

Molecular characterization of some fungi isolated from broiler chicken farms

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ABSTRACT

The study was performed on 225 chicken (72 diseased and 153 freshly dead ones) from different 45 commercial broiler farms (1- 30 days old) at Dakahlia Governorate for mycotic infection. Samples were taken from these chickens (lung; air sac; crop; liver and brain from each chicken) after clinical and postmortem examination for mycological examination. The results revealed that, fungi were isolated from 503 positive samples (44.7%); represented as 119 positive samples (10.6%) from diseased chickens and 384 positive samples (34.1 %) from freshly dead ones.651 fungal isolates (moulds and yeasts) were isolated from 1125 samples, where 219(33.6%) were isolated from lung samples followed by 199(30.6%); 119(18.3%); 91(14.0%) and 23(3.5%) from air sac, liver, crop and brain samples respectively. Moreover, A. fumigatus was the most isolated one 141(21.7%) followed by A. flavus 126(19.4%); A. niger 111(17.1%); Rhizopus spp. 67(10.3%); C. albicans 58(8.9%); Mucor spp. 42(6.5%); Penicillium spp. 32(4.9%); A. terreus 20(3.1%); Fusarium spp.19 (2.9%); C. krusei 13(2.0%); C. tropicalis 9(1.4%); A. candidus 9(1.4%) and finally A. ochraceus 4(0.6%). PCR using fungus-specific universal primer pairs (ITS1 and ITS4) was used for identification and genotypic characters of Aspergillus species (A. fumigatus; A. flavus and A. niger). They were able to successfully amplify the ITS1-5.8S rDNA region of all tested Aspergillus isolates, providing a single PCR product of about 600 bp for all tested isolates PCR using fungus-specific universal primer pairs (ITS and RPS) was used for identification and genotypic characters of C. providing a single PCR product of about 109 bp .Sequence of the internal transcribed spacer 1 reigon (ITS-1) of isolated A. flavus Gene Bank accession number for studied nucleotide sequence (Bankit 1867303) is KM 983253. The sequences obtained for ITS-1 region were more than 98% identical to the corresponding GenBank sequences (accession no. DQ467968.1; KC994648.1; LN482516.1 and KP689246.1). Sequence of the internal transcribed spacer 1 region (ITS-1) of isolated C. albicans. Gene Bank accession number for studied nucleotide sequence (Bankit 1867955) is KM 983254. The sequences obtained for ITS-1 region obtained were more than 95% identical to the corresponding GenBank (accession no. M87288.1; gb|S71769.1|S71769; emb (AL033396.1) and AP006852.1).

Key wards: C. albicans, A. flavus, A. ochraceus

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1. INTRODUCTION

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morbidity and mortality, especially in young birds and cause stunted growth; diarrhea; and fatal encephalitis (Singh et al., 2012). Risk factors, which predisposes to fungal infection and aggravate disease include malnutrition, vitamin D deficiency, poor hygiene, prolonged use of antibiotic suppressing normal bacterial flora, stress an immunosuppressive disease (Velasko, 2000). Aspergillosis and Candidiasis are the most important fungal diseases of poultry (Dhama et al., 2013a). Aspergillosis is a necrotizing and granulomatous cavity disease of the lungs with hematogenous spread caused mainly by Aspergillus fumigatus, most pathogenic fungi affecting poultry (Redig, 2005; Ganguly et al., 2011 and Dhama et al., 2013b). A. fumigatus infection occurs more frequently in poultry, as the spores of this pathogen species are smaller than those of other Aspergillus spp. (Dhama et al., 2013b). Other Aspergillus spp. that may affect birds adversely are A. flavus, A. terreus, A. glaucus, A. nidulans and A. niger (Beemaert et al., 2010and Dhama et al., 2013b). Affected birds may show gasping, dyspnea, fever, foetid yellowish diarrhea, rapid loss of condition with convulsions together with anemia and mortality range between 5-50%. Survivors often develop chronic disease due to pulmonary insufficiency or neurological fungal metastasis and may become lethargic and stunted (Atasever and Gumussoy, 2004; Beemaert et al., 2010 and Dhama et al., 2013b). Candidiasis is a fungal disease caused by yeasts of the genus Candida having nearly 200 species, among them, six are most frequently isolated. While C. albicans is the most abundant and significant species, C. tropicalis, С. glabrata, C. parapsilosis, C. krusei and C. lusitaniae have also been implicated as causative agents (Tiwari et al., 2011). C. an asporogenous albicans is and pseudomycelial dimorphic yeast having fermentation capability. It grows on ordinary media over a wide range of pH and temperature. Budding yeast forms (blastospores) are 3-4 um on epithelial surfaces whereas branching septate hyphae or pseudohyphae are 3-5 um diameter in deeper tissues. It can utilize ammonia but not nitrate; nitrogen and most strains need growth factor biotin to be supplemented for their growth (Novak et al., 2003). The identification of fungi by traditional microscopic, cultural and metabolic characteristics remains commonly used.

