JOURNAL OF ADVANCED VETERINARY AND ANIMAL RESEARCH
ISSN 2311-7710 (Electronic)
http://doi.org/10.5455/javar.2019.f366
A periodical of the Network for the Veterinarians of Bangladesh (BDvetNET)

December 2019
VOL 6, NO. 4, PAGES 445–450

SHORT COMMUNICATION

Characterization of mitochondrial COX-1 gene of *Sarcoptes scabiei* from rabbits in East Java, Indonesia

Nunuk Dyah Retno Lastuti[1], Anwar Ma'ruf[2], Wiwik Misaco Yuniarti[3]

[1]Postgraduate School and Department of Parasitology, Faculty of Veterinary Medicine, Universitas Airlangga, Surabaya 60115, Indonesia
[2]Postgraduate School and Department of Basic Medical Science, Faculty of Veterinary Medicine, Universitas Airlangga, Surabaya 60115, Indonesia
[3]Department of Clinical Sciences, Faculty of Veterinary Medicine, Universitas Airlangga, Surabaya 60115, Indonesia

ABSTRACT

Objective: The purpose of this study was to characterize the mitochondrial COX-1 gene of *Sarcoptes scabiei* in rabbits from three districts of Malang, Nganjuk, and Kediri, East Java, Indonesia. The gene was aligned with a DNA isolated from *S. scabiei* of Chong'qing rabbit (accession number: EU256388.1) to construct a molecular analysis of phylogenetic in *S. scabiei* COX-1 gene.

Materials and Methods: This study has been verified by the Committee Ethics (Faculty of Veterinary Medicine, Universitas Airlangga). The mites were collected and identified from rabbits that have an indication of scabies infection. DNA was extracted with QIAamp DNA mini kit and polymerase chain reaction (PCR) analysis was done. The PCR products were purified with the protocol of the BigDye XTerminator™ Purification Kit (Thermo Scientific) and were double-sequenced with the forward and reverse PCR primers of ABI PRISM 310 Genetic Analyzer. The sequence product was confirmed with Clone Manager Professional 9 (Sci-Ed Software) and the Neighbor-Joining method was done with MEGA6 to build a phylogenetic tree.

Results: The target product of DNA amplification in this PCR was around 290-bp. The amplicon was visualized in 2% of agarose gel electrophoresis. The homology analysis of these sequences showed that it had more than 99% similarity.

Conclusion: COX-1 gene sequences of *S. scabiei* from rabbits in Malang, Nganjuk, and Kediri were very similar to COX-1 gene sequences in *S. scabiei* acquired from several hosts according to NCBI data.

ARTICLE HISTORY

Received May 23, 2019
Revised July 24, 2019
Accepted August 01, 2019
Published September 11, 2019

KEYWORDS

COX-1; DNA mitochondrial; rabbit; *Sarcoptes scabiei*.

Introduction

Sarcoptes scabiei causes an infectious skin disease called scabies, and every year more than 300 million people are infected. Sarcoptes mites manifestation was reported to infect more than 100 mammal species, including human, domestic animal, and wild animal [1–3]. Scabies caused economic losses because it inhibits growth, decreases feed conversion rate, high in morbidity and mortality rate. Scabies is a very contagious disease, described by dermatitis, hyperkeratosis, alopecia, pruritic, and crust formation. Scabies pathogenesis was related to hypersensitivity reaction [4–6]. Many countries and international organization realize how important scabies is, that is included as one of the most common diseases and treated as "neglected tropical disease," and scabies charges as an emerging/re-emerging infectious disease [7,8].

Mites protein is known as antigen; when antigen enters the body, it will activate lymphocyte B cells to produce immunoglobulin. Several studies have shown that *S. scabiei's* protein of goat and rabbit isolates is immunogenic which can be developed for diagnostic kits and vaccine sub-units [6,9]. Vaccination is a good ecological alternative for effective parasite control. Moreover, anti-parasite vaccine that is effective against scabies is not yet developed; it is because of some factors like the intricacy of interaction between the host immune system and the parasite, also the mechanism

Correspondence Nunuk Dyah Retno Lastuti ✉ nunukdyah53@gmail.com Faculty of Veterinary Medicine, Universitas Airlangga, Surabaya 60115, Indonesia.

