

## Summary

The European Society of Evolutionary Biology (ESEB) conference is a biyearly event of large proportions organized by the European Society of Evolutionary Biology. It gathers European and non European scientists from different fields of biology, including population ecology, evolutionary biology and genetics. The ESEB commonly attracts between 1000 and 1300 participants.

The ESEB 2011 received 1023 submissions for posters and abstracts distributed in 30 symposia and 1 general session. Of these 337 slots were dedicated to talks (including 8 plenaries and 66 invited speakers). About 500 submissions were presented as a "regular" posters. The remaining 200 contributions were in the form of "essence posters" (summary mini-posters). Submissions were received from 40 countries across the globe, including US, Australia, China and Japan.

The Evolutionary Ecological Genomics symposium attracted the highest number of applications together with the general session in the entire conference. This suggests that a large community of scientists was interested in the topic we opened for discussion and that evolutionary ecological genomics is a topic that many research groups are either going toward or already addressing. Among the >100 applications we received, 17 were selected for a talk and the remaining >80 were presented as regular or essence posters. The symposium was closed by a plenary discussion that set the pace for the future developments in the field of evolutionary ecological genomics. Between 200 and 300 participants attended the symposium. Young investigators were actively involved in discussion and given the chance to present their work. The poster sessions were actively attended and lively discussions took place throughout the conference.

The symposium on Evolutionary Ecological Genomics was most appreciated by renown scientists as well as by young investigators. Participants found the scientific content of the symposium sound and stimulating, and the atmosphere encouraging new collaborations and constructive discussion. We were congratulated on the timely presentation and discussion of a highly debated topic in modern biology. It was a complete success! The most relevant contributions as well as invited contributions from top scientists in the field of evolutionary ecological genomics will be collected in a special issue that will be published in *Molecular Ecology*.

Final program of the event. The Evolutionary Ecological Symposium (sy 21) was held on Sunday 21st and Monday 22nd of August in the lecture hall N6.

## Sun 21 Aug - A

Business meetings and funding specials  
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## A - Sun 21 Aug

