insecticides can have profound negative impacts; c) conventionally bred maize varieties can differ substantially in their impact; d) different management practices have profound impacts on populations on-crop and off-crop. A number of conclusion can be drawn from the assessments: 1. The NTO ERA for Bt-maize should more strongly rely on early tier experiments; 2. Field trials are only sensible if results from earlier tiers show the possibility for negative NTO impacts; 3. A comparative approach to ERA is without alternative, also looking at conventionally bred varieties and alternative management approaches; 4. The methods and trial designs used are able to detect differences in impact of different maize varieties; 5. To fully assess the potential impacts of the cultivation of Bt- and other genetically modified plants a systems approach is needed, that also takes into account the benefits of using these plants; 6. A decision is needed on what we really want to protect and thus need to assess.

THURSDAY - 7 August

SYMPOSIUM 7 (Dis. of Benef.I Inverteb.) Thursday, 8:00-10:00 **Emerging Tools for Aquatic Pathogen Discovery and Description**

Symposium. Thursday, 8:00. 203

Early mortality syndrome is an infectious disease with a bacterial etiology

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Beginning in about 2009, a new, emerging disease called "Early Mortality Syndrome or EMS" (more descriptively called Acute Hepatopancreas Necrosis Syndrome or AHPNS) began to cause significant production losses in shrimp farms southern China. By 2010 the range of affected farms in China had expanded, and by 2011 EMS/AHPNS was confirmed in Vietnam and Malaysia, and in Thailand in 2012. EMS/AHPNS disease has caused serious losses in the areas affected by the disease, and it has also caused secondary impacts on employment, social welfare, and international market presence. EMS/AHPNS was first classified as an idiopathic disease because no causative agent had been identified. Preliminary studies conducted in Vietnam in 2012 by the Laboratory of Aquaculture Pathology at the University of Arizona (UAZ-APL) have indicated that EMS/AHPNS is infectious. Since early in 2013, the UAZ-APL was able to isolate and identify the causative agent of EMS/AHPNS in pure culture. In several separate challenge experiments, the same EMS/AHPNS pathology was reproduced consistently in experimental shrimp. In addition, the same identical agent was recovered from the challenged animals and several subsequence challenge tests using the recovered agent could also reproduce EMS/AHPNS pathology with very consistent results. The agent was identified as a unique strain of Vibrio parahaemolyticus that is commonly found in marine environment. Hence, EMS/AHPNS has a bacterial causative agent that satisfies Koch's Postulates to be a typical infectious disease. Further studies focusing on the agent of AHPNS revealed that the agent could produce toxin(s) causing the primary pathology in affected shrimp.

Symposium. Thursday, 8:30. 204

Policy, phylogeny, and the parasite Grant D. Stentiford ^{1,2}, Stephen W. Feist ², David M. Stone ², Edmund J. Peeler² and David Bass

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Animal diseases gain political attention by their inclusion on lists of global bodies such as those of the World Organisation for Animal Health. Currently, the OIE lists 116 diseases caused by viral, bacterial, fungal, protistan, and metazoan pathogens. Each is afforded a specific chapter in the regularly updated OIE 'Manual of Diagnostic Tests' series. Of these, 30 diseases are caused by eukaryotic (fungal, oomycete, protistan, and metazoan) parasites. Inclusion necessitates national governments to report outbreaks promptly but may lead to trading restrictions between nations in an attempt to limit spread. Detection therefore has consequences that may directly impact from farm to state levels. Here, we consider current approaches to discrimination of listed parasites from related, but unlisted, counterparts. We outline problems with defining 'species', propose the necessary drivers that should be required for discrimination of important taxa, and highlight how this process may be influenced by national policies. Further, we propose a set of 'best practice' measures, broadly based upon current taxonomic philosophies for protists and metazoans that should be applied when defining taxa for listing as notifiable. We will illustrate these principles with topical issues associated with the taxonomy and listing of aquatic invertebrate pathogens.

Symposium. Thursday, 9:00. 205

The Next Generation of Crustacean Health: Disease Diagnostics Using Modern Transcriptomics K. Fraser Clark ^{1,2,3}; Spencer J. Greenwood ^{1,2};

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Commercial crustacean fisheries on the Atlantic coast of Canada represent over \$(CAD) 1 billion annually. The American lobster (Homarus americanus) fishery alone represents over \$(CAD) 600 million with harvests in recent years breaking records for amount of lobster that has been landed. The Canadian and Maine USA lobster populations remain healthy but the once vibrant lobster fisheries in Southern New England USA have been devastated by a mixture of disease, ocean acidification, global warming and anthropogenic stressors. Conventional gross anatomic, microscopic and histological analysis remain the backbone of

crustacean health and disease assessment but new molecular genetic techniques are beginning to be integrated into this assessment. Modern genomics and transcriptomics have revolutionized the discovery of diagnostic and prognostic markers in human and terrestrial medicine and promise to drive crustacean health and diagnostic molecule discovery. We have recently begun to apply high-throughput transcriptomic techniques, such as microarray and RNA-Seq, to investigate American lobster health, disease and response to physiological and anthropogenic stressors. Our studies highlight the incredible potential that modern molecular biological approaches have for advancing our understanding of crustacean immunology and disease biomarker discovery.