How to cite: Lastuti NDR, Ma'ruf A, Yuniarti WM. Characterization of mitochondrial COX-1 gene of *Sarcoptes scabiei* from rabbits in East Java, Indonesia. J Adv Vet Anim Res 2019; 6(4):445–450.

of the host immune system, and large number of protein that coded by parasite is not yet known' therefore, it is very hard to find the protein that has the capacity to give protective immunity [10]. There is no immunodiagnostic test or commercial subunit vaccine available for scabies. Some research has focused on producing a recombinant protein from *S. scabiei* to investigate the host's immune response, to develop a subunits vaccine, and serodiagnostic [11–13]. Study of genetic characterization of *S. scabiei* using a marker of subunit 1 cytochrome c oxidase (COX-1) and the second internal transcribed spacer (ITS-2) are well developed to achieve the aims of molecular epidemiology investigation and the provision of subunit vaccines for scabies in animals [14–17].

COX-1 gene is the most informative for investigating molecular epidemiology and often used by researchers for a marker of genetic characterization of *S. scabiei* from animals and human [14,18,19]. Based on field observations, the number of scabies cases in rabbits in Indonesia is increasing elevately. However, there have been no case reports because the condition has been treated with acaricide [9]. Vaccination is a good ecological alternative for effective parasite control. Anti-parasite vaccine that is effective against scabies is not yet developed because there are lacks of the genetic characterization data on *S. scabiei*. The purpose of this study was to characterize the mitochondrial COX-1 gene of *S. scabiei* in rabbits from three districts of Malang, Nganjuk, and Kediri, East Java, Indonesia. The gene was aligned with a DNA isolated from *S. scabiei* of Chongqing rabbit (accession number: EU256388.1) to construct a molecular analysis of phylogenetic in *S. scabiei* COX-1 gene.

Materials and Methods

Ethical approval

This research has been approved by the Ethics Commission, Faculty of Veterinary Medicine, Universitas Airlangga, Indonesia with certificate number 630-KE.

Identification and Collecting mites of S. scabiei from rabbits

The mites were collected and identified from rabbits that have an indication of scabies infection.

Identification of *S. Scabiei* was carried out at Laboratory of Parasitology, Faculty of Veterinary Medicine, Universitas Airlangga. The selected Sarcoptes were centrifuged at 3,000 rpm for 10 min and this step was performed at least three times to get the result free of dirty materials that still carried in the scraping process. The deposit result kept in a freezer at −20°C, to be processed into DNA extraction [9,14].

DNA extraction and amplification

DNA extraction was carried out and followed the extraction protocols of the QIAamp DNA mini kit (Qiagen, Hilden, Germany) [20].

The amplification target of mitochondrial COX-1 gene in *S. scabiei* was 290-bp of polymerase chain reaction (PCR) products. DNA templates were obtained from the samples after extraction procedures. The Primers were designed, which refer to the GenBank Accession Number EU256388.1, the mitochondrial COX-1 gene of *S. scabiei* was isolated from Chongqing rabbit. The forward primer is 5′-TCT TAG GGG CTG GAT TTA GTA TG-3′ and the reverse primer is 5′-AGT TCC TCT ACC AGT TCC AC-3′. PCR amplification was constructed in Biorad iCycles IQ. PCR steps were done for 35 cycles in the following temperatures, initial denaturation (95°C 5 min), denaturation (95°C 30 sec), annealing (50°C 60 sec), extension (72°C 60 sec), and final extension (72°C 5 min). The amplicon was visualized in 2% of agarose gel electrophoresis under UV illuminator [14].

The PCR products were purified according to the protocol of the BigDye XTerminator™ Purification Kit (Thermo Scientific) and were double-sequenced with the forward and reverse PCR primers of ABI PRISM 310 Genetic Analyzer (Applied Biosystems).

Bioinformatics analysis

The sequence was analyzed with program Clone Manager Professional 9 (Sci-Ed Software) where the reverse primer was inverted to make complete alignments. The inverted result then aligns to compare with DNA from Chongqing rabbit (Accession Number EU256388.1).