		Time		0900		0950		1030		Time		1100		1120		1140		1200		1220		
		Rooms								Room												
morning	N6	Welcome, plenary talk 1				Plenary talk 2				Lecture hall centre HZ (Essence poster area) Sponsored by Ethology, Wiley-Blackwell Hot and cold drinks	N2	Sy 30: General session: <b>Behaviour</b> (p. 14)										Campus canteen Mensa (Regular poster area) Lunch
	live	Michael Siva-Jothy				Duur Aanen					N3	Sy 30: General session: <b>Life-history</b> (p. 14)										
	N5	Sex, trauma and disease: Female responses to male inflicted mating injury in cicidids				The evolution of cooperation in mushrooms					N4	Sy 30: General session: <b>Population ecology</b> (p. 14)										
	video										N5	Sy 30: General session: <b>Development</b> (p. 14)										
	N7	Female bed bugs are traumatically inseminated during mating. I examine and discuss the anatomical, behavioural and physiological responses that have evolved as a consequence.				Mushroom forming fungi engage in ecologically important mutualisms and have a highly interesting social and sex life making them excellent models to study evolution of cooperation.					N6	Sy 30: General session: <b>Disease and immunity</b> (p. 15)										
	video										N7	Sy 30: General session: <b>Evolutionary genetics</b> (p. 15)										
		Mike Siva-Jothy is professor of entomology at the Department of Animal and Plant Science, University of Sheffield. His research interests are focused on sexual conflict, ecological immunology and interactions between reproduction and immunity.				Duur Aanen is an assistant professor at the Laboratory of Genetics, Wageningen University. His main interest is the levels of selection in evolution. His current research focuses on conflicts between selection at different levels, the evolution of allorecognition and sexual selection.																
	Chair: Hinrich Schulenburg				Chair: Michael Weiss														Funding: German Science Foundation (DFG) N7 → p. 8			
afternoon	N0	Sy 08 start: <b>Predicting macroevolution from microevolution</b> (p. 16)								Lecture hall centre HZ (Essence poster area) Sponsored by Ethology, Wiley-Blackwell Hot and cold drinks	N0	Sy 08 cont.: <b>Predicting macroevolution from microevolution</b> (p. 18)										Campus canteen Mensa Regular poster session A
		Goldberg*				Pybus*					N1	Sy 25 cont.: <b>Evolutionary systems biology</b> (p. 18)										
	N1	Sy 25 start: <b>Evolutionary systems biology</b> (p. 16)									N2	Sy 11 cont.: <b>Non-genetic inheritance and evolution</b> (p. 18)										
		Reed*				Jaeger Nelson					N3	Sy 05 cont.: <b>Mutualism: Causes and consequences</b> (p. 18)										
	N2	Sy 11 start: <b>Non-genetic inheritance and evolution</b> (p. 16)									N4	Sy 27 cont.: <b>Selective sweeps</b> (p. 19)										
		Badyaev*				Day*					N5	Sy 15 cont.: <b>Division of labour</b> (p. 19)										
	N3	Sy 05 start: <b>Mutualism: Causes and consequences</b> (p. 16)									N6	Sy 21 cont.: <b>Evolutionary ecological genomics</b> (p. 20)										
		Archetti*				Lukasik Rouchet					N7	Sy 01 cont.: <b>Microbe/macrobe experimental evolution</b> (p. 20)										
	N4	Sy 27 start: <b>Selective sweeps</b> (p. 16)									N9	Sy 22 cont.: <b>Environment, G matrices and adaptation</b> (p. 20)										
		Stephan*				Chevin*																
N5	Sy 15 start: <b>Division of labour</b> (p. 17)																Funding: Volkswagen Foundation N7 → p. 8					
	Michod*				Ratcliff Hammerschmidt																	
N6	Sy 21 start: <b>Evolutionary ecological genomics</b> (p. 17)																					
	Pfeander* Orsini Coelho Bast																					
N7	Sy 01 start: <b>Microbe/macrobe experimental evolution</b> (p. 17)																					
	Lanski*				Nieuwenhuis Simons																	
N9	Sy 22 start: <b>Environment, G matrices and adaptation</b> (p. 17)																					
	Chenoweth*				Berner Beckmann																	
	* Invited speaker																					

# Mon 22 Aug - B

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# B - Mon 22 Aug

Time Rooms	0900	0950	1030	Time Room	1100	1120	1140	1200	1220	
	<b>morning</b> N6 <i>live</i> N5 <i>video</i> N7 <i>video</i>	<b>Welcome Prorector, plenary talk 1</b> <b>Julie Etterson</b> Evolution of plant populations in response to climate change: Case studies from the Great Plains, United States Two case studies are presented that examine potential adaptive responses to climate change in two plant species, a diploid annual pea and a polyploid perennial herb. Julie Etterson works as an associate professor at the Department of Biology, University of Minnesota Duluth. The goal of her research is to understand genetic and ecological factors that influence the rate of adaptive evolution in natural plant populations. Chair: Katja Tielbörger	<b>Plenary talk 2</b> <b>Michael Ruse</b> What, if anything, does a historian and philosopher have to say to real scientists? Should real working scientists take notice of the history & philosophy of science? By looking at evolution, I shall argue that there is a value in the history & philosophy of science. Michael Ruse holds a Lucyle T. Werkmeister Professorship at the Department of Philosophy, Florida State University. His research interests cover Philosophy of Biology, Ethics, the History and Philosophy of Science. He lectures globally on evolutionary issues and is a renowned debater of Creationists. Chair: Daniel Dreesmann	Lecture hall centre HZ (Essence poster area)	<b>N2</b> Sy 30: General session: <b>Behaviour</b> (p. 24) Herberstein   McNally   Purcell   Wischmann	<b>N3</b> Sy 30: General session: <b>Life-history</b> (p. 24) Bastiaans   Wit   Schärer   Lessard	<b>N4</b> Sy 30: General session: <b>Population ecology</b> (p. 24) Hadany   Mumby   Broquet   Mattila	<b>N5</b> Sy 31: <b>Outreach symposium</b> (p. 24) Carroll*   Ryan*   Andersen*   Blume*	<b>N6</b> Sy 30: General session: <b>Disease and immunity</b> (p. 25) Mappes   Roth   Otti   Wolinska	<b>N7</b> Sy 30: General session: <b>Evolutionary genetics</b> (p. 25) Sabath   Bentkowski   Guillaume   Halligan

