**SUMMARY**

Throughout the world *Mycoplasma synoviae* (MS) is an important pathogen of poultry especially for chicken and turkey. It causes respiratory tract infection and infectious sinusitis. The study was conducted to determine the seroprevalence of *Mycoplasma synoviae* (MS) infection with associated risk factors and identification of MS organism in unvaccinated flocks of commercial breeder farms of Chittagong district from January 2012 to December 2012. The risk factors were selected as farm, flock size, age and season. Blood samples were aseptically collected from the wing vein using (3-ml) sterile disposable syringes. A total of 365 serum samples were collected and tested for MS using serum plate agglutination (SPA) test for determination of *Mycoplasma synoviae* seroprevalence. On the other hand tracheal swabs were collected from each sero-positive flocks for Polymerase Chain Reaction (PCR) to determine the presence of *Mycoplasma synoviae* (MS) organism. For statistical analysis (Chi square test and Pearson correlation) was used. Among the farms the highest prevalence was found to be 69.23% and the lowest was 28.57% with the average 60%. The seroprevalence of MS infection in the breeder farms was highest 70.53% with the flock size >10000 birds whereas it was lowest 53.79% in the flocks ranging from 4000- 7000. According to age group the prevalence was found highest 69% in >60 weeks age group of birds and lowest 42.25% in 10-19 weeks group. The seroprevalence of MS in winter season was found as highest as 64.37% whereas it was found lowest 57.52% in summer season. There was significant difference (p<0.05) among the seroprevalence of MS in different breeder farms, flock size and age groups but there was statistically no significant (p>0.05) difference in seroprevalence of MS among the winter, summer and rainy season. The results showed that occurrence of MS have a significant relationship with the age, flock size and farm condition. To confirm the presence of MS in the samples PCR test was applied using specific published primers to amplify a 214 bp region of the 16S rRNA gene of the organism. The DNAs of MS were extracted using boiling method. In PCR all sero–positive flocks showed positive result for MS. As it was possible to identify MS using PCR from samples taken directly from tracheal swabs avoiding time consuming and laborious conventional culture method, it may be suggested that the PCR method could be used as an alternate of culturing method for identification of the organism.