For comparison with other related DNA sequences, the COX-1 DNA fragment sequence of *S. scabiei* isolated from Malang, Nganjuk, and Kediri rabbits was used as a query search with the program Nucleotide BLAST. All hits that have nucleotide identity of 80% or higher, along with all sequences resulted from this investigation, were aligned using the ClustalW2 program [22]. The sequence product was confirmed with Clone Manager Professional 9 (Sci-Ed Software) and the Neighbor-Joining method was done with MEGA6 to build a phylogenetic tree [23], with a COX-1 sequence from *Megaselia* sp. (GenBank accession No. KT103510.1) as an outer group.

Results and Discussion

Sarcoptes scabiei mites were isolated from Malang, Nganjuk, and Kediri rabbits, with clinical symptoms such as skin thickening, crust formation, hair loss on the areas around the eyes, ears, mouths, and legs. The amplicon products of PCR were visualized in 2% agarose gel electrophoresis and under the UV illuminator it showed a correct band 290 bp that is at the position between 200 and 300 bp of the markers (Fig. 1).

This study showed that the sequencing of COX-1 gene (Fig. 2) DNA *S. scabiei* rabbits originated from Kediri, Malang, and Nganjuk, after analyzed with Clone Manager Professional 9 program (Sci-Ed Software) using DNA