Time Room	1400	1420	1440	1500	1520	Time Room	1550	1610	1630	1650	1710	1730 - 1900	
	<b>afternoon</b> N0 N1 N2 N3 N4 N5 N6 N7 N9	Sy 08 cont.: <b>Predicting macroevolution from microevolution</b> (p. 26) Humphreys   Goldie   Santos   Vanoverbeke	Sy 20 start: <b>Chemical communication</b> (p. 26) Blows*   Hurst*	Sy 23 start: <b>Climate change and evolution</b> (p. 26) Merilä*   Husby   Moiroux	Sy 05 cont.: <b>Mutualism: Causes and consequences</b> (p. 26) Mueller*   Feldhaar   Kooij	Lecture hall centre HZ (Essence poster area)	<b>N0</b> Sy 12 start: <b>Plant epigenetics</b> (p. 28) Colot*   Verhoeven*   Zhang   Vergeer	<b>N1</b> Sy 20 cont.: <b>Chemical communication</b> (p. 28) Kappel   Schneider   Werner   Egas   Sun	<b>N2</b> Sy 23 cont.: <b>Climate change and evolution</b> (p. 29) Lohbeck   Hallsson   Rode   Grazer   Zarza	<b>N3</b> Sy 14 start: <b>Family interactions</b> (p. 29) Kölliker*   Moore*   Drummond	<b>N4</b> Sy 13 cont.: <b>Evolution outside of the nucleus</b> (p. 29) Taylor   Breton   Innocenti   Montooth   Harrison	<b>N5</b> Sy 03 cont.: <b>Evolution and human disease</b> (p. 30) Wegmann   Hollegaard   Hughes   Pavard   Pijpe	<b>N6</b> Sy 21 cont.: <b>Evolutionary ecological genomics</b> (p. 30) Domingues   Tautz   Good   Lischer   <i>Closing discussion</i>
Sy 13 start: <b>Evolution outside of the nucleus</b> (p. 27) Burton*   McCauley*		Sy 01 cont.: <b>Evolution and human disease</b> (p. 30) Stearns*   Haig*   Crespi*   Ubeda	Sy 03 cont.: <b>Evolution and human disease</b> (p. 30) Perron   Wong   Engelmoer   Becks   Millard	<b>N7</b> Sy 01 cont.: <b>Microbe/macrobe experimental evolution</b> (p. 27) Bell*   Travisano   Hollis	<b>N9</b> Sy 19 start: <b>Evolution of chirality</b> (p. 31) Barrett*   Palmer*   Klingenberg   Hosoi   Gravendeel Schilthuisen	Sy 21 cont.: <b>Evolutionary ecological genomics</b> (p. 27) Hanski*   Nadeau   Earley   Veltsos	Sy 22 cont.: <b>Environment, G matrices and adaptation</b> (p. 28) Schmitt*   Hornoy   Schoustra						

\* Invited speaker

# Tue 23 Aug - C

Business meetings and funding specials  
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# C - Tue 23 Aug

