

1257	S16	Omar	Rota Stabelli	The acne causing agent <i>P. acnes</i> transferred from human to grapevine in the Neolithic	<p>Studies which have investigated the dynamics of Bacteria/Host associations have revealed numerous cases of host switches from domestic animals to humans. Much less is known about the exchange of symbionts between humans and plants, and even less about the timing of such events. Here we report the surprising and, to our knowledge, first example of an horizontal interkingdom transfer of the human opportunistic pathogen, and agent of acne (<i>Propionibacterium acnes</i>) to the domesticated grapevine <i>Vitis vinifera</i> L. Fluorescent <i>in-situ</i> hybridization, phylogenetic and population genetic analyses suggest that this bacteria has a human origin and has adapted to the new host to the point of obligate, possibly endocellular, endophytism. Molecular dating indicates that this host transfer is compatible with a Neolithic domestication of grapevine by humans; we speculate that <i>P. acnes</i> has exploited common agronomic practices, such as grafting and pruning, to transfer to the new host.</p>
1258	S16	Frank	Portillo	Phylogeography of globe eye treefrogs from the Albertine Rift	<p>The genus of globe eye tree frogs, <i>Leptopelis</i>, occurs in multiple habitats throughout sub-Saharan Africa, and it includes several species that have highly variable color patterns, which makes taxonomic studies challenging. In this study, we examined multiple populations of <i>Leptopelis</i> from the Albertine Rift (AR), a region known for its high levels of endemism and biodiversity. Currently, five species are recognized from the AR: <i>Leptopelis fizeiensis</i>, <i>L. karissimbensis</i>, <i>L. kivuensis</i>, and two new species (being described by FP and EG in spring 2014) from the region in and around the Itombwe Plateau in Democratic Republic of the Congo. We employed both traditional gene-tree and coalescent species-tree approaches for estimating phylogenies, with a multi-locus data set consisting of two mitochondrial genes (16S and cyt b) and one nuclear gene (RAG1). Both analyses supported the recognition of several cryptic lineages within the genus, suggesting a revision of AR <i>Leptopelis</i> taxonomy is needed. Further investigations of acoustics and morphological data will clarify species delimitations.</p>
1259	S16	Maria Fernanda	Medina	Systematics of Snake-eyed Skinks in the <i>Panaspis wahlbergi</i> Complex	<p>Snake-eyed skinks are relatively small lizards of the genus <i>Panaspis</i> that are mostly endemic to the savannah areas of sub-Saharan Africa. During an expedition in January 2010, specimens of this genus were collected from a moss forest in Katanga Province, Democratic Republic of the Congo (DRC). Out of the three species known to reside in Katanga, <i>P. seydleri</i>, <i>P. smithii</i> and <i>P. wahlbergi</i>, the newly collected specimens had a congruent morphology with <i>P. wahlbergi</i>. Our well-supported genetic and morphometric datasets suggested that the Katanga</p>