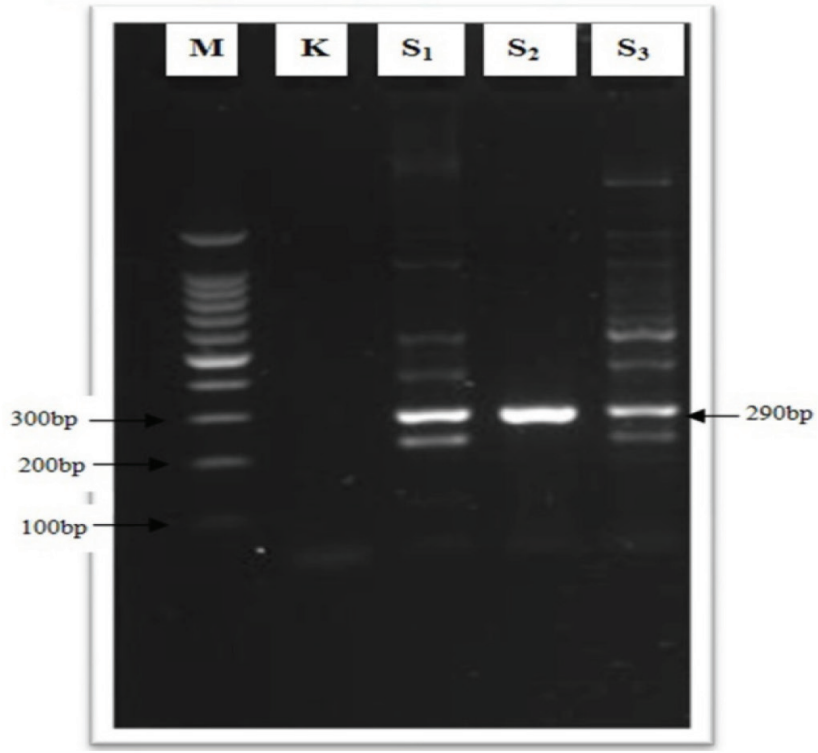

Figure 1. PCR product of *S. scabiei* from rabbit of Kediri (S1), Malang (S2), Nganjuk (S3), Negative Control (K), and Marker (M).

```
EU256388      1 TCTTAGGGGCTGGATTTAGTATGTTGATTCGATATCAATTATCTCAACCAATAGGAATTT
Kediri        1 TCTTAGGGGCTGGATTTAGTATGTTGATTCGATATCAATTATCTCAACCAATAGGAATTT
Malang        1 TCTTAGGGGCTGGATTTAGTATGTTGATTCGATATCAATTATCTCAACCAATAGGAATTT
Nganjuk       1 TCTTAGGGGCTGGATTTAGTATGTTGATTGGATATCAATTATCTCAACCAATAGGAATTT

EU256388     61 CTATAAATTCTATATTTTATAATTCAGTTGTAACCGCCCATGCTTTTATTATAATTTTTT
Kediri       61 CTATAAATTCTATATTTTATAATTCAGTTGTAACCGCCCATGCTTTTATTATAATTTTTT
Malang       61 CTATAAATTCTATATTTTATAATTCAGTTGTAACCGCCCATGCTTTTATTATAATTTTTT
Nganjuk      61 CTATAAATTCTATATTTTATAATTCAGTTGTAACCGCCCATGCTTTTATTATAATTTTTT

EU256388    121 TTATAGTAATACCTATTATAATAGGAGGATTTGGAAATTTATTAATTCCTTTAATATTAG
Kediri      121 TTATAGTAATACCTATTATAATAGGAGGATTTGGAAATTTATTAATTCCTTTAATATTAG
Malang      121 TTATAGTAATACCTATTATAATAGGAGGATTTGGAAATTTATTAATTCCTTTAATATTAG
Nganjuk     121 TTATAGTAATACCTATTATAATAGGAGGATTTGGAAATTTATTAATTCCTTTAATATTAG

EU256388    181 GCTCTGCTGATATAGCTTACCCTCGATTAAATAATATAAGTTTTTGGTTACTTCCACCAT
Kediri      181 GCTCTGCTGATATAGCTTACCCTCGATTAAATAAGGTAAGTTTTTGGTTACTTCCACCAT
Malang      181 GCTCTGCTGATATAGCTTACCCTCGATTAAATAATATAAGTTTTTGGTTACTTCCACCAT
Nganjuk     181 GCTCTGCTGATATAGCTTACCCTCGATTAAATAATATAAGTTTTTGGTTACTTCCACCAT

EU256388    241 CTTTAACTTTATTACTAATTTCTTTATTGTGTGGAACTGGTAGAGGAACT
Kediri      241 CTTTAACTTTATTACTAATTTCTTTATTGTGTGGAACTGGTAGAGGAACT
Malang      241 CTTTAACTTTATTACTAATTTCTTTATTGTGTGGAACTGGTAGAGGAACT
Nganjuk     241 CTTTAACTTTATTACTAATTTCTTTATTGTGTGGAACTGGTAGAGGAACT
```

Figure 2. Sequence alignment of COX-1 partial gene mitochondrial DNA of *S. scabiei* from rabbits of Kediri, Malang, and Nganjuk East Java, Indonesia.

sequence with the GenBank accession No. EU256388.1 showed more than 99% similarity. The phylogenetic tree of mitochondrial COX-1 gene of *S. scabiei* from Kediri, Malang, and Nganjuk was relatively close to 19 *S. scabiei* isolates obtained from the NCBI nucleotide database with their Accession Numbers (Fig. 3).

The sequence products showed that Nganjuk scabies infected rabbits had one base pair different. In the nucleotide number 30, Cytosine (C) was replaced by Guanine (G). The sequence from Kediri infected rabbits showed a different result. There were two base pair differences and the two base pairs of Thymine and Adenine (TA) were replaced by guanine (GG) in the base pair number 215–216. There was no base pair difference in Malang scabies infected rabbits.

Research by Lastuti et al. [21] demonstrated that the partial CDS of mitochondrial COX-1 gene of *S. scabiei* from Lamongan goats was very similar to Mojokerto rabbits, with a homology identity of 99%. That previous study confirmed that out of 290 bp in Lamongan scabies-infected goats, there was one base pair different. In the nucleotide number 26, Guanine was replaced by Adenine.

The guanine residue is conserved in other *S. scabiei* COX-1 gene. Based on homology analyses with marker ITS-2 by Gu et al. [24], it showed high homology of more than 96.6% among six isolates of *S. scabiei* (De Geer). Thus, high homogenity results mean that isolates from China and other locations belonged to a single and heterogeneous species.