Time Rooms	0900	0950	1030	Time Room	1100	1140	1220
	N6 <i>live</i>	Welcome, plenary talk 1	Plenary talk 2	Lecture hall centre HZ (Essence poster area)	N6 <i>live</i>	JMS-Prize Laureate	ESEB member meeting All ESEB members are invited to attend. Topics include the organisation and state of the society (finances, memberships, boards, journal, ...), current and future activities and science policy.  ESEB relies on active feedback from members (like you) during this meeting to approve and shape the decisions that keep this society successful. Please feel more than welcome to attend.
Anna Qvarnström		Johannes Krause	Rowan Barrett				
N5 <i>video</i>		Speciation – how difficult can it be?	What makes us human: Insights from sequencing extinct hominin genomes?			N5 <i>video</i>	
N7 <i>video</i>	Debated issues will form starting points for some excursions into recent studies on speciation. I conclude that divergence is easy but co-existence difficult.	We present the genome sequence of the Neandertal and an only recently described Siberian hominin in the Denisovan. Both genomes show evidence of gene flow with modern human populations.	Hot and cold drinks	N7 <i>video</i>	The genetics of adaptation: Combining theory, lab and field studies to understand the mechanisms that drive ecological and evolutionary responses to changing environments.	Lunch	
Anna Qvarnström is an associate professor at the Department of Ecology and Genetics, University of Uppsala. Her research aims at finding how new species are formed and how new species are sheltered from merging through interbreeding or from driving each other to extinction through competition.	Johannes Krause is a Junior Professor at the Center of Science-based Archaeology, University of Tübingen. His main research focus lies on the genomic comparisons of Neanderthals and anatomically modern humans to clarify their evolutionary relationship.	Rowan Barrett is a Howard Alper and FQEB fellow at the Department of Organismic and Evolutionary Biology, Harvard University. His work is motivated by a desire to understand the genetic basis of adaptation to changing environments.					
Chair: Katharina Foerster	Chair: Katerina Harvati	Chair: Sarah Otto					

Time Room	1400	1420	1440	1500	1520	Time Room	1550	1610	1630	1650	1710	1730 - 1900
	N0	Sy 09 start: Polyploid ecological genomics (p. 34)	Husband*		Mable	Griffin	N0	Sy 09 cont.: Polyploid ecological genomics (p. 36)	Wendel*		Ainouche	Van Doninck
N1		Sy 04 start: Cooperation and virulence (p. 34)	Brown*	Hughes*	Alizon	Debarre		N1	Sy 04 cont.: Cooperation and virulence (p. 36)	Ugelvig	Buechel	McKean
N2	Sy 23 cont.: Climate change and evolution (p. 34)	Hoffmann*		Kellermann	Calabria	N2	Sy 23 cont.: Climate change and evolution (p. 37)	Walters	Ronce	Laugen	Krenek	Leicht
N3	Sy 14 cont.: Family interactions (p. 34)	Gini	Szekely	Arce	Andrews	N3	Sy 14 cont.: Family interactions (p. 37)	Cant	Jacob	Fromhage	Priest	Closing discussion
N4	Sy 28 start: Functional population genomics (p. 35)	Meyer*	Jiggins*	Storz	Runcie	N4	Sy 28 cont.: Functional population genomics (p. 37)	Schmidt	Hahn	Papakostas	Müller	Marquez
N5	Sy 06 start: Speciation by natural versus sexual selection (p. 35)	Servedio*	Merrill	Haller	Kozak	N5	Sy 06 cont.: Speciation by natural versus sexual selection (p. 38)	Hendry*	Smadja	Crochet	Kaufmann	Groot
N6	Sy 02 start: Coevolution from parasitism to mutualism (p. 35)	Jokela*	Kerstes		Hall	N6	Sy 02 cont.: Coevolution from parasitism to mutualism (p. 38)	Lion	Lefèvre	Mennerat	Restif	Refardt
N7	Sy 01 cont.: Microbe/macrobe experimental evolution (p. 35)	Kawecki*		Uusi-Heikkilä	Chen	N7	Sy 26 start: Parallel evolution (p. 38)	Bernatchez*		Hoekstra*	Chan	Funding: Humboldt Foundation (AvH) N7 → p. 8
N9	Sy 24 start: Adaptation in large populations (p. 36)	Barton*		Hermisson*		N9	Sy 24 cont.: Adaptation in large populations (p. 39)	Weissmann	Weich	Hartfield	Ross	Teotonio

