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Morphological, molecular and histopathological identification of *Sarcoptes scabiei* infection in a goat herd at Goa, India

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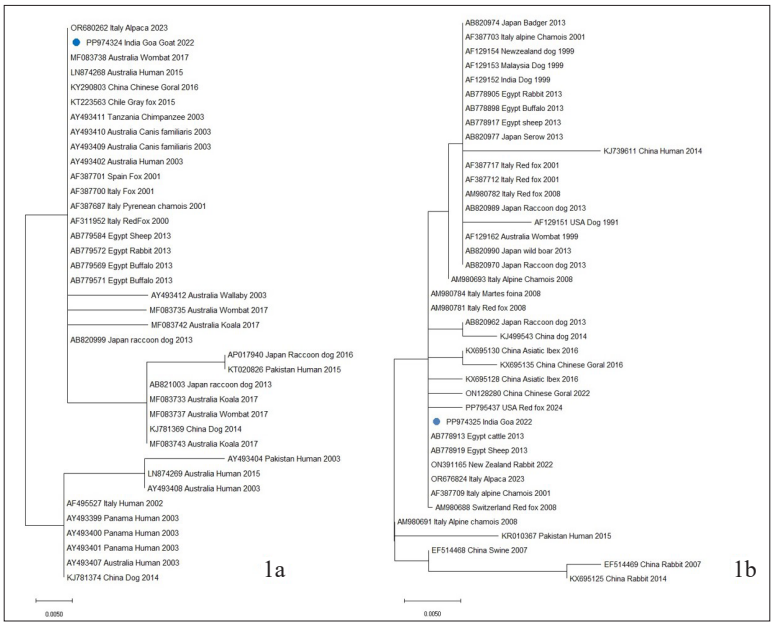
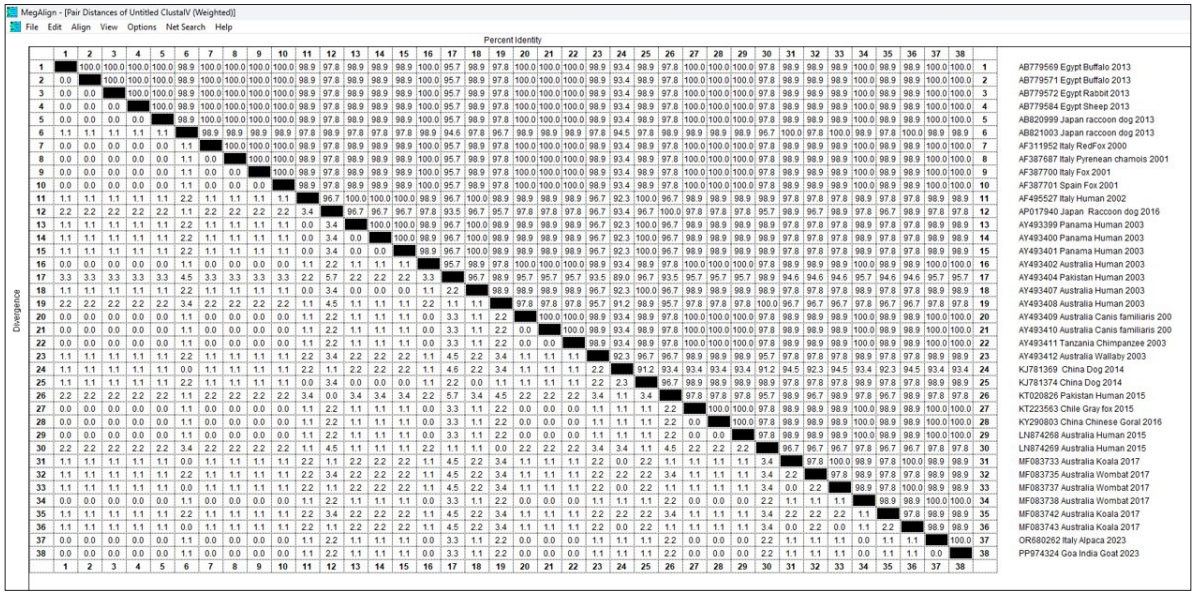
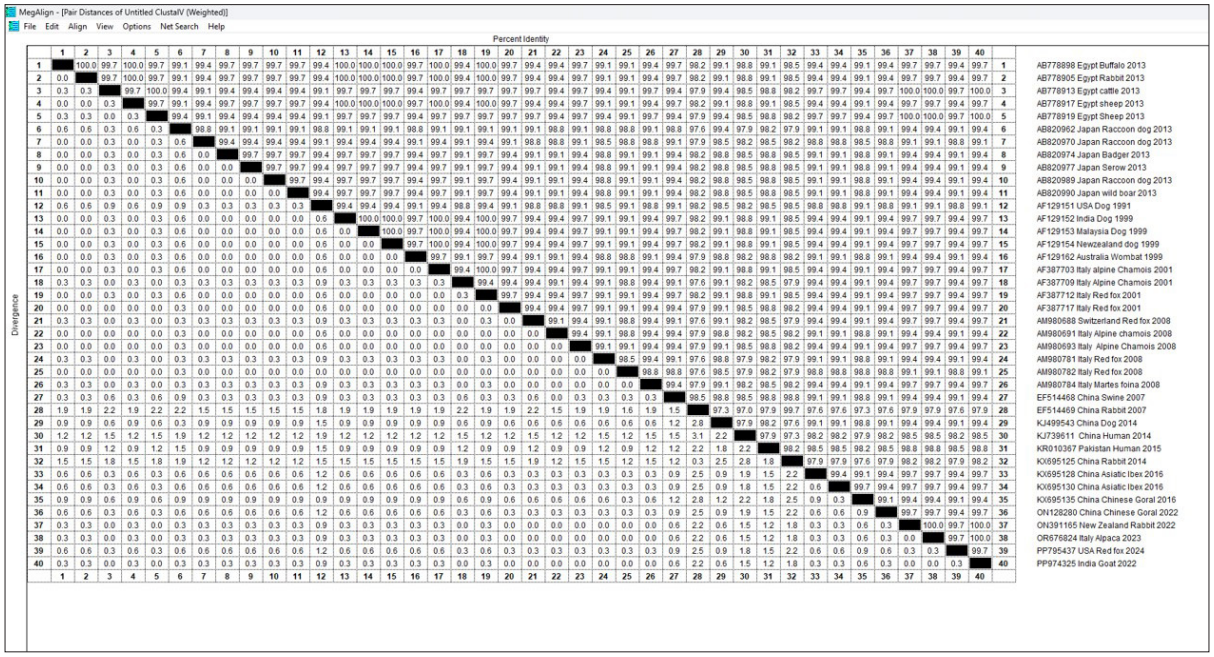


Supplementary Fig. 1. Phylogenetic tree based on the *16s rRNA* gene (1a) by Maximum Likelihood method of MEGA X, showing the clustering of strains in 3 major groups, and the Phylogenetic tree based on the *ITS* gene (1b) showed three clades on the ML tree with the isolate from the present study marked as blue.



Supplementary Fig. 2. Percentage identity of *16srRNA* gene sequence of Goan isolate PP974324 with NCBI sequences revealed by MEGALIGN program of DNASTAR software.



Supplementary Fig. 3. Percentage identity of *ITS* gene sequence of Goan isolate PP974325 with NCBI sequences revealed by MEGALIGN program of DNASTAR software.