According to the literature, guanine found in Guanosine Triphosphate plays a role in cellular processes such as cell growth regulation, signal transduction, and protein transport [25], possibly related to the pathogenesis of scabies. Mites of *S. scabiei* originated from rabbits that showed clinical symptoms of severe scabies, with histopathological changes such as parakeratosis, acanthosis, inflammatory cell infiltration, degeneration, and congestion [6,26]. *Sarcoptes scabiei* antigen induces cytokine expression in fibroblast and keratinocytes cells. The secretion of cytokine will stimulate eosinophils to secrete granules which cause allergic reactions such as edema, mucous secretion, and leukocyte infiltration [27].

The *S. scabiei* mites that were genetically characterized were from rabbits infected with severe scabies from rabbit

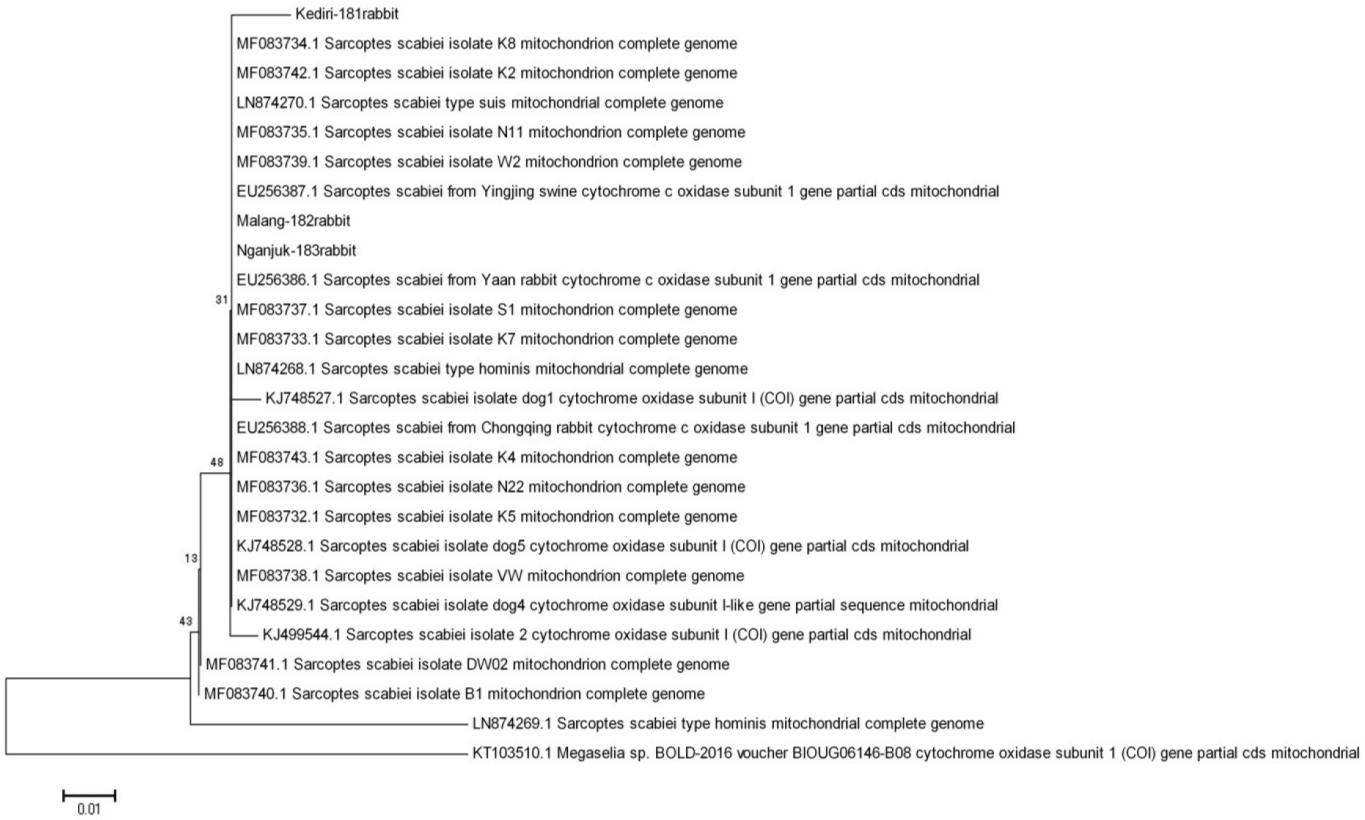

Figure 3. Phylogenetic analysis of partial CDS of COX-1 gene of *S. scabiei* isolated from several different species. All sequences were aligned by using ClustalW2 and the cladogram was built using the Neighbor-Joining method.

