



International Society of Hymenopterists

2020 Business meeting and Virtual Symposia

12 November 2020

General Information:

- The ISH Business meeting will take place in the Americas symposium at 15:30 CST (UTC¹ – 6).
- Three virtual symposia will be taking place across three time zones as below (conversion of the three sessions' start times to various Time Zones can be found on the last page).
- All Talks are 15 minutes total (12 minutes with 3 minutes for questions is suggested).
- Please raise hand in zoom to ask a question, or post in the chat.
- Presenters: you will be made a co-host to share your screen. Please ensure you are on a good internet connection. Also, please send a pdf of your slides to the moderator by November 11th just in case.
- Presentations will not be recorded.
- Students are automatically entered into the student competition across all Time Zones. First Place = \$100 prize + 1 year membership, 2nd place (\$50 prize + 1 year membership), 3rd place (\$50 prize + 1 year membership).
- Break out rooms can be made for socials to make it easier to chat.
- Titles of all talks are below with the name of the presenter only; abstracts and full authorship + affiliation are listed in the second part of the document.

VIRTUAL SYMPOSIA PROGRAM

Australasia session

Start Time: 10:00 JST (UTC +9) i.e. 01:00 GMT

Moderator: Erinn Fagan-Jeffries

10:00 **Introductory remarks (Erinn Fagan-Jeffries)**

10:05 **Morphometric comparisons and novel observations of diurnal and low-light-foraging bees**

Presenter: James B Dorey - Twitter handle @JamesDoreyPhoto

(Student competition)

¹ UTC (Universal Time Coordinated) and GMT (Greenwich Mean Time) share the same current time

- 10:20 **Systematics of black and orange spider wasps of Australia**
 Presenter: Mahin Sadat Chavoshi Jolfaei (Student competition)
- 10:35 **Temporal variation in parasite pressure: niche partitioning of seven parasitoids driven by host resource utilisation**
 Presenter: Lucas Hearn - Twitter handle @LRHearn (Student competition)
- 10:50 **Break**
- 11:00 **Genomic phylogeny of sawfly**
 Presenter: Niu Gengyun
- 11:15 **The Taxonomy Australia initiative and its potential for documenting Australia's hymenoptan diversity**
 Presenter: Andy Austin
- 11:30 **Tri-trophic interactions delimiting the potential of natural enemies targeting invasive alien species of pests and weeds in India**
 Presenter: Ankita Gupta
- 11:45 **Concluding remarks + mini social**

Europe, Middle East, Africa Session

Start Time: 10:00 CET (UTC+1) i.e. GMT 09:00

Moderator: Lars Krogmann

- 10:00 **Introductory remarks (Lars Krogmann)**
- 10:05 **Karyotypic study of the superfamily Chalcidoidea: An update**
 Presenter: Vladimir E. Gokhman
- 10:20 **Transferring Wolbachia endosymbionts across species boundaries in Spalangia (Hymenoptera: Pteromalidae) and Trichopria (Hymenoptera: Diapriidae) wasps**
 Presenter: Lucian Fusu
- 10:35 **In search for efficient Trichogramma application for organic agriculture in Ukraine**
 Presenter: Maryna Kaliuzhna - Twitter handle @marinka_kma - She/Her
- 10:50 **Morphological and COI fragment-based identification of Pauesia species (Hymenoptera: Braconidae: Aphidiinae) attacking Eulachnini aphids (Homoptera: Aphididae: Lachninae) on coniferous plants in Lithuania**
 Presenter: Maryna Kaliuzhna - Twitter handle @marinka_kma - She/Her