The species level identification is very complex. Macro-morphological identification is done based on conidial and mycelial color, colony diameter, colony reverse color, production of exudates and pigments. Microscopic soluble identification is mainly dependent on seriation, shape and size of vesicle, conidia and stipe morphology (Chakranarayan and Pati, 2013). These methods are laborious, time-consuming (may take days to weeks), require significant technological expertise and sometimes unsuccessful because of the atypical features of some isolates. Therefore, Molecular approaches have been developed to provide more rapid and accurate identification of pathogenic fungi comparing to traditional phenotypic methods (Makimura et al., 1994 and Yamakami et al., 1996). The internal transcribed spaces 1 and 2 regions (ITS 1 and ITS 2) have been used extensively for molecular analysis of fungi. length

2. MATERIAL AND METHODS

2.1. Samples collection

A total of 225 chicken were collected from different 45 commercial broiler farms (1-30 days old) at Dakahlia Governorate were inspected for mycotic infection. Samples were taken from 72 diseased chicken and 153 freshly dead ones (lung; air sac; crop; liver and brain from each chicken) after clinical and postmortem examination. Each examined organ was taken alone in sterile plastic bags, kept in icebox and transferred with minimum delay to the laboratory for mycological examination.

2.2. Mycological culture examination

The surface of organs were seared by hot spatula, then a sterilized loopful was introduced through seared portion of the organ. Loopfuls were inoculated on modified Sabouraud's dextrose broth under aseptic condition and incubated aerobically at 37° c for 3-days. Two Loopfuls were taken, the first was streaked on the following media: Sabouraud's dextrose agar media: Malt Extract agar and Rose Bengal agar and incubated for 10 days at 37° c. and fungal growth colonies were picked up and kept in Sabouraud dextrose agar slopes and Malt Extract slope ager then incubated at 22-25°C for 5-7 days. The purified colonies were identified by careful observation and measurements of the macroscopically microscopically and characteristics of the mould colonies according to Jand and Singh (1995); David et al., (2007) and Markey et al., (2013). The second was streaked on Sabouraud's dextrose agar media and incubated for 48h at 30°C. The yeast growth colonies were sub- cultured onto the following media: Eosin methylene blue agar; Rose Bengal agar and CHROM Candida agar and incubated at 30°C for 48 h. The yeast growth colonies were picked up and kept in Sabouraud dextrose agar slopes then incubated at 22-25°C for 5-7 days. The purified colonies were identified by careful observation and measurements of the macroscopically; microscopically characteristics of the yeast colonies and biochemically according to Lodder and Krieger Van Rij (1970); David et al., (2007) and Markey et al., (2013).

2.3. Genotypic methods of identification:

PCR was applied by using fungus-specific universal primer pairs (ITS1 and ITS4) was used for identification and genotypic characters of15 random isolated Aspergillus species (*A. fumigatus; A. flavus and A. niger*) and (ITS and RPS) for 5 random isolated *C. albicans*, following QIAamp DNeasy Plant Mini kit instructions (Catalogue no. M501DP100), Emerald Amp GT PCR master mix (Takara) with Code No. RR310Aand 1,5% agarose gel electrophoreses (Sambrook et al., 1989).