farms from Kediri, Malang, and Nganjuk. Rabbits originating from the area in addition to meeting their region needs, also sold to other areas, especially East Java to meet the needs of rabbit meat, animal experiment, and kept as a pet. Most of the rabbits were traditionally maintained with humid cage conditions and lack of sanitation, thus causing transmission among rabbits, especially in one population, making it possible that *S. scabiei* mites have adapted to their hosts and have grown long enough [9]. The incidence of scabies in America and Australia is an emerging infectious disease. Transmission occurs through direct contact between individual or contaminated materials with mites. The life cycle of *S. scabiei* mites takes about 3 weeks [16].

The study of genetic detection of *S. scabiei* by several researchers showed a change in the nucleotide of mitochondrial DNA COX-1 gene sequencing between animal species and geographical differences. Whereas sequencing ITS-2 gene did not show geographical differences and host adaptation [10,17]. Detection of *S. scabiei* genetic with COX-1 gene as a marker can be used as epidemiology study of *S. scabiei* mites from various animal species and geography to control scabies infection [10,16].

Sarcoptes scabiei mite was a single species but has many variants according to its host (rabbit, goat, and dog) [15,24,28]. Mitochondrial DNA of *S. scabiei* isolated from rabbits originated from Kediri, Malang, and Nganjuk, East Java, Indonesia, all show COX-1 partial gene sequences that are highly similar (>99% identity) to those found in GenBank. Molecular analysis of phylogenetic in COX-1 sequences confirmed that it has three branches of *S. scabiei*: (1) large, unresolved branch, including sequences from Kediri, Malang, and Nganjuk rabbits, and sequences obtained from the GenBank of *S. scabiei* from different host and regions; (2) branch of *S. scabiei* from Australia wombats and *S. scabiei* isolate B1; and (3) Branch of *S. scabiei* type *hominis* from Australia and *Megaselia* sp. from Canadian insects, used as an outer group in this analysis.

The haplotypes of *S. scabiei* between koala and wombat have very high similarity (99.1%–100%). Close to a full-length phylogenetic analysis of mitochondrial genomes confirmed three branches of *S. scabie* (in human and two marsupial), no apparent difference in geographic or host species [16].

This research could be further developed to explore the genetic diversity of *S. scabiei* from animals species in Indonesia to produce subunit vaccines for scabies infection [29,30].

Conclusion

COX-1 gene sequences of *S. scabiei* from rabbits in Malang, Nganjuk, and Kediri were very similar (>99%) with COX-1 gene sequences of *S. scabiei* acquired from several hosts according to NCBI data.

Acknowledgments

The authors would like to thank the Rector of Universitas Airlangga and Director of Postgraduate School Universitas Airlangga. This study was supported by Universitas Airlangga research Grant, No.1131/UN3.1.15/LT/2018.

Conflict of interest

The authors declared that they have no conflict of interest related to this research

Authors' contribution

NDRL, as a research coordinator, designed the plan research work. AM and WMY did the laboratory works and analyzed the results. All authors read and approved the final manuscript.

References

[1] Bhat SA, Mounsey KE, Liu X, Walton SF. Host immune responses to the itch mite, *Sarcoptes scabiei,* in humans. Parasit Vectors 2017; 10:385–90; https://doi.org/10.1186/s13071-017-2320-4

[2] Walton SF, Currie BJ. Problems in diagnosing scabies, a global disease, in human and animal populations. Clin Microbiol Rev 2007; 20(2):268–79; https://doi.org/10.1128/CMR.00042-06

[3] Fraser TA, Shao R, Fountain-Jones NM, Michael Charleston M, Martin A, Whiteley P, et al. Mitochondrial genome sequencing reveals potential origins of the scabies mite *Sarcoptes scabiei* infesting two iconic Australian marsupials. BMC Evol Biol 2017; 17:233–42; https://doi.org/10.1186/s12862-017-1086-9

