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**CLINICAL, HAEMATOLOGICAL AND
MOLECULAR STUDY OF *SARCOPTIC SCABIEI*
IN HUMAN AND SHEEP IN SOME REGIONS OF
DIYALA PROVINCE**

A Thesis

**Submitted to the Council of the College of Veterinary
Medicine/University of Diyala in partial fulfilment of Requirements for
The Degree of Master of Science in Veterinary Medicine (Zoonosis)**

By

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بِسْمِ اللَّهِ الرَّحْمَنِ الرَّحِيمِ
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Supervisors Declaration

We certify that this thesis has been prepared under my supervision at the Department of Internal and Preventive Medicine / University of Diyala entitled "**Clinical, hematological and molecular study of *Sarcoptic scabiei* in human and sheep in some regions of Diyala province**" As a partial fulfillment of the requirements for the degree of Master of Science in Veterinary Medicine (Zoonosis).

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Examination committee certification

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DEDICATION

Is dedicated to my family, whom has been a constant source of support and encouragement during the challenges of graduate studies and life. I am truly thankful for having you in my life.

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Abstract

The study was conducting on sheep and human, in Diyala, Iraq. 146 sheep consist from 61 male and 85 female .were submitted to investigation, during the period, November 2021 to March 2022. Skin scraping were collected, undergo laboratory examination for *Sarcoptes scabiei*. The main clinical signs, were increase in respiratory and heart rate, wool loss, crusted, pityriasis, pustules. Infestation rate 56(38.35%); 19(13.01%) among male and 37(25.34%) female. The maximum prevalence was during January and February, 12.33% and 17.12% respectively. The infestation was high in young sheep of one year old. Also in those of poor and malnutrition condition and those under bad management. Hematological there were a significance difference in TECs and TLCs and Hb concentration, in addition to low pcv% value. Histologically there were hyperkeratosis, acanthosis, hemorrhage, inflammation, neutrophils, eosinophilic layer and macrophage.

In the diagnosis using technology of the PCR eight samples were taken from samples that diagnosed positive microscopically six sample were molecular identified sizes polymer chain reaction products for *Sarcoptes scabiei*. Show that size 700bp and sequence result show 80% identities.

In humans, (60) suspected cases of scabies were examined, and the results showed that 24(40%) patients tested positive for microscopic examination, infestation rate male was 13 (21.7%) and female was 11 (18.3%) with on significant deference, study found high patient rate in group age 20-50 years and the Illiterate persons, higher rates of infestation in rural residents and infestation was commonest in house wife and student. During the study we asked the patients if they contact or breeding sheep and we found (5) patients that breed sheep from total (24) patient. We found that the typical scabies infestation features such as bubbles, blisters, papules and linear burrows itching have been showed on the hand area. Diagnosis using technology of

the PCR eight samples were taken from samples that positive diagnosed microscopically five sample were molecular identified sizes polymer chain reaction products for *Sarcoptes scabiei*. Show that size 700bp. The phylogenic tree showed that the sheep sample 1, 2 and 3 isolate clade was close to MF503258 *Sarcoptes scabiei* human Pakistan and AB779577 *Sarcoptes scabiei* Rabbit Egypt and the phylogenic tree show that human sample clade was close to KJ499544 *Sarcoptes scabiei* Dog China EU256387 *Sarcoptes scabiei* swine China OK510218 *Sarcoptes scabiei* Camel iraq OK510217 *Sarcoptes scabiei* Camel Iraq and show there is close between human sample and sheep sample.

In a conclusion, the present study has shown that mange still constitutes a notable problem, the phylogenic tree show there is close between human sample and sheep sample.

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List of Abbreviations

RNA	Ribonucleic Acid
rRNA	Ribosomal Ribonucleic Acid
ITS-2	Internal Transcribed Spacer
WHO	World Health Organization
rDNA	Recombinant DeoxyriboNucleic Acid
mtDNA	Mitochondrial DeoxyriboNucleic Acid
COX1	Cyclooxygenase-1
BCE	Before Common Era
qPCR	Quantitative Polymerase Chain Reaction
µm	Micrometers
RH	Relative Humidity
LTCHs	Long-Term Care Hospital
HIV	Human Immunodeficiency Virus
(OS)	Ordinary Scabies
(CS)	Crusted Scabies
IgE	Immunoglobulin E
EDTA	Ethylenediaminetetraacetic Acid
KOH	Potassium Hydroxide
R.B.C.	Red Blood Cells
W.B.C.	White Blood Cells
Hb	Hemoglobin
PCV	Packed Cell Volume
MCV	Mean Corpuscular Volume
MCHC	Mean Corpuscular Hemoglobin Concentration
MCH	Mean Corpuscular Hemoglobin
TLC	Total Leucocytes Count
DLC	Differential Leucocytes Count
(Pg)	Pico Gram
cm	Centimeter
hrs	Hours

