Molecular characterization of encoding gene of second internal transcribed spacer (ITS-2) of *Sarcoptes scabiei* in rabbits from several areas of East Java, Indonesia

Nunuk Dyah Retno Lastuti, Nur Rusdiana, Poedji HastutieK
Faculty of Veterinary Medicine, Universitas Airlangga, Surabaya, Indonesia

**Background**

*Sarcoptes scabiei* mites is the causal agent of the highly contagious skin disease that affects animals and humans worldwide. Scabies as an emerging/re-emerging parasitic disease that threatens human and animal healthy globally. Many country and international organization realize how important scabies is, that included as one of 50 most common diseases worldwide and treated as “neglected tropical disease”. Scabies is one of the most economically important diseases in goats and rabbits in Indonesia. This study purpose to determine the molecular characterization of encoding gene of the ITS-2 of *S. scabiei* in rabbits from several areas of East Java.

The PCR product of the samples showed the DNA band tape at 304 bp. Homology analysis results from the five samples showed identity with the range of 91.23-98.68% with *S. scabiei* originate isolate from China (KX695125.1). Phylogenetic tree analysis results showed that the sample from several areas of East Java close to *S. scabiei* samples from *Capricornus crispus*, Japan isolates (AB820977.1), Rabbit, Chinese isolates (KX695125.1 and EF514469.2) and Ferral raccoons, Japan isolates (AB36384.1) and many other isolates present on NCBI data.

**Materials and Methods**

*S. scabiei* mites collected from rabbits scabies from Surabaya, Sidoarjo, Mojokerto, Pasuruan and Nganjuk; DNA extraction with minikit QIAamp DNA; PCR amplification; nucleotide sequence analysis; homology and phylogenetic tree using the Neighbor-Joining method in the program MEGA-7.

**Conclusion:** The homology analysis of all samples showed identity more than 91.23% with isolate China (KX695125.1). The sequences of ITS-2 gen of *S. scabiei* from rabbits in several area were relatively close to *S. scabiei* obtain various hosts from NCBI data.