\* Invited speaker

# Wed 24 Aug - D

Business meetings and funding specials  
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# D - Wed 24 Aug

morning	Time	0910	0930	0950	1010	1030	Time	1100	1120	1140	1200	1220	
	Room						Room						
	N0	Sy 07 start: <b>Fossils and evolutionary biology</b> (p. 42) Smith* Joyce*				Lecture hall centre HZ (Essence poster area)	Hot and cold drinks	N0	Sy 07 cont.: <b>Fossils and evolutionary biology</b> (p. 44) Bocherens Matschiner Höhna Sims				Campus canteen Mensa (Regular poster area)
	N1	Sy 18 start: <b>Perceptual manipulation and mimicry</b> (p. 42) Johnson* Egger Whitehead						N1	Sy 18 cont.: <b>Perceptual manipulation and mimicry</b> (p. 44) Fuller* Kikuchi Wehrle				
	N2	Sy 16 start: <b>Viviparity, placentation and conflict</b> (p. 42) Reznick* Wildman*						N2	Sy 16 cont.: <b>Viviparity, placentation and conflict</b> (p. 44) Leinweber Ala-Honkola Capellini Kühnel				
	N3	Sy 17 start: <b>Novel techniques in behavioural ecology</b> (p. 42) Chapman* Manier Reinhardt						N3	Sy 17 cont.: <b>Novel techniques in behavioural ecology</b> (p. 44) Polak* Callander Robinson				
	N4	Sy 10 start: <b>Causes of epistasis</b> (p. 42) Weinreich* Kishony*						N4	Sy 10 cont.: <b>Causes of epistasis</b> (p. 45) Agrawal Østman Chou Ebert				
	N5	Sy 06 cont.: <b>Speciation by natural versus sexual selection</b> (p. 42) Maan* Havens Tuomaala Gonzalez						N5	Sy 06 cont.: <b>Speciation by natural versus sexual selection</b> (p. 45) Svensson* Gante Aguilée Thomassen				
	N6	Sy 02 cont.: <b>Coevolution from parasitism to mutualism</b> (p. 43) Hurst* Schraghammer Nash						N6	Sy 02 cont.: <b>Coevolution from parasitism to mutualism</b> (p. 45) Lemoine Duneau Schulenburg Parker				
	N7	Sy 26 cont.: <b>Parallel evolution</b> (p. 43) Hendrickx Mundy Le Rouzic Barluenga						N7	Sy 26 cont.: <b>Parallel evolution</b> (p. 45) Schwander Jones Santos Bailey				
N9	Sy 29 cont.: <b>Can drift facilitate adaptive evolution?</b> (p. 43) Masel* Salverda*				N9			Sy 29 cont.: <b>Can drift facilitate adaptive evolution?</b> (p. 46) Guggisberg Krug Steiner Gossmann					

afternoon	Time	1400	1420	1440	1500	1520	Time	1550 - 1650	1930 - 0100			
	Room						Room					
	N2	Sy 30: General session: <b>Human impact</b> (p. 46) Huijben Pennings Sundin Warmuth				Lecture hall centre HZ (Essence poster area)	Hot and cold drinks	N6	<p><i>Presidential address, closing session, prizes</i></p> <p><b>Brian Charlesworth</b></p> <p>How population genomics can solve a lot of our problems</p>	Shuttles to farewell party → p. 83		
	N3	Sy 30: General session: <b>Inbreeding</b> (p. 46) Postma Pekkala Jordan Szulkin						N5			Farewell party Monastery Bebenhausen	
	N4	Sy 30: General session: <b>Evolutionary genetics</b> (p. 47) Beldade Smith Kaiser Kousathanas						N7				
	N5	Sy 30: General session: <b>Evolution of sex</b> (p. 47) Peck Lehtonen Balbi King										
	N6	Sy 30: General session: <b>Primates</b> (p. 47) Kanitz Fickenscher Courtiol Hellmann										
	N7	Sy 30: General session: <b>Disease and immunity</b> (p. 47) El Nagar Lattorff Tack Olsson										

\* Invited speaker

Brian Charlesworth is a Senior Honorary Professorial Fellow at the Institute of Evolutionary Biology, University of Edinburgh. His recent research has focused on three main areas: Molecular evolution and variation, evolution of genetic and sexual systems, and quantitative genetics of life-history traits.