[4] Zhang R, Jise Q, Zheng W, Ren Y, Nong X, Wu X, et al. Characterization and evaluation of a *Sarcoptes scabiei* allergen as a candidate vaccine. Parasit Vectors 2012; 5:176–82; https://doi.org/10.1186/1756-3305-5-176

[5] Casais R, Granda V, Balseiro A, Cerro Ad, Dalt N, González, et al. Vaccination of rabbits with immunodominant antigens from *Sarcoptes scabiei* induced high levels of humoral responses and pro-inflammatory cytokines but confers limited protection. Parasit Vectors 2016; 9(1):435; https://doi.org/10.1186/s13071-016-1717-9

[6] Lastuti NDR, Yuniarti WM, Hastutiek P, Suwanti LT, Chrismanto D. Humoral and cellular response induced by antigenic protein of *Sarcoptes scabiei* var. *caprae*. Vet World 2018; 11:819–23; https://doi.org/10.14202/vetworld.2018.819-823

[7] Alasaad S, Rossi L, Heukelbach J, Perez JM, Hamarsheh O, Otiende M, et al. The neglected navigating web of the incomprehensibly emerging and re-emerging sarcoptic mite. Infect Genet Evol 2013; 17:253–9; https://doi.org/10.1016/j.meegid.2013.04.018

[8] Walton SF, Holt DC, Currie BJ, Kemp DJ. Scabies: new future for a neglected disease. Adv Parasitol 2004; 57:309–76; https://doi.org/10.1016/S0065-308X(04)57005-7

[9] Lastuti NDR, Hatutiek P, Suwanti LT, Chrismanto D. Exploration of *Sarcoptes scabiei* antigenic protein which play roles in Scabies pathogenesis in goats and rabbits. Iran J Parasitol 2018; 13(3):466–72.

[10] Amer S, Wahab TAE, Metwaly AEN, Ye J, Roellig D, Feng Y, et al. Preliminary molecular characterizations of *Sarcoptes scaibiei* (Acari: Sarcoptidae) from farm animals in Egypt. PLoS One 2014; 9(4):1–6; https://doi.org/10.1371/journal.pone.0094705

[11] Zheng Y, He R, He M, Gu X, Wang T, Lai W, et al. Characterization of *Sarcoptes scabiei* cofilin gene and assessment of recombinant cofilin protein as an antigen in indirect-ELISA for