- 11:05 **Break**
- 11:20 **Enhancing pollinator biodiversity in agricultural landscapes**
Presenter: Francisco Javier Peris Felipo
- 11:35 **Using modern insect taxonomy to revise the morphologically variable ants *Camponotus* subgenus *Myrmosaga* (Hymenoptera: Formicidae) from the Malagasy region**
Presenter: Jean Claude Rakotonirina
- 11:50 **Effects of climate, host plant, and parasitoids on hornworm distributions**
Presenter: Emelia Obodum Kusi - Twitter handle @ObodumKusi - She/Her (Student competition)
- 12:05 **A rare genus calls into question the morphological monotomy of *Trissolcus* Ashmead**
Presenter: Cristina Vasilița (Student competition)
- 12:20 **Break**
- 12:35 **The Perils of *Platygaster***
Presenter: Jessica Awad - Twitter handle @parasitoidrex - She/Her (Student competition)
- 12:50 **Taxonomic revision of the Malagasy *Camponotus* Subgenus *Mayria* (Hymenoptera: Formicidae) through morphological, morphometric and molecular analyses**
Presenter: Nicole Rasoamanana (Student competition)
- 13:05 **Ancient amber meets modern methods: Using micro-CT scanning to describe new species of *Spalangiopelta* from Baltic amber**
Presenter: Marina Moser - Twitter handle @MarinaMoser_ - She/Her (Student competition)
- 13:20 **Molecular and morphological diversity of *Torymus sinensis* Kamijo (Hymenoptera, Torymidae) in France**
Presenter: Ionela-Madalina Viciriuc (Student competition)
- 13:35 **The Waterston's Organ of Ceraphronidae: A morphological barcode to a cryptic taxon**
Presenter: Jonah M Ulmer (Student competition)
- 13:50 **Concluding remarks + mini social**

Americas Session

Start Time: 10:00 CST (UTC-6) i.e. GMT 16:00

Moderator: Barbara Sharanowski

- 10:00 **Introductory remarks (Barbara Sharanowski)**
- 10:05 **Genomic architecture of endogenous polydnaviruses revealed by whole genome sequencing of ichneumonid wasps**
Presenter: Bernardo Santos - Twitter handle @bernardo_santos
- 10:20 **Progress toward an inventory of the ants (Formicidae) of Santa Barbara County, California**
Presenter: Zachary Brown - Twitter handle browndzsch
- 10:35 **One Hundred and Sixty Years of Taxonomic Confusion Resolved: Belonocnema Mayr (Hymenoptera: Cynipidae, Cynipini) Gall Wasps Associated with Live Oaks in the USA**
Presenter: Y. Miles Zhang - Twitter handle @ymilesz - He/Him
- 10:50 **Break**
- 11:05 **Native bees from the Oklahoma City Zoo**
Presenter: Jose Montalva - Twitter handle @jmmontalva (Student competition)
- 11:20 **Using Diachasma wasps to measure mutation accumulation as a consequence of asexual reproduction**
Presenter: Benjamin Trendle - He/Him (Student competition)
- 11:35 **Mitochondrial evolution in the subfamilies of the parasitoid wasps family Braconidae (Hymenoptera: Ichneumonoidea)**
Presenter: Jovana Magdalena Jasso Martinez (Student competition)
- 11:50 **Systematics and evolution of different phytophagous strategies in Allorhogas (Braconidae: Doryctinae) and other gall-associated related genera**
Presenter: Ernesto Samacá (Student competition)
- 12:05 **Concluding remarks + mini social**

ISH Business meeting starts at 15:30 CST (UTC-6) i.e. 21:30 GMT

International Society of Hymenopterists 2020 Virtual Symposia

PRESENTATIONS ABSTRACTS

Australasia session (all times in UTC +9)

10:05 Morphometric comparisons and novel observations of diurnal and low-light-foraging bees

James B. Dorey (Flinders University and South Australia Museum), Erinn P. Fagan-Jeffries (University of Adelaide), Mark I. Stevens (South Australian Museum), Michael P. Schwarz (Flinders University)

Abstract

Low-light adapted bees are substantially understudied components of the bee fauna, particularly in Australia. Whilst several species in Australia are thought to be adapted to low-light conditions, explicit records of these taxa actually foraging at twilight or night are absent from the scientific literature. We present the first observations of Australian bees foraging in low-light conditions as well as the first evidence of low-light foraging behaviour in the colletid bee subfamily, Hylaeinae. Using morphometrics of Australian and more broadly-distributed diurnal, facultative low-light and obligate low-light adapted bees, we explore the use of morphological traits to objectively assess possible low-light behaviour and corroborate low-light collection events. Our results show that it is possible to morphologically distinguish between diurnal and low-light adapted bees, and that there is a spectrum of characters that are associated with low light conditions. We use GIS to show that low-light adapted species occur mostly in the tropics, but that some species have subtropical, arid and even temperate distributions. As low-light foraging behaviour in bees is infrequently reported, it appears that low-light foraging behaviour is more common than currently appreciated, highlighting the need for extended bee-sampling periods and more consistent collection data to increase the understanding of this little-understood aspect of bee behaviour.

