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6. Summary

The most important FMDV features is its highly potential genetic and antigenic variation. So, this study was designed to Isolation and identification of FMDV from Sharkia, Monofia, Kalubia and Beni- Seuf governorates, Characterization of VP1 gene of FMDV serotypes (O_1 and A) circulating field strain and Comparing the VP1 neucleotide sequence of the field isolates

The collected sample, were Two T.E samples and 70 OP samples collected from El-Monofia, Three T.E samples and 50 OP samples collected from El-Kaluobia, Two T.E samples and 50 OP samples collected from Benisuef, Three T.E samples and 80 OP samples collected from El-Sharkia along the year 2009- 2010 according to the notification of the FMD outbreaks

The virological samples were submitted to FMDV isolation in baby mice and tissue culture and to identification by indirect ELISA.The results showed that both FMDV serotypes (O_1 and A) were present in the OP samples collected from Monofia governorate. FMDV serotype (O_1) was detected in Kusina, Sheben El- Kom and Tala by 26%, 30% and 15% respectively while FMDV serotype (A) was detected in Kusina, Sheben El-Kom and Tala by 6.6%, 5% and 5% respectively. Monof location (OP) samples were free from the both serotypes.

The (OP) samples collected from Kalubia showed that serotype (O_1) of FMDV present in Toukh, Benha and Metnama localities as 20%, 13.3% and 15% respectively, while the percentage of positive collected OP samples for FMDV serotype (A) was 5% in Metnama, while Toukh and Benha were free from serotype (A) FMDV.

Also results showed that the serotype (O_1) was present in Seds, Beba and Naser localities (Beni- Suef governorate) collected (OP) samples as 20%, 20% and 6.7% respectively. Fashn was free from type (O_1) according to OP samples collected. The result showed also that Fashn and Naser localities collected OP samples detected serotype FMDV (A) by 15% and 6.7% respectively, while Seds and Beba samples were free from serotype (A).

The (OP) samples collected from Sharkia governorate exhibited that, both FMDV serotypes (O_1 and A) are circulating in all the localities of Sharkia governorates when the OP samples collected. FMDV serotype (O_1) was detected from Belbis, Abohamad, Kafr- Sager and Zagazig by 12%, 10%, 4% and 20% respectively, while FMDV serotype (A) were detected in Belbis, Abohamad, Kafr- Sager and Zagazig by 4%, 10%, 8% and 5% respectively.

Isolation and identification of FMDV from Epithelial tongue samples collected from Monofia, Kalubia, Beni- Seuf and Sharkia by baby mice inoculation, tissue culture and indirect ELISA indicated that both FMDV serotypes (O_1 and A) were detected from Monofia, Kalubia and Beni- Suef which FMDV serotype (A) was detected only in Sharkia samples.

Reverse transcriptase polymerase chain reaction (RT- PCR) was performed by using specific primer for O and A serotypes for amplification of VP1 gene. Serotype (O_1) gave positive result with RT- PCR at 402bp, while FMDV serotype (A) gave positive RT- PCR results at 800bp with variable intensity on ethidium bromide gel. Eight PCR product samples were selected as one for FMDV serotype (O_1) and one for FMDV serotype (A) from each governorate (Monofia, Kalubia, Beni- Suef, and Sharkia). The eight PCR products were submitted for performing the sequencing. Results

of the sequencing of VP1 gene was (1D) of FMDV serotype (O_1) revealed that there is a similarity between the isolated strains, the similarity of the 3 end of the 1D gene was 99.8% to 98.6% among them, while there was a divergence from other compared FMDV strains. A phylogenetic tree based on the VP1 (1D) region of FMDV is used for genetic characterization so as to Compare the VP1 nucleotide sequence of the field isolates and the results of the aligament revealed that the FMDV serotype O1/ manias iso 87 is most nearly identity to samples O/ Monofia, O/ Kalubia, O/ Beni- Suef and O/ Sharkia. While thhe results of sequencing of VP1 gene (1D) of FMDV serotype (A) revealed that there is no significant divergence between the isolated strains as the similarity was 99.4% to 98.2% among them, while there is a divergence from other compared FMDV strains. The results revealed that the FMDV serotype A/ Egy/ 2006 is the most nearly identity to samples A/ Monofia, A/ Kalubia, A/ Beni- Suef and A/Sharkia.

From this study its clear that:

1. FMDV serotype O_1 and A/ Egy/ 2006 still existing and circulating in Monofia, Kalubia, Beni- Suef and El Sharkia governorates.

2. The phylogenic study showed that the 2 FMDV serotypes isolated from these governorates are highly related to the traditional serotype isolated before in Egypt and being used in vaccine production.