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Serological and Molecular Detection of Foot and Mouth Disease Virus in Diyala Province

A Thesis

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وزارة التعليم العالي والبحث العلمي

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كلية الطب البيطري

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رسالة مقدمة الى

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وهي جزء من متطلبات نيل درجة الماجستير في علوم الطب البيطري / الاحياء المجهرية

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غزوان خضير علوان

بكالوريوس طب وجراحة بيطرية عامة (2004)

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Chapter one

1.1.Introduction

Foot-and-mouth disease (FMD) is one of the most important diseases of animal husbandry that affected cloven-hoofed ruminants and pigs. It is viral disease that characterized by formation of vesicles in skin junction (coronate) with hooves (Foot) and mucous membrane of mouth and tongue, Other parts like teats were also affected (Alexandersen *et al.*, 2003a ; Arzt *et al.*, 2010).

Furthermore, the disease was associated with increased body temperature, salivation, and loss of appetite that indirectly affected body weight gain of infected animal and sometimes sudden death of young infected animals (Quinn *et al.*, 2005). The disease is contagious and reported in more than 70 wild life animal species (Alexandersen *et al.*, 2003a ; Arzt *et al.*, 2010).

Economically importance, this diseace was attributed to the lossing of high morbidity, treatment, vaccination and veterinary services, secondary infections, as well as losses in body weight gain of infected animals, mortality that might reach 2% in adults and 20% (Radostits *et al.*, 2007) to 50% (MacLauchlan and Dubovi, 2011) among young animals, reduction in milk production , increased abortions that might lead to fertility impairment (Admassu *et al.*, 2015) , and restriction regulations that applied on countries affected with FMD outbreaks (Geering and Lubroth, 2002; Dosky *et. al.* 2006; Al Gharrawyi ,2009; Knight-Jones and Rushton, 2013).

More than 100 countries were reported endemic by FMD. Some developed countries were reported free, whereas it was the main problem in most developing countries (Jamal and Belsham, 2013).

The disease was caused by an RNA virus that classified as a member in the genus *Aphthovirus*. This genus was grouped with the family *Picornaviridae*. Its RNA genome is a single stranded, linear and positive sense. There are seven serotypes of the virus named: A, O, C, Asia 1 and three Southern African Territories (SAT) serotypes recognized as SAT1, SAT2, and SAT3. These serotypes were included subtypes and confined to specific geographical distribution (Vosloo *et al.*, 2006; Valdazo-González *et al.*, 2012).

Foot and Mouth Disease Virus was reported to be transmitted by many methods that involved direct transfer of infected droplets between diseased and healthy susceptible animals, or indirectly through contaminated personals and equipment that might aid in transmission of the disease from farm to farm, werwas Infected pigs that produced large quantities of the virus with their exhalation were reported to cause airborne transmission to susceptible ruminants (Alexandersen *et al.*, 2002a).

Each serotype of FMD virus dose not elicits acceptable immunity against other serotypes. This is because FMD virus characterized by high antigenic diversity that make the disease not easy to be controlled (Knight-Jones and Rushton, 2013).

Genetic variations among serotypes and subtypes might be attributed to the variations in surface viral protein 1 (VP1) that responsible for attachment to susceptible cells, antigenicity and entry of the virus (Jamal and Belsham, 2013).This made VP1 gene the most important target to study the antigenic variations between different strains and sub-strains of FMD (Longjam and Tayo, 2011).

In Iraq, cattle and sheep husbandry and rearing is one of the important national economic facts. Most Iraqi foods supplement of meat was depending on such industry. Accordingly, spread of a viral disease of such type (FMD) might greatly affected animal production and led to huge economic losses among such animals as it was reported many FMD outbreaks were occurred in the last decades (Dosky *et. al.* 2006;Al Gharrawyi ,2009).

In 1988 in Iraq, FMD virus was isolated, serotyped, and characterized by Al-Bana and Shoney (1988). During the period of 1998 to 2000 many outbreaks among Iraq cattle were reported and the virus was isolated from Holstien cattle and identified as serotype O (Al-Janabi, 2001).

Outbreaks in Iraqi cattle were occurred in 2009 due to FMDV, and some of collected samples were sent to Pribright laboratories. The isolated virus was identified as a subtype related to Turkish FMD isolate. This A/IRQ/24/2009 isolate was found to 99.69% matched in identity to A/IRQ/10/2009, and A/KUW/6/2009. The same isolate was found to be closely related in 95.46% identity to A/IRN/1/2005 and, in 84.75% to A/SAU/41/91 isolate, and finally it was related in 82.16% identity to A22/IRQ/24/64 (vicinal strain)(FAO 2010).

The major role in controlling FMD is vaccination programs and quarantine restrictions. Most available vaccines are tissue derived, but many biotechnological techniques were performed to replace the conventional inactivated FMD vaccines (Parida, 2009; Rodriguez and Gay, 2011).

Many FMD cases were reported among cattle in some villages of Diyala province. Some of these animals were subjected to vaccination programs by veterinary services. Occurrence of FMD in vaccinated animals in Iraq had been reported nine years ago and attributed to misuses of scientific and accurate methods for FMD control. Additionally, random doses of the vaccine were used, and such vaccine did not match the antigenicity of circulating field FMDV in Iraq (FAO 2009a; WrLfmd, 2009).

1.2. Aims of the study

the present study aimed to:

1- Serologic screening of FMDV antibodies in cattle of Diyala province by 3ABC ELISA kit that differentiate infected cattle regardless their vaccination.

2- Molecular detection(RT- PCR) of FMD from actively infected animals.

3- Molecular bio-typing of detected virus to point up the type of circulating field virus in comparison to vaccine strain.