diagnosis. BMC Infect Dis 2016; 16:21; https://doi.org/10.1186/s12879-016-1353-1
[12] Casais R, Granda V, Balseiro A, Del Cerro A, Dalton KP, González R, et al. Vaccination of rabbits with immunodominant antigens from *Sarcoptes scabiei* induced high levels of humoral responses and pro-inflammatory cytokines but confers limited protection. Parasit Vectors 2016; 9(1):1717–79; https://doi.org/10.1186/s13071-016-1717-9
[13] Xu J, Huang X, Dong X, Ren Y, Wu M, Shen N, et al. Serodiagnostic potential of alpha-enolase from *Sarcoptes scabiei* and its possible role in host-mite interactions. Front Microbiol 2018; 9:1–16; https://doi.org/10.3389/fmicb.2018.01024
[14] Makouloutou P, Suzuki K, Yokoyama M, Takeuchi M, Yanagida T, Sato H. Involvement of two genetic lineages of *Sarcoptes scabiei* mites in a local mange epizootic of wild animals in Japan. J Wild Dis 2015; 51(1):69–78; https://doi.org/10.7589/2014-04-094
[15] Arlian LG, Morgan MS. A review of *Sarcoptes scabiei*: past, present and future. Parasit Vectors 2017; 10:297; https://doi.org/10.1186/s13071-017-2234-1
[16] Fraser TA, Shao R, Fountain-Jones NM, Charleston M, Martin A, Whiteley P, et al. Mitochondrial genome sequencing reveals potential origins of the scabies mite *Sarcoptes scabiei* infesting two iconic Australian marsupials. BMC Evol Biol 2017; 17:233; https://doi.org/10.1186/s12862-017-1086-9
[17] Nas S, Chaudhry FR, Rizvi DA, Ismail M. Genetic characterization of *Sarcoptes scabiei* var. hominis from scabies patients in Pakistan. Trop Biomed 2018; 35(3):796–803.
[18] Desiandura K, Lastuti NDR, Suwanti LT, Handijatno D. Molecular identification of *Sarcoptes scabiei* var. *cuniculi* from Surabaya and Malang regions of East Java. I J T I D 2017; 6(6):150–3; https://doi.org/10.20473/ijtid.v6i6.5436
[19] Pentinsaari M, Salmela H, Mutanen M, Roslin T. Molecular evolution of a widely-adopted taxonomic marker (COI) across the animal tree of life. Sci Rep 2016; 6:35275; https://doi.org/10.1038/srep35275
[20] Dale JW, Schantz M. From genes to genomes. Concepts and applications of DNA technology. John Wiley & Sons Ltd. The Atrium, Southern Gate, Chichester, UK, vol. 17, pp 143–61, 2003.
[21] Lastuti NDR, Rohman A, Handiyatno D, Chrismanto D, Desiandura K. Sequence analysis of the cytochrome c oxidase sub unit 1(COX-1) gene of Sarcoptes scabiei isolated from goats and rabbits in East Java, Indonesia. Vet World 2019; 12:959–64; https://doi.org/10.14202/vetworld.2019.959-964
[22] Larkin MA, Blackshields G, Brown NP, Chenna R, McGettigan PA, McWilliam H, et al. Clustal W and Clustal X version 2.0. Bioinformatics 2007; 23(21):2947–8; https://doi.org/10.1093/bioinformatics/btm404
[23] Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. MEGA6: molecular evolutionary genetics analysis version 6.0. Mol Biol Evol 2013; 30(12):2725–9; https://doi.org/10.1093/molbev/mst197
[24] Gu XB, Yang GY. A study on the genetic relationship of mites in the genus Sarcoptes (Acari: Sarcoptidae) in China. Int J Acarol 2009; 34(2):183–90; https://doi.org/10.1080/01647950808683722
[25] Boron, WF, Boulpaep EL. Medical physiology. Elsevier Saunders, Philadelphia, England, p 90, 2005. Updated edition. ISBN 1-4160-2328-3.
[26] Kraabøl M, Gundersen V, Fangel K, Olstad K. The taxonomy, life cycle and pathology of *Sarcoptes scabiei* and *Notoedres cati* (Acarina, Sarcoptidae): a review in a Fennoscandian wildlife perspective. Fauna Norvegica 2015; 35:21–33; https://doi.org/10.5324/fn.v35i0.1652
[27] Arlian LG, Morgan MS, Neal JS. Modulation of cytokine expression in human keratinocytes and fibroblasts by extracts of scabies mites. Am J Trop Med Hyg 2003; 69:652–6; https://doi.org/10.4269/ajtmh.2003.69.652
[28] Erster O, Roth, Pozzi PO, Bouznach A, Shkap V. First detection of *Sarcoptes scabiei* from domesticated pig (*Sus scrofa*) and genetic characterization of *S.scabiei* from pet, farm and wild hosts in Israel, Division of Parasitology. Kimron Veterinary Institute. Exp Appl Acaroll 2015; 66(4):605–12; https://doi.org/10.1007/s10493-015-9926-z
[29] Harumal P, Morgan M, Walton SF, Holt DC, Rode J, Arlian LG, et al. Identification of a homologue of a house dust mite allergen in cDNA library from *Sarcoptes scabiei* var.*hominis* and evaluation of its vaccine potential in a rabbit/*S. scabiei* var. *canis* model. Am J Trop Med Hyg 2003; 68:54–60; https://doi.org/10.4269/ajtmh.2003.68.54
[30] Gu X, Xie Y, Wang S, Peng X, Lai S, Yang G. Immune response induced by candidate *Sarcoptes scabiei* var. *cuniculi* DNA vaccine encoding paramyosin in mice. Exp Appl Acarol 2014; 63:401–12; https://doi.org/10.1007/s10493-014-9780-4