



ESEB

XVI Congress

Groningen, The Netherlands



20-25 August 2017

Caribbean lizard, *Anolis sagrei*

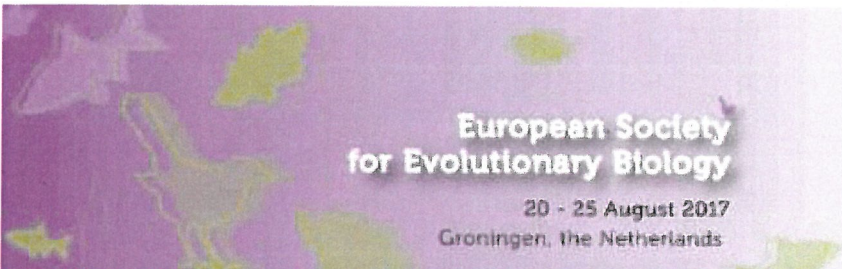
Landscape wide effects of Pgi genotypes on population dynamics of the Glanville fritillary butterfly	Schulz T. et al.	43
Population dynamics and developmental mode variation of a spionid polychaete - nature vs. nurture.	Thonig A. et al.	45
A global analysis of the role of habitat in avian diversification.	van Els P. et al.	47
Genetic diversity in fluctuating environmental conditions through ddRAD sequencing	Vasileiadou K. et al.	49
Host-parasite coevolution promotes the evolution of seed banking as a bet hedging strategy	Verin M. et al.	51
Investigating host-pathogen coevolution in associations between human HLA and <i>Mycobacterium tuberculosis</i> genetics	Winternitz J. et al.	53
Can we infer diversity-dependent diversification from phylogenies under multiple locations model?	Xu L. et al.	55

Symposium 34. Applications of evolutionary biology in agriculture and industry

Linking pollinator behavior to gene flow risk to predict transgene escape in insect-pollinated crops	Brunet J. et al.	1
The spatial and temporal genetic structure of <i>Rhopalosiphum padi</i> in the UK	Morales-Hojas R. et al.	2
SNP assay validation for introgression analysis in the dark honey bee using MALDI-TOF MS	Muñoz I. et al.	3
The genome of <i>Drosophila subpulchrella</i> and the importance of sister-species comparison in agricultural pest science	Rota-Stabelli O. et al.	4

Symposium 35. Open symposium

Population structure and linkage disequilibrium of the dengue mosquito across Thailand using nuclear DNA sequences	Arunyawat U. et al.	2
TiBi – Teaching the importance of biodiversity at lower organizational levels	Becks L. et al.	4
Evolving brain morphology in prey-predator interactions	Bijl W. et al.	6
The breeding brain: Increased neural investment during reproduction in stickleback	Buechel S. et al.	8
The age of morphological stasis: absence of interspecific morphological differentiation despite pronounced genetic divergence	Cerca de Oliveira J. et al.	10
Genome-wide evidence for adaptive evolution in two wild passerine species with different effective population sizes	Corcoran P. et al.	12
Is bigger better? The relationship between size and reproduction in female Asian elephants	Crawley A. et al.	14
Ontogenetic stage, plant vigor and sex mediate herbivory loads in dioecious <i>Mercurialis perennis</i>	Cvetkovic C. et al.	16
Value based decision making in cellular metabolic pathway activation	Encarnación Segura A. et al.	18
Coevolution of cancer defences and body size: can birds beat cancer?	Erten E. et al.	20
What doesn't kill you makes your offspring stronger	Fuchs M. et al.	22
Sperm characteristics vary with social environment but not male age	Girndt A. et al.	24
Estimation of diversification rates of dragonflies and damselflies (Insecta: Odonata)	Gutiérrez-Ramírez L. et al.	26
Karyotype analysis and multiple sex chromosome system in	Hladová I. et al.	28



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View abstract data

Abstract title	SNP assay validation in honey bee populations and allele frequency determination in DNA pools by MALDI-TOF MS
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Abstract text	

Single nucleotide polymorphisms (SNPs) have a great potential in genetic identification and introgression studies of honey bees (*Apis mellifera*). To achieve SNPs full power in genetic analysis, they must be screened in a rapid, accurate and cost-effective manner. Matrix-assisted laser desorption-ionization-time-of-flight (MALDI-TOF) mass spectrometry is a promising tool for the high-throughput screening of SNPs at an affordable cost in the post-genome sequencing era. In this study, a reduced SNP panel has been validated for Iberian honey bees (*A. m. iberiensis*) and a pooling strategy is presented for allele frequencies determination by using MALDI-TOF technology. The reduced SNP panel contains 127 most ancestry-informative loci design in the dark honey bee (*A. m. mellifera*). We demonstrate the utility of this methodology in samples of Iberian honey bees (*A. m. iberiensis*) selected for its pathogen tolerance and in genomic DNA pools. The described method reduces costs and time and enables genotyping of up to thousands of honey bee samples by taking advantage of the high-throughput MALDI-TOF technology.

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