3. RESULTS

3.1. Clinical and postmortem examinations:

The clinical examination of studied chicken showed clinical manifestations as dyspnea,

gasping, accelerated breathing, depression, emaciation, ruffled feathers, over distention of crops with watery stink smelling discharge from the mouth, profuse watery diarrhea, blindness, torticollis, lack of equilibrium, and stunting growth. Meanwhile, the postmortem lesions of diseased and freshly dead chicken from which fungi (moulds and yeasts) were isolated showed congestion of the lungs, air saculitis, ulcer formation in the crop with excessive secretion covering the inner surface of the crop, mucous enteritis with sloughing of the intestinal mucosa and some of them showed greenish gray lesions and caseated nodules of 1-2mm thickness distributed in lungs, livers, proventriculus, gizzard intestine and abdomen.

3.2. Isolation and identification of fungi (moulds and yeasts) isolates

Prevalence of positive samples for fungi isolation from examined chickens broiler farms

The results of fungi (moulds and yeasts) isolation (Table1) showed that, 503 out of 1125 samples (44.7%) were positive for fungi isolation, where 119 positive samples (10.6%) from diseased chickens and 384 positive samples (34.1 %) from freshly dead ones. Moreover, the highest positive samples in diseased and freshly dead chickens were in both lung (43&128) and air sac (35&119) samples. Most samples showed mixed fungi (moulds and yeasts). Total number and percentage of fungi isolated from examined chickens broiler samples. The results of mycological examination (Table, 2) revealed that, a total number of 651 fungal isolates (moulds and yeasts) were isolated from 1125 samples, where 219(33.6%) were isolated from lung followed 199(30.6%); samples by 119(18.3%); 91(14.0%) and 23(3.5%) from air sac, liver, crop and brain samples respectively. Moreover, A. fumigatus was the most isolated one 141(21.7%) followed by A. flavus 126(19.4%); A. niger 111(17.1%); Rhizopus spp. 67(10.3%); C. albicans 58(8.9%); Mucor spp. 42(6.5%);

Penicillium spp. 32(4.9%); A. terreus 20(3.1%); Fusarium spp.19 (2.9%); C. krusei 13(2.0%); C. tropicalis 9(1.4%); A. candidus 9(1.4%) and finally A. ochraceus 4(0.6%) 3.2.1.2. Total number and percentage of fungal species isolated from examined organs. Out of 651 fungi isolated from examined organs, 411(63.1%) Aspergillus species were isolated mostly from lung samples 162 (39.4%), followed by 142(34.6%), 64(15.6%), 37(9.0%) and 6(1.5%) from air sacs, liver, crops and brain samples respectively. Other mould species isolated were160 (24.6%) mostly from air sac samples55 (34.4%) followed by 54(33.8%); 22(13.8%); 17(10.6%) and 12(7.5%) from lung, liver, brain and crop samples respectively. Moreover, Candida species isolated were 80 (12.3%) mostly from crop samples 42(52.5%) followed by 33(41.3%); 3 (3.7%) and 2 (2.5%) from liver, lung and air sac samples respectively meanwhile, they could not isolated from brain samples (Table, 2). Total number and percentage of fungal species isolated from lungs; air sacs; crops; liver and brain of studied chickens were tabulated in (Tables 3-7).

3.3. Identification of fungi isolates using polymerase chain reaction (PCR) (Genotypic characters)

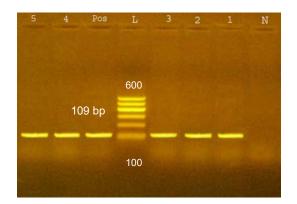
Genotypic characters of Aspergillus species (A. fumigatus; A. flavus and A. niger) PCR using fungus-specific universal primer pairs (ITS1 and ITS4) was used for

identification and genotypic characters of Aspergillus species (A. fumigatus; A. flavus

Fig. (1). c. albicans I^{ts1} L.100bp – 600bpDNA ladder, N. negative control, Pos. positive control (at 109bp), Lane 1 to 5 positive C. albicanis and A. niger). They were able to successfully amplify the ITS1–5.8S rDNA region of all tested Aspergillus isolates, providing a single PCR product of about 600 bp for alltested isolates as shown in photo (1, 2 & 3).

