

The 1st International One Health Congress – Individual Oral Abstract Template
14 – 16 February 2011

*** A maximum of 250 words applies***

Your abstract title and author names will be published as you have entered in the online system

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| <p>Abstract Title:</p> | <p>Parasite community ecology and epidemiological interactions at the wildlife/domestic/human interface: can we anticipate emerging infectious diseases in their hotspots?</p> |
| <p>Author(s): Please BOLD those authors who will present this paper. Name, affiliations eg. John Smith, University of Melbourne; Lisa Jones, University of Monash, Melbourne.</p> | <p>Alexandre Caron, Cirad UPR AGIRs, Michel de Garine-Wichatitsky, Cirad UPR AGIRs, Serge Morand, ISEM - CNRS</p> |
| <p>Sub-Theme: List the corresponding subtheme for your abstract i.e. Session 2: Disease Emergence Emerging Zoonoses</p> | <p>Session 2: Disease Emergence - <i>Pathogen Discovery and Early Detection</i></p> |
| <p>Please follow the format outlined on the congress website www.onehealth2011.com/coa.php</p> <p>Abstract: Text should be Arial Font 10 point single spaced.</p> <p>Maximum of 250 words</p> <p>- Your abstract must fit on one page.</p> <p>- Margins of text box are not be altered.</p> <p>Should your abstract not follow the above guidelines, it will not be accepted.</p> <p>Focus on the practical implementation of a project/case study where the outcomes/results have led to changes (i.e. what did you achieve? How did you achieve it? What worked? What didn't work?)</p> <p>State what your presentation adds to what is already known i.e. how/why is your work innovative?</p> | <p>Identified hotspots of emerging infectious diseases are often characterised by an extensive wildlife/domestic/human interface in tropical ecosystems, thus creating complex multi-hosts and multi-pathogens systems. How can we anticipate emerging events in these hotspots?</p> <p>The parasite communities shared by wild and domestic populations at this interface reflect the historical of epidemiological interactions between them. A new pathogen entering this host system is most likely to use the transmission pathways already used by other pathogens. Using recent advances in community ecology and evolutionary molecular biology, we present a research framework to identify these transmission pathways.</p> <p>We applied this framework to 34 macroparasites and 7 microparasites shared by 14 rodents and the human species in a study site in Thailand. Based on a comparative study of component communities between host populations using the Jaccard index (presence/absence data), we build a network of interactions between the host populations. This network is characterised by the frequency, intensity and direction of interactions and can be explored using classical network analysis.</p> <p>We discuss the challenges and possibilities of this innovative approach. It provides a description of the transmission pathways between host species the most used by pathogens. This network can provide direct inputs for targeted disease surveillance at the wildlife/domestic/human interface to detect pathogen emergence when it occurs or host most likely to provide a source for future emergence.</p> <p>More generally, this approach could support the exploration of hypothesis about the general properties of transmission ecology at the wildlife/livestock/human interface.</p> |

Please check spelling and grammar before you submit.