



Federal Ministry
of Food
and Agriculture

LEAPAgri

A long EU Africa research and innovation partnership on
Food and Nutrition Security and Sustainable Agriculture

Project Acronym: MUSBCEA

country/countries	Uganda, Kenya, Egypt, Spain, Germany
funding agency	Federal Ministry of Food and Agriculture – BMEL
project management	Federal Office for Agriculture and Food – BLE
project coordinator	Prof Dr Joseph Erume, Makerere University, Kampala, Uganda
project partner(s)	<ul style="list-style-type: none">• PD Dr. Wolfgang Beyer, Universität Hohenheim, Stuttgart• Prof Dr Ignacio Moriyon, University of Navarra, Pamplona, Spanien• Prof Dr Jose Blasco, Centro de Investigacion y Technologica Alimentaria de Aragon, Zaragoza, Spanien• Prof Dr Lilly Bebora, Faculty of Veterinary Medicine University of Nairobi, Kenia
associated partners	<ul style="list-style-type: none">• Animal Health Research Institute (AHRI), Mansoura, Ägypten• Faculty of Veterinary Medicine, Benha University, Ägypten• Friedrich-Löffler-Institut, Jena• Bundesinstitut für Risikobewertung (BfR) Berlin
project budget	282.553,80 EUR

project duration	August 2018 – December 2021
key words	Brucellosis, Epidemiology, Genotyping, Whole Genom Sequencing
background	<p>Livestock breeding in Eastern Africa as well as in Egypt represents a very high economic factor and is of great importance for nutrition and health. Brucellosis, caused by <i>Brucella</i> spp. is a zoonosis and one of the main causes which negatively influence the health and productivity of livestock and thus has a negative impact on food security, socio-economic development and the health of the population in these countries. In Kenya up to 25%, in Uganda up to 56% and in Egypt up to 38% of livestock herds are infected with <i>Brucella</i>. Important to emphasize is that the majority of these livestock are kept by small farmers.</p> <p>Governmental control programs are not in force or not effective.</p>
objective	<p>The main part of the German project partner has been the isolation, characterization and genotyping of <i>Brucella</i> spp. from African countries. Using genetic and epidemiological data, phylogeographic maps of the distribution and spread of <i>Brucella</i> outbreak strains in those countries are created. The genotyping results are analyzed following a hierarchical scheme using canSNP analysis (for <i>B. melitensis</i>), fragment analysis (Bruce-ladder PCR, Multilocus Variable Number of Tandem Repeats Analysis (MLVA)) and whole genome sequencing with a subsequent core genome SNP (cgSNP) analysis. The raw sequencing data will be made available in and compared to international databases.</p>
results	<p>In order to analyze the spread and diversity of outbreak strains of <i>Brucella</i> spp. 47 isolates of <i>B. abortus</i> from 11 Governments and 137 isolates of <i>B. melitensis</i> from 17 Governments in Egypt could be used. Samples were available from years 2001-2020.</p> <p>Genotyping based on differences in cgSNPs or the fragment lengths of VNTR-markers revealed a very fine differentiation of strains on the level of isolates from the outbreaks. Epidemiological metadata on date and site of sampling and the animal species as well were used to correlate genotypes with outbreak strains.</p> <p>Results revealed from cgSNP analysis and their comparison to the appropriate MLVA data do not support the recently published and commonly followed idea on the epidemiological interpretation of Brucella-MLVA data. Identical MLVA genotypes do not indicate identical outbreak strains and vice versa.</p> <p>Our analyses give a new picture on diversity and spread of <i>Brucella abortus</i> and <i>Brucella melitensis</i> in Egypt. Results indicate the presence of rather old outbreak strains which might have been imported with animals from European countries like Italy and Great Britain. On the other hand there are rather young and very diverse outbreak strains identified indicating recent imports of animals as a source.</p> <p>In some cases outbreak strains could be defined having spread among and between up to five Governments. These results indicate the spread of the pathogens by live animal transports or via contaminated animal products, mainly dairy products.</p> <p>Such phylogeographic correlations are of great relevance for every analysis of the epidemiological situation of the presence, routes and causative factors of</p>

spread of Brucellosis in Egypt. The know-how and methodology developed in this project can provide a tool for targeted control programs. Such an approach can also be transferred to other regions endemic for Brucellosis.

One of the main milestones in this project has been the establishment of a bioinformatic pipeline on the „BinAC“-Server in Tübingen as developed at the reference laboratory on Brucellosis, the IBIZ FLI Jena. Access for scientists from IBIZ and the University of Hohenheim was provided, appropriately. With this tool the basics for analysis of bacterial whole genome sequences are made available for the University.

recommendations

The establishment of a tool for differentiation of *Brucella* genotypes by cgSNP-analysis and correlating genomic data with epidemiological metadata to define outbreak strains allows for the analysis of diversity and spread of the disease Brucellosis. This tool should become part of every future programs on the control of Brucellosis.



Workshop und Training at the University of Nairobi, March 2019

photos



Workshop in Mansoura, Egypt, November 2019



Meeting at Animal Health Research Institute, Cairo, Egypt, November 2019