0	0	0	0	0
	Bekoji 14/15	breeder	0	0	0	0	0	0	0	0	0
	CI-1652 17/18	breeder	0	0	0	0	0	0	0	0	0
gomenzer	S-67 17/18	breeder	100	0	0	0	0	0	0	0	0
	Yellow Dodola15/16	breeder	100	0	0	0	0	0	0	0	0
	Holetta-1 11/12	breeder	100	0	100	0	0	100	0	0	0

Afl = Aspergillus flavus, Anig = Aspergillus niger, Alt = Alternaria sp., Bipo = Bipolaris sp., Botr = Botrytis sp., Foxy = Fusarium oxysporum, Peni = Penicillium sp., Rhiz = Rhizosporium sp., Asc = Ascochyta sp.

Fungal Incidence of Sample Crops

The variation regarding the percentage of infection of different fungal species was observed for samples of crop seeds of HARC storage (Table 2). Maximum fungal infection (100%) was observed in most varieties followed by 97.5% (HB1307 of barley and Alidoro of wheat), 95% (Kingbird of wheat and RIB13/14 of nug), 90% (Kuncho of teff), 50% (Holetta-1 11/12 of gomenzer), 20% (Ginchi-1 11/12 of nug and Yellow Dodola15/16 of gomenzer), 10% (Shambu 17/18 of oat), and 5% (Shambu 11/12 of oat, S-67 17/18 of gomenzer and Fogera 10/11 of nug) except linseed variety with 0% fungal infection observed. Infection percentage varied from 0-100% in seed storage of the crops HARC (EIAR). Maximum fungal infection (100%) was observed in barley, wheat, teff, oat, faba bean, nug, and field pea varieties of different seed classes (Table 2).

Moreover, contamination of wheat grains by fungal species at different locations and storage times with different frequencies was reported and the highest fungal incidence (98.62%) was recorded after six months of storage of wheat grain [33]. Similarly, as reported by Asela and Worku [20], the infection percentage varied from 5-100 %. Also agreed with the study of Zafar *et al*., [23], the infection percentage varied from 10-100% in all the wheat accessions tested. There is a need for proper

storage of seeds to minimize fungal infection and mycotoxin production during storage and provide disease free seeds for crop production and human consumption.

Table 2: Frequency of occurrence of seed-associated fungi isolated from samples of crops

Incidence (%)												
Crop	**Variety**	**Seed class**	**Afl**	**Anig**	**Alt**	**Bipo**	**Botr**	**Foxy**	**Peni**	**Rhiz**	**Asc**	**Total**
barley	Iboni	breeder	80	25	5	0	0	5	0	0	0	100
		prebasic	55	55	15	10	0	5	0	0	0	100
	Holker	breeder	100	15	0	0	0	0	0	0	0	100
		prebasic	75	20	10	20	0	5	0	0	0	100
	HB1307	breeder	90	0	5	0	0	0	0	0	0	95
		prebasic	55	25	15	30	0	0	0	0	0	100
	HB1966	breeder	100	0	5	0	0	5	0	0	0	100
	HB1963	breeder	85	15	15	0	0	0	0	0	0	100
	EH1493	breeder	100	0	10	0	0	0	0	0	0	100
	EH1847	breeder	100	0	15	0	0	0	0	0	0	100
	CI4198	breeder	100	0	10	0	0	0	0	0	0	100
wheat	Kingbird	breeder	55	5	20	0	0	15	0	0	0	95
	Alidoro	breeder	80	15	0	0	0	0	0	0	0	95
		prebasic	90	0	5	5	0	0	0	0	0	100
	Lemu	breeder	90	10	5	0	0	0	0	0	0	100
		prebasic	85	15	5	0	0	0	0	0	0	100
	Tay	prebasic	95	0	5	0	0	0	0	0	0	100
	Danda'a	basic	75	20	5	0	0	5	0	0	0	100
teff	Degem	prebasic	60	10	0	30	0	0	0	0	0	100
	Kuncho	prebasic	75	15	0	0	0	0	0	0	0	90
	Kora	prebasic	70	35	20	0	0	0	0	0	0	100
fababean	Didia	breeder	0	0	0	0	100	0	0	0	100	100
	Wolki	breeder	0	0	0	0	100	0	0	0	100	100
		prebasic	0	0	0	0	100	0	0	0	100	100
	Dosha	breeder	0	0	0	0	100	0	0	0	100	100
		prebasic	0	0	0	0	100	0	0	0	100	100
	Chalew	breeder	0	0	0	0	100	0	0	0	100	100
	Gebelcho	prebasic	0	0	0	0	100	0	0	15	90	100
	Tumsa	breeder	0	0	0	0	100	0	0	0	100	100
	Gora	breeder	0	0	0	0	100	0	0	0	100	100
	Moti	breeder	0	0	0	0	90	0	15	10	80	100
	Hachalu	breeder	0	0	0	0	100	0	0	15	100	100
	Degaga	breeder	0	0	0	0	100	0	0	0	100	100
fieldpea	Tegegnech	breeder	15	0	0	0	85	0	0	0	85	100
		prebasic	5	0	5	0	95	0	0	30	100	100
	Burkitu	breeder	0	0	0	0	80	0	15	20	80	100
		prebasic	15	0	0	0	70	0	0	30	90	100
	Jeldu	breeder	30	0	0	0	60	15	0	35	75	100
	Bursa	prebasic	15	0	0	0	65	0	0	0	85	100
oat	CI8237	basic	45	5	65	0	0	5	0	0	0	100
nug	Pb0101	prebasic	85	0	15	0	0	0	0	0	0	100
	Shambu 17/18	breeder	10	0	0	0	0	0	0	0	0	10
	Shambu 11/12	breeder	5	0	0	0	0	0	0	0	0	5
	RIB13/14	breeder	65	0	10	0	0	15	5	0	0	95
	Fogera 10/11	breeder	5	0	0	0	0	0	0	0	0	5
	Ginchi-1 11/12	breeder	20	0	0	0	0	0	0	0	0	20
linseed	Chilalo 16/17	breeder	0	0	0	0	0	0	0	0	0	0
	Belay-96	breeder	0	0	0	0	0	0	0	0	0	0
	Berene	breeder	0	0	0	0	0	0	0	0	0	0
	Tolle 15/16	breeder	0	0	0	0	0	0	0	0	0	0
	Kulumsa 15/16	breeder	0	0	0	0	0	0	0	0	0	0
	Kassa-2 13/14	breeder	0	0	0	0	0	0	0	0	0	0