Chair: Siv Andersson

## **Description of the scientific content of the Evolutionary Ecological Genomics symposium**

The European Society of Evolutionary Biology (ESEB) is among the largest societies in Europe and organizes biyearly conferences that attracts scientists from all over the world. The ESEB 2011 was held in the historical town of Tuebingen, Germany, where the University has a long tradition in the field of evolutionary biology. The conference attracted representatives from >40 countries, including US, Canada, Japan and China. The conference was divided in symposia organized by the scientific community on a voluntary basis. Call for symposia generally open one year before the actual conference and symposia are chosen on the scientific quality and innovation of the topic open for discussion. The selection of the symposia is decided by the scientific committee of the ESEB society, composed of renown scientists in different fields of Biology. In the ESEB 2011 there were 30 parallel symposia, including the general session, and a total of 1023 attendees.

The symposium on evolutionary ecological genomics received the largest consensus from the scientific committee for the timely presentation of a highly debated topic in evolutionary biology. It also received the largest number of applications together with the general session, once again confirming the general interest of the scientific community in the proposed topic. The symposium ran throughout 2 entire afternoons, each divided in two sessions. Each session was lead by a renown scientist in the field of ecological evolutionary genomics. Our keynote speakers were (in order of presentation):

- 1) Michael Pfrender is interested in a broad range of topics in the area of evolutionary and ecological genomics. These topics range from detailed investigation of the molecular genetic basis of adaptive traits and phenotypic plasticity, to the relationship between genetic diversity and ecosystem function. He is particularly interested in the relationship between short-term organismal responses to environmental stresses and long-term adaptive changes in novel environments. Michael Pfrender has contributed together with John Colbourne to promote the waterflea *Daphnia* as the model system in environmental and ecological genomics.
- 2) Catherine Peichel is interested in identifying the genetic and molecular mechanisms that underlie evolutionary processes. For her research she uses the model system threespine stickleback (*Gasterosteus aculeatus*). These fish have evolved incredible diversity in their behaviors, morphologies and life histories in a relatively short evolutionary time scale. Current research in the Peichel Lab is aimed toward understanding the genetic basis for reproductive isolation, the evolution of morphological, behavioral, and life history traits, and the evolution of sex chromosomes. Catherine Peichel has an impressive record of publications in top scientific journals.
- 3) Ilkka Hanski is the director of the Metapopulation Research Group (MRG) at the University of Helsinki. His research focuses on the biology of species inhabiting fragmented landscapes. The strength of his research is the ability to combine ecological, molecular, computational, and theoretical approaches to answer question of central relevance in biology and evolution. Ilkka Hanski and his group have been awarded the

position of Centre-of-Excellence in research by the Academy of Finland for 3 terms of 5 years: 2000-2005 2006-2011 and 2012-2017. Ilkka Hanski received the Crafoord Price in Biosciences in 2011.

- 4) Hopi Hoekstra's research focuses on understanding how variation is generated and maintained in natural populations. Her research interests range from population genetic to evolution and development and ecological speciation in vertebrates. For her research, she uses an integrative approach combining molecular genetics techniques, theoretical modeling, experimental tests, breeding studies and fieldwork. She uses as model systems natural populations of rodents. Hopi Hoekstra is a world renown scientist with an impressive record of publications in top scientific journals such as Science, MBE, Evolution, TREE, and Current Biology.

Our keynote speakers are the excellence in their field. In addition, the other speakers of the symposium were selected based on the excellence of their study in evolutionary ecological genomics and for the innovative aspects they presented. This guaranteed the excellence of the symposium.

Talks selected for oral presentation in the Evolutionary Ecological Genomics symposium were carefully chosen to give equal attention to a wide range of organisms and approaches. In addition special attention was taken in mixing the talks in every session so that research both in genetic model and non model species was presented. This formula attracted interest from a large audience and stimulated an animated conclusive discussion on the future developments of the field of evolutionary ecological genomics.