Symposium. Thursday, 9:30. 206

Environmental DNA as a tool for detection and identification of aquatic parasites: known unknowns and iust plain unknowns

just plain unknowns <u>Hanna Hartikainen</u>^{1,5}; Grant D. Stentiford^{2,3}; Kelly Bateman^{2,3}; Stephen W. Feist³; David M. Stone³; Matt Longshaw^{3,4}; Georgia Ward¹; Charlotte Wood¹; Beth Okamura¹ and David Bass¹

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The increasing application of massively parallel sequencing technology to environmental DNA samples (e.g. from water, sediment, soils, whole animals) is providing unprecedented resolution of microbial community structure, diversity and functioning. Application of general and specific primer approaches, amplicon sequencing and metagenomics have enormous potential for the detection of known, novel and otherwise cryptic pathogen lineages. We use such techniques to detect invertebrate pathogens of potential significance to fisheries and aquaculture. Using specific-primer approaches, we have revealed unknown diversity of haplosporidian parasites from eDNA and show shifts in parasite communities along an offshore gradient. At the other end of the spectrum, we have used a metagenomic approach to identify a mikrocytid pathogen of juvenile edible crabs that had eluded molecular characterization using specific- and general primer approaches. We highlight the current methods for discovery and detection of potential pathogens in eDNA samples and show how such studies can inform on ecology, life-cycle and transmission dynamics of aquatic pathogens. Finally, we predict a re-emergence in the importance of classical approaches to disease investigation (e.g. histopathology, electron microscopy) to enable meaningful links to be drawn between presence within the matrix and outcomes in hosts. eDNA analyses should therefore be considered as a 'tool in the box', rather than the toolbox per se, for investigating pathogens of concern to aquatic hosts.

CONTRIBUTED PAPERS Thursday 8:00-10:00

Contributed paper. Thursday, 8:00. 207

The Role of biocontrol agents within IPM of *Tuta* absoluta on tomato in Egypt <u>Mahfouz Abd-Elgawad</u>

Nematodes 3

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Since its arrival in Spain, the tomato leafminer Tuta absoluta has rapidly spread around Europe and has become an extremely important pest of tomato crops in Mediterranean Basin countries. This pest arrived to Egypt early in 2010 and there soon followed an outbreak in many tomato-planted areas where it caused extensive damage by mining in tomato leaves, stems and fruit. Egyptian entomopathogenic nematode species (EPN) induced 89.3-96.4% mortality to T. absoluta larvae. Also, the other biocontrol agents Trichogramma achaeae and Macrolophus pygmaeus are suggested as effective components within a new control strategy against the insect on tomato in the present study. M. pygmaeus may prey on T. absoluta eggs and larval stages, but due to more suitable climate of Egypt to T. achaeae, earlier release of the latter bug is preferable in order to start the control on the first generations of the pest eggs. EPN have both foliar and soil applications in the strategy. On the foliage, EPN can control efficiently feeding larvae of T. absoluta in and outside the leaf galleries while the soil nematodes kill both last instar larvae, when they slide down from the leaves to pupate, and emerging adults from the buried pupae. In addition to such natural enemies, the strategy is supported by prophylactic measures, light and pheromone traps, and IPM compatible insecticides.

Contributed paper. Thursday, 8:15. 208

Insecticidal activity of Heterorhabditis bacteriophora Shandong toward Brontispa longissima and Cryptothelea variegate

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Heterorhabditis bacteriophora nematodes kill many insect species, but its potencies toward *Brontispa longissim and Cryptothelea variegate* pests are unknown. Initially, four isolates of *H. bacteriophora*, UV resistant *H. bacteriophora* Shandong (HbSD), Hb I, Hb II, and Hb III were bioassyed against standard insect *Galleria mellonella*. The UV resistant HbSD isolate was chosen for next bioassay against the last-instar of *B. longissima* and *C. variegate* compared with *G. mellonella* in the laboratory. After exposure of insects to infective juveniles of nematodes (IJs) for six days, mortality was correlated with dosage, and the LC₅₀ was \approx 9.35 IJs for *B. longissima* and \approx 11.76 IJs for *C. variegate*, as compared with that \approx 8.56 IJs for *G. mellonella*. There are no statistically different in potency among these three hosts. Thus, the insecticidal potencies of the nematodes to these three pests