Incidence (%)												
Crop	**Variety**	**Seed class**	**Afl**	**Anig**	**Alt**	**Bipo**	**Botr**	**Foxy**	**Peni**	**Rhiz**	**Asc**	**Total**
	Jeldu 14/15	breeder	0	0	0	0	0	0	0	0	0	0
	Bekoji 14/15	breeder	0	0	0	0	0	0	0	0	0	0
	CI-1652 17/18	breeder	0	0	0	0	0	0	0	0	0	0
gomenzer	S-67 17/18	breeder	5	0	0	0	0	0	0	0	0	5
	Yellow Dodola15/16	breeder	20	0	0	0	0	0	0	0	0	20
	Holetta-1 11/12	breeder	15	0	20	0	0	15	0	0	0	50

Afl = Aspergillus flavus, Anig = Aspergillus niger, Alt = Alternaria sp., Bipo = Bipolaris sp., Botr = Botrytis sp., Foxy = Fusarium oxysporum, peni = Penicillium sp., Rhiz = Rhizosporium sp., Asc = Ascochyta sp.

CONCLUSSION AND RECCOMMENDATION

The present work was carried out to investigate the presence and determine the identity and incidences of major fungal pathogens associated with crop seeds. In this study a total of 9 fungi belonging to 8 genera viz. *Aspergillus flavus*, *Aspergillus niger*, *Alternaria* sp., *Bipolaris* sp., *Botrytis* sp., *Fusarium oxysporum*, *Penicillium* sp., *Rhizopus* sp., and *Ascochyta* sp. were isolated from samples of the crops. None of the fungi were isolated from linseed. The most predominant fungus isolated was *Aspergillus flavus* (62.07%) followed by *Alternaria* sp. (37.93%). Results of the current study revealed heavy contamination of seeds by *Aspergillus flavus*. The infection percentage of seeds varied from 0-100 % in the seed multiplication store. Most varieties of crops showed 100% infection of different seed classes and the linseed variety showed 0% fungal infection.

Generally, seed-borne pathogens were present in most seed samples of cereals, oils, and legume crops of different seed classes. That most of the samples were infected by several species of fungi in the crop seed varieties tested except linseed samples. Some of the identified fungi are potential producers of mycotoxins, thus their presence is important in terms of reduced food safety for humans and animals. In addition, some seed-borne fungi were also the causal agents of diseases of the roots, stems, and leaves of crops. Therefore, an early and accurate diagnosis and pathogen surveillance will provide time for the development and application of disease management strategies. Finally, looking at the alarming rate of crop production in the country to feed the ever-increasing population, this study suggests that research on the biology, ecology, and management of major fungi associated with the crops should be given due attention in the country.

Author Contributions:

Asela Kesho, Yitagesu Tadesse, Girma Ababa, and Dereje Amare wrote the manuscript to its final version, read and approved the final version of the manuscript.

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