10:20 Systematics of black and orange spider wasps of Australia

Dr. Juanita Rodriguez (CSIRO-ANIC), Mahin Chavoshi (ANU)

Abstract

This project mainly aims to combine traditional taxonomy with molecular methods to revise the taxonomy of black and orange spider wasps of Australia.

10:35 Temporal variation in parasite pressure: niche partitioning of seven parasitoids driven by host resource utilisation

Ben Parslow (South Australian Museum), Mark Stevens (South Australian Museum), Michael Schwarz (Flinders University)

Abstract

Brood parasitism has been emphasised as a major component contributing to decreased reproductive success in bees. The effects of brood parasitism are generally associated at a single point in a bee's phenology and rarely observed across the full life-cycle, meaning the full impact of parasitism is rarely understood. In the only known social colletid bee, *Amphylaeus morosus*, brood parasitism appears from the outset to involve several pressures occurring at various times throughout the life-cycle. Our results indicate that *A. morosus* is strongly

pressured by seven different parasite species operating at different colony phenology phases – four species of Gasteruption wasp that operate during the very early stages of brood provisioning, Anthrax maculatus throughout the middle of brood rearing, and two mutillid wasps towards the end of brood rearing. The pattern in sequence of attack displayed by these parasitoids is likely driven by resource utilisation for a specific host stage; the predator-inquiline larvae of Gasteruption exploiting the provisions and egg of *A. morosus*, *A. maculatus* the larval stage, while both mutillid species preference the prepupal stage which is more likely to be found later in the season. These temporal selection agents could have important implications for understanding how parasitism influences social nesting across the entire colony phenology.

11:00 Genomic phylogeny of sawfly

Niu Gengyun (Jiangxi Normal University), Wei Meicai (Jiangxi Normal University)

Abstract

Phylogenetic studies are increasingly reliant on next-generation sequencing. We assembled 76 whole sawfly genomes using second-generation sequencing results and obtained 115,955,145 nucleotide sites in 3583 single-copy genes. We implemented five different methods (partition 、ASTRAL、GHOST、Dayhoff6、PMSF) on five datasets to get eleven evolutionary trees with nearly identical topologies. We recover a well-supported phylogenetic structure for the basal hymenopteran. After the divergence of Xyelidae in 200Ma, the tree is split into two major branches. One is consistent with Pamphilioidea, Siricoidea, Cephidae, and vespina, which includes Orussidae. The other is formed by eight highly supported clades: Blasticotomidae, ((Pergidae, Argidae), (Athaliidae, ((Cimbicidae, Diprionidae), (Heptamelidae, Tenthredinidae))))). The rapid divergence of Tenthredinoidea occurred around 145~176Ma, which coincides with a period of the rapid evolution of angiosperms.

11:15 The Taxonomy Australia initiative and its potential for documenting Australia's hymenoptan diversity

Andy Austin and Erinn Fagan-Jeffries (Australian Centre for Evolutionary Biology & Biodiversity, School of Biological Sciences, Darling Building, The University of Adelaide)

Abstract

Taxonomy Australia (taxonomyaustralia.org.au) is a national initiative aimed at galvanising the taxonomic community in an aspirational endeavour to describe the continent's fauna in a generation. Launched in 2018, the initiative has had strong support from the Australian Academy of Science, the Potter Foundation, the various systematics' societies and the taxonomic community. Although only in the early stages of development, we take this opportunity to explore how the initiative can be effectively used to approach the daunting task of documenting the Australian hymenopteran fauna, and training a new generation of workers to undertake this task.

11:30 Tri-trophic interactions delimiting the potential of natural enemies targeting invasive alien species of pests and weeds in India

Ankita Gupta (ICAR-National Bureau of Agricultural Insect Resources)

