CONTENTS

LIST OF ABBREVIATION

AFLP	Amplified-fragment length polymorphism.
AGP	Agar gel precipitation.
APS	Ammonium persulfate.
AP-PCR	Arbitrarily primed PCR.
AIV	Avian influenza virus.
bp	Base pair.
CIEP	Counter immune electrophoresis.
CO2	Carbon dioxide.
CRD	Chronic respiratory disease.
DNA	Deoxy ribo nucleic acid.
ELISA	Enzyme linked immunosorbant assay.
FA	Fluorescent agar block technique
GI	Growth inhibition.
GP	Grand parent.
HI	Haemagglutination inhibition.
IF	Immunofluorescence.
IgM	Immunoglobulin M.
IBV	Infection bronchitis virus.
ILTV	Infection laryngeotracheitis.
kDa	Kilodalton.
MAT	Microagglutination test.
MA	Mili amber.
MG	***Mycoplasma gallisepticum***.
μg	Microgram.

µl	Microliter.
µm	Micrometer.
MS	***Mycoplasma synoviae*.**
NAD	Nicotinamide dinucleotide.
NDV	Newcastle disease virus.
NPIP	National poultry improvement program.
OiE	Office international des epizootic.
PCR	Polymerase chain reaction.
PD	Plate dilution.
PFGE	Pulsed field gel electrophoresis.
PBS	Phosphate buffer saline.
PCR-RFLP	Polymerase chain reaction- Restriction fragment length polymorphism.
PPLO	Pleuropneumonia-Like organism.
RAPD	Random amplified polymorphic DNA.
Rf	Rate of flow.
RFLP	Restriction fragment length polymorphism.
RPA	Rapid plate agglutination test.
r.p.m	Round per minute.
rRNA	Ribosomal ribo nucleic acid.
RSA	Rapid serum agglutination test.
SAT	Serum agglutination test.
SDS-PAGE	Sodium dodecyl sulfate polyacrylamide gel electrophoresis.
SPA	Serum plate agglutination test.
SPF	Specific pathogen free.
TEMED	Tetrametylethylene diamine.

7- SUMMARY

The prevalence of ***Mycoplasma*** species from diseased chickens from different poultry farms and individual breeders in Egypt (Sohag, Assiut and Cairo Governorates) was studied by both culturing and serological methods. A total of three hundred and twenty five samples including swabs from tracheal, nasal cleft and conjunctiva as well as 325 serum samples were collected from chickens showing respiratory manifestations. These birds were of different ages (four weeks - two months) and of different breeds (native and leghorn).

Mycoplasma species were biochemically identified as ***M. gallisepticum*** or ***M. pullorum*** in 220/325 swab samples with the percentage of 68%, ***M. gallinarum*** was isolated from 20/325 with the percentage 6.2% and ***M. arginini*** was isolated from 15/325 with the percentage 4.6%.

By serological identification of the ***Mycoplasma*** spp. using growth inhibition test, ***M. gallisepticum*** in 148/255 with the percentage of 58%, ***M. pullorum*** in 77/255 with the percentage of 30.2% and ***M. gallinarum*** in 30/255 with the percentage of 11.8% were founded.

The serological identification of ***Mycoplsama*** spp. using serum plate agglutination test proved that 277/325 were ***M. gallisepticum*** with a percentage of 85.2 % and 48/325 were ***M. synoviae*** with the percentage of 14.8%.

Four field isolates were tested by PCR and compared with standard ***M. gallisepticum*** referance strains (F, PG31 and S6). All of the examined field isolates were identified as ***M. gallisepticum*** (gave characteristic 330 bp fragment), while ***M. pullorum*** and ***M. gallinarum*** were not amplified by these primers.

RAPD-PCR is a more recent technique used for differentiation among different strains of the same ***Mycoplasma*** species. Also, it is a reproducible method for comparing the ***Mycoplasma*** field isolates in epidemiological studies. The technique detects the genetic diversity in natural populations among field isolates. DNA profiles of 4 ***M. gallisepticum*** field isolates were compared with that of ***M. gallisepticum*** reference strains (F, PG31 and S6) using Geary 1 and Geary 2 primers. Using Geary (1) primer, it was clear that RAPD fingerprinting is capable of distinguishing the ***M. gallisepticum*** field strains from vaccinal strains. On the other hands, It was interested to note that Geary (2) primer was not sufficient to differentiate ***M. gallisepticum*** strains (reference and field).

SDS-PAGE was used for differentiation between ***M. gallisepticum*** standard and field strains. In the present study, comparison of the protein profiles of standard and field strains ***M. gallisepticum*** whole cells was carried out for detection of similarity and /or variations among the compared strains. Each protein analysis of ***M. gallisepticum*** reference strains (PG31. F, S6 and R strains) and 10 of the field isolates yielded a characteristic profile banding ranged from (18-25) bands. From the results of SDS-PAGE analysis, it was clear that most isolates were related to S6 and R reference strains.