The first afternoon sessions were opened by Michael Pfrender and Ilkka Hanski. Michael Pfrender introduced the new emerging environmental model system, the waterflea *Daphnia*. The waterflea is a renown ecological model system with growing functional genomic tools. With the available genome sequence of one of the *Daphnia* species, *D. pulex*, and the wide ecological background available for several *Daphnia* species, the genome organization and the functional genomics of adaptation to multiple environmental stressors are being understood. M. Pfrender showed how functional genomics approaches examining adaptive divergence in natural populations set the stage for a greater understanding of genome X environment interactions, and the relationship between short-term transcriptional responses and genetic adaptation to accommodate environmental challenges. In the same session Luisa Orsini showed how the use of detailed ecological and environmental data with cutting-edge genomic techniques can advance our understanding of adaptation in natural populations. Using a genome scan approach in space, time and experimental evolution trials, Orsini and coworkers showed solid evidence of selection at genome level under well-characterized environmental gradients in the wild and identified candidate genes linked to the three environmental stressors. The first afternoon session continued with special focus on genetic non model species for which emerging genomics tools are being developed. Susana Coehlo showed how the application of genomics tools to the brown alga *Ectocarpus* has helped identifying sex determination in this major eukaryotic lineage. In his presentation, Jens Bast dealt with a very interesting topic, the link between transposable elements and the persistence of asexual species. From the study of Bast and coworkers seems that transposable elements may be the way asexual species purge out their negative mutations and in this way determine their evolutionary success.

The second session of the afternoon was lead by Catherine Peichel. She focused on the genetic basis of phenotypic variation between species and on how these differences may lead to speciation. Her research model system is *Gasterosteus aculeatus*, commonly known as stickleback. This species has become an ideal system to identify the genetic changes that contribute to adaptation to new environments. An elegant application of the available genomics tools on sticklebacks was presented by Philine Feulner. Feulner and co workers resequenced the entire genome of 16 sticklebacks, evaluating structural variation of the genome within and between parapatric lake-stream population. The innovation of this work as well as of the work on the waterflea *Daphnia*, is the application of cutting edge genomics combined with detailed ecological and environmental data to natural populations. The second session of the first afternoon continued with focus on genetic non model species. The study present by Tonia Schwartz was an elegant combination of transcriptomics and physiology to understand adaptive stress response in natural populations of snakes. The authors demonstrated the existence of parallel evolution in ecotypes evolved in similar stress conditions. The study of Kim Kang Wook and coworkers was more oriented toward a functional genomics approach. Through extensive target sequencing they identify the gene responsible for melanism in Gouldian finches. The intriguing implication of this study is that the identified gene may be linked to incipient speciation in Gouldian finches. The last speaker of the session was Francesco Angeloni, that presented a study on inbreeding depression, a topic of central relevance for the persistence of populations in the wild. By comparing the change in gene expression level of several different families of inbred and outbred individuals of the plant genus *Scabiosa*, Angeloni and Ouborg could estimate how many genes are associated with inbreeding depression.

Ilkka Hanski opened the second day of the symposium introducing a new perspective to the field of evolutionary ecological genomics, the importance of eco-evolutionary dynamics in complex population systems. His talk summarized the opportunities to combine ecological and genomic research in the context of long-term observational studies of natural populations and showed how mathematical modeling can be employed to address eco-evolutionary dynamics. The session that followed Hanski's presentation was a well balanced mix between population and functional genomics. Nicola Nadeau showed how new genetic techniques can be used to address questions about adaptive evolution, divergence and mimicry at the genome level in a typically “non-model” system. Nadeau and co workers identify genomic regions under divergent selection linked to mimicry in races and close species of *Heliconius* butterflies, integrating the ecological understanding of mimicry with genomics. The talk of Eric Earley was more oriented toward a functional genomics approach. Earley and coworkers combined next-generation whole genome sequencing with ecological and behavioral assays in order to find causative genetic changes accompanying behavioral adaptation in *Drosophila sechellia*. The talk of Paris Veltsos concluded this session, presenting the application of a QTL approach to explain behavioral traits potentially associated with adaptation and mating success in *Drosophila montana*.

