Regal Setting Showcases Crown Jewels of SMBE 2015 Science

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Ancient genomes, archean explorations, new computational tools and methods, some serious hominid introgression, and the “good, bad and ugly” of transposon elements were among just a few of the scientific highlights at the 2015 Society for Molecular Biology and Evolution (SMBE)’s annual conference in Vienna, Austria.

More than 1,400 evolutionary scientists from 44 countries gathered at the magnificent, sprawling, marbled and frescoed hallways and grounds of the Hofburg Palace, the former royal center of the Hapsburg Empire and incomparable venue—where Beethoven and Mozart once premiered symphonies and operas, and King Franz Joseph and Queen Elizabeth “Sisi” last held court.

The University of Vienna officially served as gracious local hosts as Christian Schlötzer welcomed visitors for the biggest SMBE meeting ever. Four jam-packed days featured 29 scientific symposia with 343 talks, the best of student research achievements presented at the Fitch symposium, and 750 posters.

To help navigate the overflowing conference, SMBE had even developed a fully customizable conference guidebook app, while the twitter-verse was also buzzing with the hashtag #smbe15, which at one point, become one of the top trends on all of Twitter. Many social media followers were in awe of the extraordinary talents of graduate student Alex Cagan (@ATJCagan), whose artistic summaries covered the conference in real time (as well as the more than 8,000 tweets from others) for those who couldn’t attend.

SMBE president Joe Felsenstein kicked off the meeting with a provocative talk in the “very intimidating” room of the Hofburg, the Festival Hall (Festaal) throne room, but reassured to the audience that “no molecular sequences will be harmed in this talk or considered.” Rather, he challenged the SMBE community into thinking about an evolutionary equivalent to rival particle physics, a quest for a grand unified theory by integrating thermodynamics with natural selection.

“Can we find a simple model where I can make a connection between natural selection, thermodynamics and entropy?” he asked. “The whole idea of connecting thermodynamics with natural selection is a holy grail. It would unite the paradigms of biology and physics. Perhaps, there is a connection to be made between increase in entropy and increase in biological information.”

After a fitting champagne-filled opening reception in the Hofburg foyer and royal galleries, the following morning, Diethard Tautz gave his plenary talk on the de novo evolution of new genes. He highlighted trends such as the transcriptome age index, where the oldest, most conserved genes are found in embryos, and the youngest (and those that contribute the most to adaptation) come on later in adults. For the evolutionary birth of new genes, “the pattern is universal: The highest rates of gene emergence are seen in the youngest lineages.” Tautz said that this can’t be explained by the well-established gene duplication/divergence model, but rather, can only be explained by de novo evolution, which implies a faster turnover of de novo genes. Within a timespan of just 10 My, he noted, a whole genome would have been subject to transcription at one point in time. Tautz said that much work still needs to be done to understand the dynamic life and death cycle of genes, and what is still missing is looking at the rates of emergence of new genes.

The 29 concurrent symposia immediately followed, often with a half-dozen sessions ongoing and attendees racing back and forth amidst the crystal chandeliers and mural bedecked ceilings in the conference rooms and hallways. The symposia proved to be an overabundance of riches, and simply too numerous to fully capture the breadth of the talks. Joshua G. Schraiber (@jgschraiber) perhaps best expressed what many attendees must have felt by his tweet: “the number of interesting talks is just too damn high.”

Among just a few research highlights from the talks were:

- **Microbiomes**—This hot and still emerging field was covered in talks by Peer Bork, Asha Ram, and Andrew Moeller, as they explored the links between the gut microbiome, ecosystems, and more than 30 diseases. They demonstrated an incredible microbiome variation, where each species harbors a compositionally distinct gut microbiome, every human has 20% different Escherichia coli, and ocean microbial biodiversity has the potential to become a new climate change indicator.

- **Bar-coded yeast**—With asexual cell populations accounting for 30% of deaths worldwide, much work needs to be done to get at the root causes of disease. Sasha Levy demonstrated a bar-coded yeast technology to trace single-cell lineages. Levy calls this remarkable technology “genomic cartography” and can now get 10 × 10 barcodes in a yeast library. His team is now on adapting the technology to your favorite organisms” and is working on Candida albicans and breast cancer cells to track lineages at high resolution.

- **Ancient hominid hanky panky**—The Joshua Akey lab demonstrated that a little Neanderthal goes a long way. Although just 1–4% of Neanderthal is found in modern humans, at least 30% of Neanderthal genome can now be excavated from ongoing sequencing data in modern humans. Michael Dannemann and Corrinne Simonti also found many new associations between Neanderthal alleles, clinical phenotypes and disease risk, such as long-term depression, keratosis, and obesity, with 22% more neanderthal DNA found in East Asian populations. Is this due to chance? Selection? Demographic history? More research to follow…

- **Archae are awesome**—A fantastic lineup in final Archaea symposium, which are now recognized to be a major

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proportion of the world’s biomass Graeme Nicol explored the evolutionary history of adaptation, with Manolo Gouy showing that long branches in archae are explained by adaptation to mesophily. This is a nice example of convergent evolution if true. David Moreira covered the phylogenomic rooting of the domain Archaea and taxonomic and evolutionary implications, whereas Anja Spang focused on Lokiarchaeota.

“Dmitri Petrov’s plenary” explored the essential role of rapid adaptation in health, including cancer, viral infections, and other conditions. “The time for mutations of $10^4$ to $10^8$ generations is depressing if you are an experimental evolutionist, but also liberating. There is more or less, nothing to do.” One of the most remarkable findings is that pesticide resistance occurs rapidly over decades and often at same loci in different species. “Now we can study evolution as a movie rather than a static photo—it’s just a lot of fun!”

“Doris Bachtrog’s final, spaghetti western themed” plenary was focused on the biology of “The Good, The Bad, and the Ugly” of repetitive DNA. Among the more sobering findings, particularly for men in the audience, was her work showing that Y chromosomes were responsible for shorter lifespan in flies, with XXY females also living shorter, whereas X0 males lived longer.

The Walter Fitch symposium underscored the critical importance of new computational tools, with about two-thirds of the student presentations devoted to developing software. In the end, the most transformative talk and 2015 recipient of the Fitch award was Aline Muyle, for her elegant work on imprinting in *Silene*.

Attendees were often reenergizing at the renowned Viennese coffee houses nearby or spreading out with the boxed lunches al fresco style on the palace grounds. The final evening was capped with an excursion to a traditional “heurigen,” enjoying fine Austrian hospitality at a local wine maker and restaurant.

Finally, Joe Felsenstein bookended the conference with a sneak peak at SMBE 2016, which will be held on the Gold Coast of Australia. Next year in the land down under promises even more childcare support, more speaker support, more travel grants, and even more great science. Visit [http://smbe2016.org/](http://smbe2016.org/) and follow @OfficialSMBE See you in 2016!