

Dear colleagues,

APHAEA (harmonized Approaches in monitoring wildlife Population Health, And Ecology and Abundance, www.aphaea.org) is an European EMIDA ERA-NET (www.emida-era.net) project closely associated with EWDA (European Wildlife Disease Association, www.ewda.org) activities. The project aims to establish an European wildlife disease surveillance network that is capable of providing reliable estimates on abundance of wildlife species and pathogen distribution and occurrence in key wildlife species in order to improve wildlife health surveillance in general. APHAEA will enhance international collaboration expected to continue after the end of the project to use the potential for monitoring pathogen distribution of selected wildlife diseases which impact on human and livestock health.

First, literature reviews in respect of methods for estimating wildlife population abundance (Species cards) and on methods for wildlife disease diagnostics (Diagnosis cards) were conducted with the aim to propose selected methods for data harmonization, both at national and European level. External partners are encouraged to provide feedback on the Species and Diagnosis cards and to indicate whether they would apply the proposed harmonized protocols in future studies.

The second part of the project consists in testing the proposed harmonized protocols and demonstrating the advantages of harmonization. For this purpose, three host-pathogen combinations have been selected:

Wild boar (*Sus scrofa*) and Aujeszky's disease virus (Pseudorabies)
Red fox (*Vulpes vulpes*) and *Echinococcus multilocularis* (Fox tapeworm)
Common vole (*Microtus arvalis*) and *Francisella tularensis* (Tularemia).

The respective questionnaires aim at evaluating which data may already be available or could be collected for the second part of the project. **External partners are invited to share existing data or contribute to collecting new ones.** On the one hand, **new data will be collected** about **host abundance** and **pathogen occurrence** for each host-pathogen combination following harmonized protocols. **Pathogen occurrence is no prerequisite for study participation.** On the other hand, **existing data should be compiled** to complement the field studies. Results will be discussed at network meetings to identify strengths and weaknesses of the proposed schemes. The overall aim of this work besides harmonization is to deliver European maps with data on abundance of key host species and on occurrence of important pathogens.

Please **find attached the three questionnaires** indicated above, designed to collect information regarding historical records, data currently available or potentially accessible in the future. You may decide, which of the host-pathogen combinations are applicable for your country. Could you please complete the respective questionnaire(s) until **30th of November 2013**? After potential co-operation partners have been identified on basis of the answers in the questionnaire, we will provide further information, protocols and Excel-sheets to facilitate data exchange.

Any data you provide to the APHAEA project will be treated as strictly confidential and will only be used within the framework of the project for the selection of feasible studies for the evaluation of harmonized sampling protocols. It is planned to publish the harmonization efforts, strengths and maybe occurred problems of the protocols based on the evaluation of the provided data. The manuscript will be send to the data providers prior to publication and your co-authorship will be recognized. In any case, it is planned to share the results of the questionnaire evaluations in an aggregated, anonymous form among the participants of the survey.

If you are not able to fill the questionnaires, please feel free to pass this information to other potentially interested persons. If there are any questions, please do not hesitate to contact us for further information via feedback@aphaea.eu.

Thank you very much for your co-operation.

Best regards,

WP3 APHAEA project team