Hopi Hoekstra and Vera Domingues opened the last session of the symposium. The main theme of this session was population genomics and adaptation. The work of Hoekstra and Domingues focused on the use of phylogenetics and population-genomics to determine the source, timing and strength of selection acting on beneficial mutations in natural populations. The model system used in this study is the beach mouse, a species with high ecological relevance in coastal ecosystems for which a large battery of genomics tools is currently available. The approach used



in the study of Domingues and co workers goes beyond the typical candidate gene approach because it identifies the alleles responsible for adaptive evolution in natural populations. In the same session Diethard Tautz and coworkers touched upon another interesting aspect in evolutionary biology, the role of hybridization between species in promoting adaptation in island populations. Jeffrey Good examined the selective forces driving the evolution of the male ejaculate in the great ape, using population genomics. Good compared male ejaculate of gorillas, chimpanzees, humans, and bonobos and linked genomic differences to divergent mating ecologies. Finally, Heidi Lischer and coworkers proposed a more technical talk in which they showed how to overcome the issue of anonymous location of AFLPs in the now established genome scans approach.

The high quality of the talks presented during the symposium stimulated a lively discussion at the end of the session. We adopted an innovative new formula by dedicating uniquely to discussion an entire slot of 20 minutes. The discussion was chaired by the four keynote speakers and the symposium organizers. The discussion particularly attracted young investigators, but experienced scientists were not scarce. Critical aspects in the field of Evolutionary Ecological Genomics as well as future perspectives were discussed.

Public genetic databases are strongly biased toward data on developmental and structural functions. This is because most of the genetic work done so far revolved around model species such as *Drosophila*, *Caenorhabditis*, mice etc. Only recently we start gaining a mechanistic and functional understanding on how natural populations adapt to an ever changing environment by developing new genomics tools for ecologically relevant species. There are two main ways in which the field of Evolutionary Ecological Genomics can develop and contribute to our understanding of adaptive responses in natural populations. (a) An ecological component can be introduced in the study of genetic model species (e.g. Balanya *et al.* 2006; Sokolowski 2001; Umina *et al.* 2005) and/or (b) genomics tools can be developed for species of central ecological value (e.g. Cock *et al.* 2010; Colbourne *et al.* 2011; Hohenlohe *et al.* 2010). The two approaches are not mutually exclusive, but a common consensus on which of the two will receive most attention from the scientific world is lacking. Most likely we will gain a better understanding of the adaptive responses acting at genome level in natural populations combining the best of the two approaches.

Regardless of what approach will be most promising, bioinformatic tools remain a bottleneck. Sequencing technologies progress at amazing fast pace (Stapley *et al.* 2010) but bioinformatics is struggling to catch up with the new technologies. Because of the fast development of genomics technologies, costs for running large experiments are drastically reduced. As a consequence, many medium to small research groups can afford genomics and start producing large amount of data. However, this goes to the expenses of data analysis because bioinformatics on one end and data storage on the other are serious bottlenecks. There seemed to be a general consensus that more training is needed for the next generation of scientists in the field of bioinformatics in order to handle the large amount of data becoming available and affordable with the now-generation sequencing technologies.

Some critical aspects also emerged from the conclusive discussion of the symposium. Given the relative ease with which nowadays genomics data can be produced, there is a tendency in modern biology to "genomicise" many organisms without a clear biological questions driving the "genomicisation". We sometimes forget that genome-wide signals are not always necessary to answer ecological evolutionary questions. Most importantly we should learn to combine cutting

edge genomics with ecological and environmental data. Only combining the best of two worlds we will significantly advance in our knowledge of adaptive potential of natural populations. A final important aspect emerged from the conclusive discussion. The field of Evolutionary Ecological Genomics can have important applications in other fields. In particular it can be a key asset for the rapidly developing field of eco-evolutionary dynamics (Fussmann *et al.* 2007; Pelletier *et al.* 2009; Urban *et al.* 2008) to better understand and predict community and ecosystem responses to environmental change, mediated by evolutionary changes in individual species.

The symposium attracted the attention of the reporter of Science Elisabeth Pennisi and of the managing editor of Molecular Ecology, Tim Vines. We agreed with Dr Vines to edit a special issue on Evolutionary Ecological Genomics in the Molecular Ecology journal. In this issue we will collect the most relevant contributions of the symposium as well as invited contributions from top scientist in the field. The publication of this special issue is expected in the fall 2012 and will give a large visibility to the symposium.

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