



Grant agreement no. 243964

QWeCI

Quantifying Weather and Climate Impacts on Health in Developing Countries

M1.1a: Completion of main phase of data entry to database

Start date of project: 1st February 2010

Duration: 42 months

Lead contractor : UNILIV
Coordinator of milestone : UNILIV
Evolution of milestone

Due date : M15
Date of first draft : M15
Start of review : M15
Milestone accepted : M15

Project co-funded by the European Commission within the Seventh Framework Programme (2007-2013)		
Dissemination Level		
PU	Public	PU
PP	Restricted to other programme participants (including the Commission Services)	
RE	Restricted to a group specified by the consortium (including the Commission Services)	
CO	Confidential, only for members of the consortium (including the Commission Services)	

As a part of the ERA NET funded ENHanCE project, the ENHanCEd Infectious Diseases (EID) database has been developed. This described the pathogens of humans and animals, along with detail on their vectors and the host species they affect, the location of pathogens and their hosts and information on the sources from which the above information came. Location information is derived from information given in the NCBI Nucleotide database (see <http://www.ncbi.nlm.nih.gov/nuccore>) or for automated literature searches of PubMed for pathogen names and the MeSH terms for country names.

During further discussion between Andy Morse and Matthew Baylis it was decided that literature would be examined for climate links to disease for a short-list of pathogens as opposed to examining climate links for 'diseases of importance in Africa partly described by stakeholders', as originally defined. This short list includes Rift Valley Fever, Malaria and tick-borne diseases of Africa.

A sequence of specific steps are in the process of being undertaken in order to incorporate the information described above into the EID, and thereafter to fulfill the tasks described in the work-package description. These include:

Description of step:	Status of step:
1. Incorporate information on the location of pathogens provided by sequences sent to the NCBI Nucleotide database into the EID. After a trial study in which no false information was identified from within a subsample, it will be assumed that of information supplied from the NCBI nucleotide database, 100% is correct.	Finished
2. Incorporate information on pathogen, vector and host interactions provided by the NCBI Nucleotide database into the EID using the same assumption of validity.	Finished
3. Further information on the location of pathogens provided by automated literature searches of the PubMed database using pathogen names and the MeSH terms for country names will then be incorporated in the EID, based upon defined inclusion thresholds. As this information will be based upon the frequency of pathogen names and their locations occurring in the literature, it will be supplied with confidence intervals for the likelihood of the relationship being true.	Ongoing - to be completed end M16 (May 2011)

Access to the database <http://www.zoonosis.ac.uk/EID2/> is available for bona fide researchers.