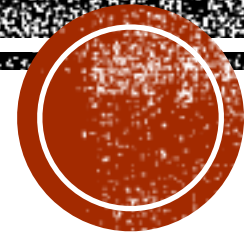
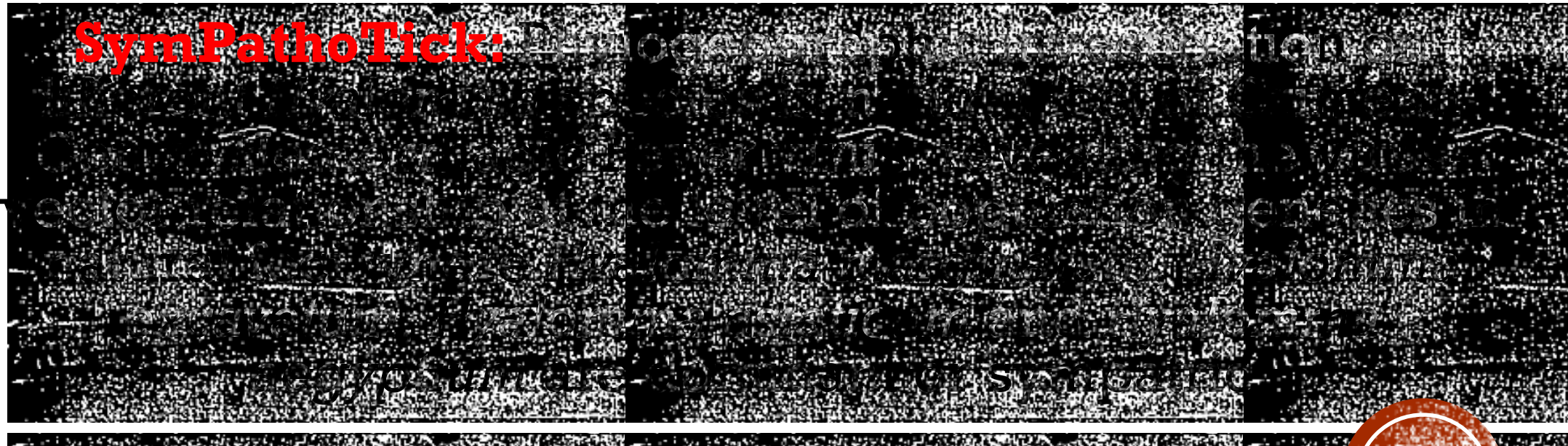


## SymPathoTick:



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Ticks and Tick-Borne Diseases Lab.