Genotypic characters of C. albicans. PCR using fungus-specific universal primer pairs (ITS and RPS) was used for identification and genotypic characters of C. albicans. They were able to successfully amplify the ITS1-5.8S rDNA region of all tested C. albicans isolates, providing a single PCR product of about 109 bp for all tested isolates as shown in fig (4). Sequence of the internal transcribed spacer 1 reigon (ITS-1) of isolated A.flavus Gene Bank accession number for studied nucleotide sequence (Bankit 1867303) is KM 983253. The sequences obtained for ITS-1 reigon were more than 98% identical to the corresponding GenBank sequences (accession no. DO467968.1; KC994648.1; LN482516.1 and KP689246.1).

Sequence of the internal transcribed spacer 1 region (ITS-1) of isolated C.albicans Gene Bank accession number for studied nucleotide sequence (Bankit 1867955) is KM 983254. The sequences obtained for ITS-1 region obtained were more than 95% identical to the corresponding GenBank (accession no. M87288.1; gb|S71769.1|S71769; emb (AL033396.1) and AP006852.1). Finally, Aspergillus species mainly A. fumigatus; A. flavus; A. niger and C. albicans were the most important causes of mould infection and candidiasis in broiler chicken farms.



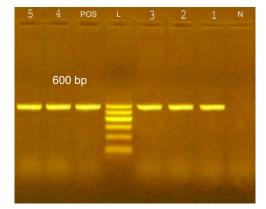
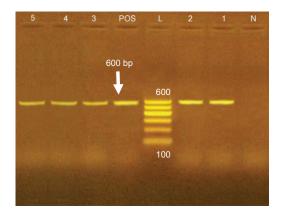


Fig. (2) A. Flavus ITS1L. 100 -600bp DNA Ladder POS. positive control (at 600bp) N. negative control. L1 to 5 positive A.Flavus

5 4 3 POS L 2 1 N 600 bp ↓ 600 100

Fig (3). A. Fumigatous ITS1, L. 100-600bp DNA Ladder, P OS. Positive control N. negative control, L1 to 5 positive A. Fumigatous

Fig (4) A. Niger I^{TS} L.100-600bp DNA Ladder, POS. positive control at 600bp N. negative control, L1 to 5 positive A. Niger



Chicken case	Number	Number of positive samples					Positive percentage			
	of	Lung	Air	Crop	Liver	Brain	Total	% ¹	% ²	% ³
	sample		sacs							
Diseased (72)	360	43	35	17	19	5	119	33.1	23.7	10.6
Freshly dead (153)	765	128	119	54	70	13	384	50.2	76.3	34.1
TOTAL(225)	1125	171	154	71	89	18	503	44.7	100.0	44.7

Table (1): Total number and Percentage of positive samples for fungi isolation from studied chickens

¹Percentage in relation to total number of cases in each row. ² Percentage in relation to total number of positive samples (503). ³ Percentage in relation to total number of collected samples (1125)