(H & E)	Hematoxylin and Eosin
rpm	Rounds Per Minute
μl	Microliter
volt	Voltage
UV	Ultraviolet
nm	Nanometer
ml	Milliliter
EtBr	Ethidium Bromide
H ₂ O	Chemical Symbol for Water
NCBI	National Center Biotechnology Information
BCE	Before the Christian Era
LTCHs	Long-term care hospitals
fl	femtoliter
LCs	Langerhans cells

Chapter One

Introduction

1.1 Introduction

Scabies is a disease caused by mange mite *Sarcoptic scabiei*, it's a widespread on domestic and wild mammals. The mite was initially properly named and described by Linnaeus as *Acarus humans subcutaneous* and *Animals with acarus exulcerans*. Renucci dubbed the newly discovered mite *Acarus scabiei* from a human in Paris in 1834 cited by **(Currier et al., 2011)**. They are microscopic ectoparasites that can infect a variety of hosts, including domestic, farm, and wild animals, and produce the mild to chronic skin condition known as "Mange." **(Pence and Ueckermann, 2002)**.

One of the first human diseases with a documented origin was scabies, which has been known to exist in humans since the time of the Bible. **(Pence and Ueckermann, 2002)**.

Mange, often known as scabies, is a contagious zoonotic skin condition that affects both humans and animals. It is brought on by the mite *Sarcoptes scabiei*. More than 300 million people are thought to get the disease annually **(Banerji, 2015)**. Animals can serve as reservoirs or carriers of infections that might affect humans (zoonosis). Also, a number of diseases shared by both livestock and wild mammals present a danger for indirect zoonotic transmission and result in financial losses **(Gortázar et al., 2016)**.

In humans, *sarcoptic scabiei* causes disease known as scabies, and in animals the disease is referred to as *sarcoptic mange* **(McCarthy et al., 2004)**.

There are more than 100 mammalian species in this parasite's host range, which spans 27 families and 10 orders **(Bornstein et al., 2001)**. In addition to having the potential to result in significant economic loss due to decreased productivity and higher animal

mortality (**Dagleish et al., 2007**). *Scabies* is an emerging/re-emerging infectious disease that poses a global danger to human and animal health (**Fthenakis et al., 2001**). Many of the various animal populations affected by sarcoptic mange globally lack reliable estimates of its prevalence. But there are numerous instances of how severe a *S. scabiei* outbreak may be, resulting in catastrophic morbidity (**Bornstein et al., 2001**).

According to tanneries research, skin disorders induced by external parasites are cause of 35% sheep skin. Ectoparasite-related skin diseases are among the most common illnesses of small ruminants that generate severe economic losses to small-scale farmers and the tanning industry (**Kassa, 2005**).

Sheep serve as a significant supply of animal protein, including meat and milk in the food production systems, and serve as a significant source of wool and skins, which are valued as the foundation of some nations' economies (**Hagos et al., 2018**). Mange mites are a potential threat to sheep production that could cause serious economic losses because of the harm they do to the skin and wool, anemia, poor physical condition, decreased milk and meat production, growth rates, and general weakness that makes the affected animals more vulnerable to other diseases (**Al-Ezzy et al., 2015**).

The utility of molecular identification techniques, with potential use in countries with low endemicity, PCR amplification and its variations, for example, appear to be the most precise and speedy procedure for detecting scabies (**Siddig &hay, 2021**). Histology may also reveal indications of infestation but is thought to be less accurate; PCR could be more accurate than cytology in situations when the load of mites is less (**Cypher et al., 2017**). Numerous

animal species, including humans, have successfully used conventional and real-time polymerase chain reactions targeting the 16S ribosomal RNA, rRNA, ITS-2, and/or COI genes, as well as microsatellites, to detect *S. scabiei* DNA from skin scrapings (**Peltier et al., 2017**).

Scabies is primarily present in regions with high rates of poverty and malnutrition, and it is spread by close contact with infected people or animals (**Wardhana and Manurung, 2002**). Scabies in humans is now a neglected tropical illness, according to the World Health Organization (WHO), although more than 200 million individuals worldwide are affected (**Umut et al., 2021**).

An original area of study into the biology of scabies mites and interactions between the mites and their hosts has been made possible by the development of molecular techniques (**Mofiz E et al., 2016**). The mitochondrial 16S DNA (mtDNA 16S) and ribosomal second internal transcribed spacer DNA (rDNA ITS2) of *Sarcoptes* mites taken from several host species have not discovered any interspecific variations (**Alasaad et al., 2009**).

1.2 Aims of the study

- 1- Detected the prevalence of sheep mange in Diyala province.
- 2- Assessment of clinical, hematological and histopathological changes in sheep that infected with mange.
- 3- Using molecular technique (PCR) by using specific primers targeting the COX1 gene.
- 4- Study the genotyping of *Sarcoptes scabiei* mites isolated from human and sheep by sequencing.