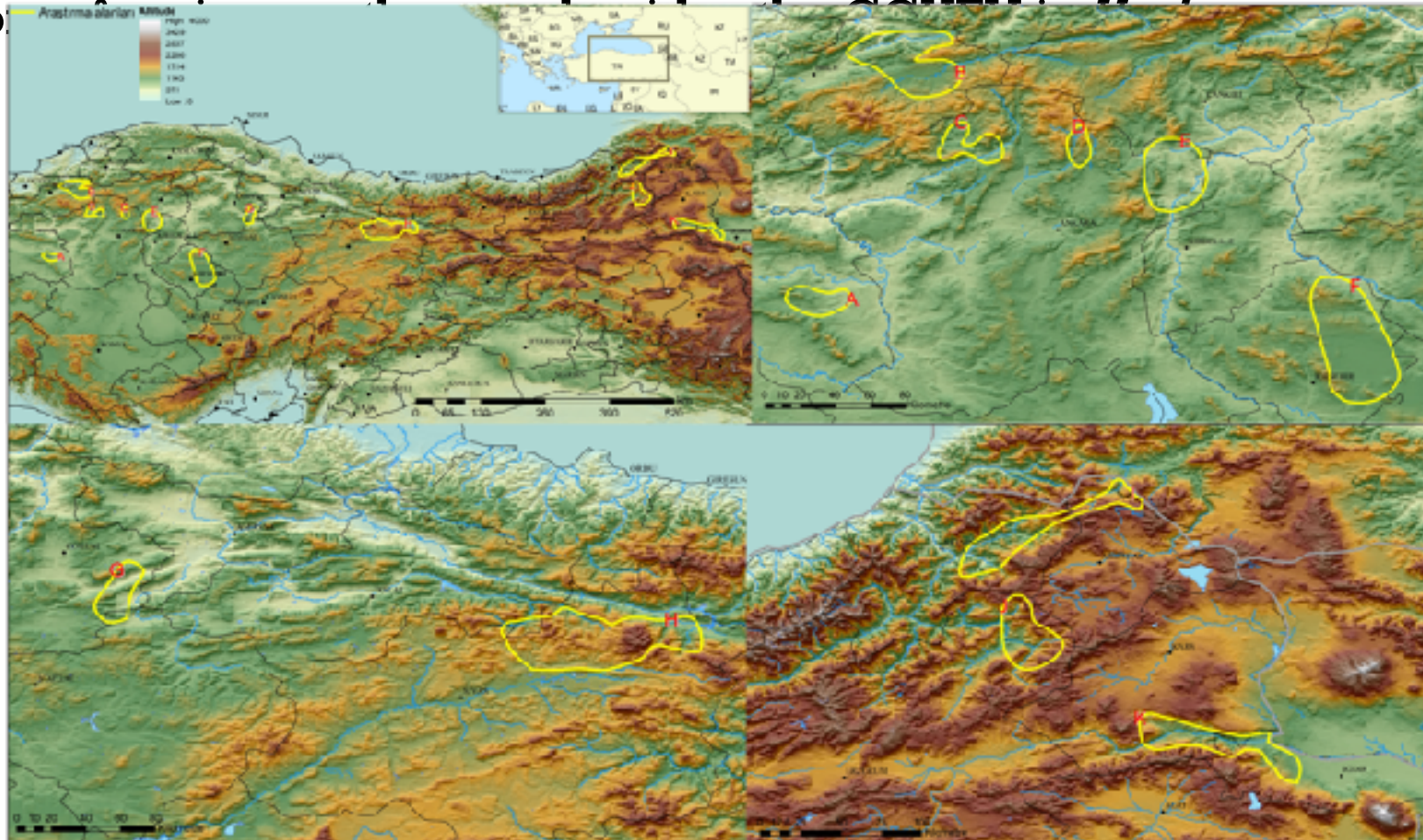
- **Project code:** TÜBİTAK COST2515
- **Project number:** 224O312
- **Project name:** Phylogeographic investigation on different *Hyalomma* species in natural foci of Crimean-Congo Hemorrhagic Fever virus: Revealing the virus-vector relationship at the level of population genetics in natural foci where *Hyalomma marginatum*, *Hyalomma excavatum*, *Hyalomma asiaticum* and *Hyalomma aegyptium* are dominant or sympatric.
- **Project duration:** 3-years
- **Related COST action:** PRAGMATICK
- **Funded by:** TÜBİTAK





- **Aim:** to investigate the presence of the virus in sympatric and dominant Hyalomma populations (*H. marginatum*, *H. excavatum*, *H. asiaticum* and *H. aegyptium*) in natural CCHF foci located in endemic and hyperendemic zones of Anatolia from a comparative population genetic and phylogeographic perspectives.

- The secondary objective is to phylogeographically investigate the potential vector species.



Other pathogens

Aigai virus  
*Babesia* spp.  
*Theileria* spp.  
*Anaplasma* spp.  
 SFG rickettsiae  
*C. burnetii*  
*F. tularensis*  
*Ehrlichia* spp.



## ■ Objectives are:

- To comparatively reveal the role of exophilic *Hyalomma* species in different natural foci of CCHFV in Anatolia,
- To characterize the S-segment-based population genetic structure of CCHFV to be detected in different *Hyalomma* species in hyperendemic and endemic regions,
- To investigate the potential roles of *H. asiaticum* and *H. excavatum* species,
- To characterize the population structure of CCHFV positive *Hyalomma* specimens based on the *cox1* gene,
- To investigate the presence of the Asian genotype of CCHFV, which is not known to exist in Türkiye but is circulating in the neighboring country Iran,
- To characterize the genetic diversity of various CCHFV variants observed in *Hyalomma* species by revealing their whole genome sequences,
- To determine the potential enzootic cycles and phylogenetic structure of CCHFV in *Hyalomma* ticks other than *H. marginatum*,
- To reveal the presence of various bacterial and protozoan pathogens as well as CCHFV and mixed infections in target *Hyalomma* populations,
- To elucidate the potential phylogeographic correlation of all pathogen and tick population genetic structure,
- To generate eco-epidemiological and genetic data that can potentially be utilized in the development of early warning systems and the mitigation of CCHF at both national and global levels.





# THANK YOU

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