4. DISCUSSION

The mycotic infection of chicken is one of the most serious problems that affect chicken causing high economic losses due to not only high morbidity and mortality in young chicken but also they are the leading cause of immunosuppression in birds, lowering their resistance level to various viral and bacterial diseases and increased mortality. On the other hand, an increase in the incidence of the mycotic diseases can be expected due to the wide use of antibiotics preparations in the treatment of many diseases as well as the extensive use of antibiotic as feed additives, which enhance mycotic complications. Therefore, this study was planned for mycological examination in broiler chicken farms. The results of clinical and postmortem examinations of studied chicken were similar to that reported by (Sajid et al., 2006 ; Zafra et al., 2008; Cacciuttolo et al., 2009; Arne et al.,2011; Dhama et al.,2011; Dhama et al.,2013 ; Amin et al., 2014 ; Musa et al.,2014 and Salem and Ali, 2014). The results of fungi isolation, (Table, 1) revealed that 503 samples (44.7%) out of 1560 samples were positive for fungi isolation; represented as 119 positive samples (10.6%) from diseased chickens and 384 positive samples (34.1 %) from freshly dead ones. Moreover, the highest positive samples in diseased and freshly dead chickens were in both lung (43&128) and air sac (35&119) samples. These results came in accordance with that obtained by (Zhao et al., 1994; Garcia et al., 2003; Steinlage et al., 2003 and Sajid et al., 2006). Culturing is regarded as the gold standard for confirming diagnosis of fungal infection with variable sensitivity due to sample collection techniques, storage and transport conditions (Bradsher et al., 2003 and Koneman et al., 2007). The use of different media for fungi isolation was performed to avoid false results and ensure accuracy. This is because misidentification of fungi species has been previously reported in results from the use of single identification media (Lo et al., 2001). Also, they helps to accelerate growth rate and the production of conidia (Odds and Bernaerts, 1994; Baumgartner et al., 1996; Chakranarayan and Pati, 2013). Moreover, Culture CHROM agar contains a chromogenic, 5bromo-6-chloro -3- indolyl phosphate Ptoluidine (chromogenic substrates) and 5bromo-4-chloro-3-indolyl/ N-acetyl-P-Dglucosaminide, which reacts with species specific enzymes to give yeasts colonies which are different in colour (Ghelardi et al., 2008).

F		Lung			Air Sac	;		Crop			Liver			Brain		Т	otal
Fungus	No	%	%**	No	%*	%**	No	%*	%**	No	%*	%**	No	%*	%**	No	%***
Aspergillus spp.																	
A.fumigatus	55	25.1	39.0	57	28.6	40.4	8	8.8	5.7	15	12.6	10.6	6	26.1	4.3	141	21.7
A.flavus	48	21.9	38.1	45	22.6	35.7	7	7.7	5.6	26	21.9	20.6	0	0.0	0.0	126	19.4
A.niger	39	17.8	35.1	32	16.1	28.8	17	18.7	15.3	23	19.3	20.7	0	0.0	0.0	111	17.1
A.candidus	6	2.7	66.7	3	1.5	33.3	0	0.0	0.0	0	0.0	0.0	0	0.0	0.0	9	1.4
A.terreus	11	5.0	55.0	4	2.0	20.0	5	5.5	25.0	0	0.0	0.0	0	0.0	0.0	20	3.1
A.ochraceus Total	3	1.4	75.0	1	0.5	25.0	0	0.0	0.0	0	0.0	0.0	0	0.0	0.0	4	0.6
Aspergillus spp. Other fungal species	162	74.0	39.4	142	71.3	34.5	37	40.7	9.0	64	53.8	15.6	6	26.1	1.5	411	63.1
Rhizopus spp.	21	9.6	31.3	20	10.1	29.9	4	4.4	6.0	5	4.2	7.5	17	73.9	25.4	67	10.3
Mucor spp.	16	7.3	38.1	18	9.1	42.9	3	3.3	7.1	5	4.2	11.9	0	0.0	0.0	42	6.5
Fusarium spp.	6	2.7	31.6	6	3.0	31.6	2	2.2	10.5	5	4.2	26.3	0	0.0	0.0	19	2.9
Penicillium spp.	11	5.0	34.4	11	5.5	34.4	3	3.3	9.4	7	5.9	21.9	0	0.0	0.0	32	4.9
Total other spp. Candida spp.	54	24.6	33.8	55	27.6	34.4	12	13.2	7.5	22	18.5	13.7	17	73.9	10.6	160	24.6
C. albicans	3	1.4	5.2	2	1.0	3.4	40	44.0	69.0	13	10.9	22.4	0	0.0	0.0	58	8.9
C. krusei	0	0.00	0.00	0	0.0	0.0	2	2.2	15.4	11	9.2	84.6	0	0.0	0.0	13	2.0
C. tropicalis	0	0.00	0.00	0	0.0	0.0	0	0.0	0.0	9	7.6	100.0	0	0.0	0.0	9	1.4
Total Candida spp.	3	1.4	3.7	2	1.0	2.5	42	46.2	52.5	33	27.7	41.3	0	0.0	0.0	80	12.3
Grand total	219	100.0	33.6	199	100.0	30.6	91	100.0	14.0	119	100.0	18.3	23	100.0	3.5	651	100.0

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Table (2): Incidence of fungi (moulds and yeasts) isolated from different organs of studied chickens in relation to number of isolates

* Percentage in relation to total number of isolates in each column,

** Percentage in relation to total number of isolates in each row. ***Percentage in relation to total number of isolates (651)

Fungus	NO.	%*	%**
A. Fumigatus	55	25.1	24.4
A. flavus	48	21.9	21.3
A. niger	39	17.8	17.3
A. candidus	6	2.7	2.7
A. terreus	11	5.0	4.9
A. ochraceus	3	1.4	1.3
Total Aspergillus spp.	162	74.0	72.0
Rhizopus spp.	21	9.6	9.3
Mucor spp.	16	7.3	7.1
Fusarium spp.	6	2.7	3.1
Penicillium spp.	11	5.0	4.9
Total other mould spp.	54	24.6	24.0
C. albicans	3	1.4	1.3
C. krusei	0	0.00	0.0
C. tropicalis	0	0.00	0.0
Total Candida spp.	3	1.4	1.3
Grand total	219	100.0	97.3

Table (3): Total number and percentage of fungi (moulds and yeasts) isolated from lung samples of studied chickens

* Percentage in relation to total number of isolates (219). ** Percentage in relation to total number of examined lung samples (225).

Table (4): Total number and percentage	of fungi (moulds	and yeasts)	isolated from	air sacs
samples of studied chickens				

Fungus	NO.	%	%**
A.fumigatus	57	28.6	25.3
A.flavus	45	22.6	20.0
A.niger	32	16.1	14.2
A.candidus	3	1.5	1.3
A.terreus	4	2.0	1.8
A. ochraceus	1	0.5	0.4
Total Aspergillus spp.	142	71.3	63.1
Rhizopus spp.	20	10.1	8.9
Mucor spp.	18	9.1	8.0
Fusarium spp.	6	3.0	2.7
Penicillium spp.	11	5.5	4.9
Total other mould spp.	55	27.6	24.4
C. albicans	2	1.0	0.9
C. krusei	0	0.0	0.0
C. tropicalis	0	0.0	0.0
Total Candida spp.	2	1.0	0.9
Grand total	199	100.0	88.4

* Percentage in relation to total number of isolates (199). ** Percentage in relation to total number of examined air sacs samples (225).

Fungus	NO.	%*	0⁄0**
A.fumigatus	8	8.8	3.6
A.flavus	7	7.7	3.1
A.niger	17	18.7	7.6
A. candidus	0	0.0	0.0
A.terreus	5	5.5	2.2
A. ochraceus	0	0.0	0.0
Total Aspergillus spp.	37	40.7	16.4
Rhizopus spp.	4	4.4	9.3
Mucor spp.	3	3.3	1.3
Fusarium spp.	2	2.2	0.9
Penicillium spp.	3	3.3	1.3
Total other mould spp.	12	13.2	5.3
C. albicans	40	44.0	17.8
C. krusei	2	2.2	0.9
C. tropicalis	0	0.0	0.0
Total Candida spp.	42	46.2	18.7
Grand total	91	100.0	40.4

Table (5): Total number and percentage of fungi (moulds and yeasts) isolated from crop samples of studied chickens

* Percentage in relation to total number of isolates (91). ** Percentage in relation to total number of examined crop samples (225).

Table (6): Total number and percentage of fungi (moulds and yeasts) isolated from liver samples of studied chickens

Fungus	NO.	%	%**
A. fumigatus	15	12.6	6.7
A. flavus	26	21.9	11.6
A. niger	23	19.3	10.2
A. candidus	0	0.0	0.0
A. terreus	0	0.0	0.0
A. ochraceus	0	0.0	0.0
Total Aspergillus spp.	64	53.8	28.4
Rhizopus spp.	5	4.2	2.2
Mucor spp.	5	4.2	2.2
Fusarium spp.	5	4.2	2.2
Penicillium spp.	7	5.9	3.1
Total other mould spp.	22	18.5	9.8
C. albicans	13	10.9	5.8
C. krusei	11	9.2	4.9
C. tropicalis	9	7.6	4.0
Total Candida spp.	33	27.7	14.7
Grand total	119	100.0	52.9

* Percentage in relation to total number of isolates (119). ** Percentage in relation to total number of examined liver samples (225).

Fungus	NO.	%*	%**
A. fumigatus	6	26.1	2.7
A. flavus	0	0.0	0.0
A. niger	0	0.0	0.0
A. candidus	0	0.0	0.0
A. terreus	0	0.0	0.0
A. ochraceus	0	0.0	0.0
Total Aspergillus spp.	6	26.1	2.7
Rhizopus spp.	17	73.9	7.6
Mucor spp.	0	0.0	0.0
Fusarium spp.	0	0.0	0.0
Penicillium spp.	0	0.0	0.0
Total other mould spp.	17	73.9	7.6
C. albicans	0	0.0	0.0
C. krusei	0	0.0	0.0
C. tropicalis	0	0.0	0.0
Total Candida spp.	0	0.0	0.0
Grand total	23	100.0	10.2

Table (7): Total number and percentage of fungi (moulds and yeasts) isolated from brain samples of studied chickens

* Percentage in relation to total number of isolates (23). ** Percentage in relation to total number of examined brain samples (225).

The main features of isolated fungi in the present study is concided with the description of Moneer (2008); Tartor (2010); Taha (2011); Klich (2002); Mohamed (2012); Chakranarayan and Pati (2013) and Musa et al., (2014). Rapid and accurate differentiation of pathogenic species of Aspergillus and Candida has become particularly important for selecting effective antifungal therapy. In addition, information about species identity is important for epidemiological and control purposes, such as for outbreaks of invasive aspergillosis, for surveillance of the emergence of new species and accurate determination of incidence rates (Henryet al., 2000; Hinrikson et al., 2005). Moreover, the molecular characterization of Aspergillus spp. and C. albicans carried out by using of PCR and sequencing of the PCR products. The identification systems for Aspergillus spp. and C. albicans depend on the PCR were based on using 18S or 28S rDNA as target DNA. However, the sequences in these regions are conserved across a wide range of fungi; it is therefore difficult to be used for identification of

variable elements that allow sequencebased identification of Aspergillus species and C. albicans; therefore, the region offers a possible template for identification of different Aspergillus spp. and C. albicans either by using primers designed from this region for the different spp. or sequencing of the amplified region by using primers for amplification of the ITS region (Lim and Lee, 2000 and Makimura, 2001). Regarding to Aspergillus species, in this study, the primers used for identification of PCR designed for amplification of the ITS region (Mirhendi et al., 2007). The examined 15 samples were identified as A.fumigatus, A.flavus and A.niger by the traditional methods and all 15 samples were successfully amplified a product of 600 bp and give + ve with the PCR examination which confirm the results of the traditional methods. The PCR products of 15 samples which were identified as A. fumigatus, A. flavus and A. niger were subjected for sequencing. These results came in accordance with those recorded by Sujita et al., (2004); Mirhendi et al., (2007) and

Aspergillus spp. The ITS region contains

Khaphagy et al., (2012). Regarding to C. albicans, in this study, the primers used for identification of PCR designed for amplification of the ITS region (Tarini et al.,2010). The examined 5 samples were identified as C. albicans by the traditional methods and all 5 samples were successfully amplified a product of 109 bp and give + ve with the PCR examination which confirm the results of the traditional methods. The PCR products of 5 samples which were identified as C. albicans were subjected for sequencing. These results came in accordance with those recorded by Tarini et al., (2010).

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