Abstract

A detailed case study highlighting the role of Opiinae parasitoids in delimiting the efficacy of bioagents belonging to *Merochlorops* species complex, considered as a potential biological solution for serious invasive weed *Hedychium gardnerianum* Sheppard ex Ker Gawl. (Zingiberaceae), originating from the Himalayas, still continues as a serious environmental concern in many tropical and subtropical regions of the world including New Zealand, Hawaii

and the Azores. The observations on various plant-pest-natural enemy complex-hyperparasitoids and their interactions for the three recent invasive pests during the last five years in India viz., cassava mealybug *Phenacoccus manihoti* Matile-Ferrero (Hemiptera: Pseudococcidae) (a neotropical pest with earliest record from Argentina, entered India in 2020); fall armyworm *Spodoptera frugiperda* (J. E. Smith) (Lepidoptera: Noctuidae) (a global transboundary pest originating from the American continent, invaded India in 2018) and rugose spiraling whitefly *Aleurodicus rugioperculatus* Martin (Hemiptera: Aleyrodidae) (originally described from Belize, invaded India in 2016), provide interesting yet alarming insights into the role of predominant native hyperparasitoids targeting predators actively involved in controlling the alien pest naturally. The case studies reveal that the situation becomes of serious concern with non availability of native parasitoid to control the alien pest accompanied with increased rate of parasitism of native predators.,,

Europe, Middle East, Africa Session (all times in UTC +1)

10:05 **Karyotypic study of the superfamily Chalcidoidea: An update**

Vladimir E. Gokhman (Botanical Garden, Moscow State University, Moscow, Russia)

Abstract

Chromosomes of about 240 chalcid species are studied up to now. Techniques for analyzing karyotypes of this superfamily include the so-called “traditional” (chromosome morphometrics, C-banding, AgNOR-banding etc.) and “modern” methods of differential segmentation of chromosomes (e.g. staining with base-specific fluorochromes) as well as fluorescence in situ hybridization (FISH), chromosome microdissection and immunocytochemical assays. Among the Chalcidoidea, the haploid chromosome number can vary from $n = 3$ to $n = 11$, with a clear mode at $n = 6$ and a second local maximum at $n = 10$. Previously, chalcid families were generally subdivided into the so-called “low-numbered” and “high-numbered” ones having $n = 3-7$ and $8-11$ respectively, with just a few exceptions. Most families belonged to the first group, whereas higher chromosome numbers were characteristic of Mymaridae, Eurytomidae, Encyrtidae and some Aphelinidae. However, main lineages of Chalcidoidea now include both “high-numbered” and “low-numbered” members. In this group, most chromosomes have two long arms, i.e. they are either metacentric or submetacentric, but acrocentrics and/or subtelocentrics also can predominate, especially within karyotypes of certain Chalcidoidea with higher chromosome numbers. The following main types of chromosomal mutations are characteristic of chalcid karyotypes: inversions, fusions, translocations, polyploidy, aneuploidy and B-chromosome variation. Although karyotype evolution of this superfamily was mainly studied using phylogenetic reconstructions based on morphological and/or molecular characters, chromosomal synapomorphies of certain groups, e.g. particular members of the Eurytomidae, were also revealed. Taxonomic implications of karyotypic features of the Chalcidoidea are apparently the most important at the species level, especially among cryptic taxa.

10:20 **Transferring Wolbachia endosymbionts across species boundaries in Spalangia (Hymenoptera: Pteromalidae) and Trichopria (Hymenoptera: Diapriidae) wasps**

Lucian Fusu, Mălina Atodiresei, Maria-Magdalena Dascălu, Daniela Gherghel, Lucian Hânceanu, Mircea D. Mitroiu, Ovidiu A. Popovici, Crstina Vasilița, Ionela-Mădălina Viciriu & Gabriela

Vochița (Faculty of Biology, 'Al. I. Cuza' University of Iasi and NIRDBS, Branch Institute of Biological Research Iasi, Romania)

Abstract

Synanthropic flies are insect pests related to major human activities such as food processing and animal husbandry. They include among others the house fly *Musca domestica* L. and the common stable fly *Stomoxys calcitrans* (L.) that cause major health problems to both humans and livestock. Most natural enemies of the synanthropic flies are small parasitoid wasps (Insecta: Hymenoptera) that develop as larvae in the flies' puparia killing them in the process. We are presenting our current project that aims to experimentally transfer *Wolbachia* endosymbionts across species boundaries in parasitic Hymenoptera. This might result in a locally adapted and improved thelytokous line of parasitoid wasps. As there are no naturally thelytokous Spalangia (Hymenoptera: Pteromalidae) or *Trichopria* (Hymenoptera: Diapriidae) species known (some of the main parasitoids attacking flies), we intend to obtain them experimentally, since thelytoky could be induced by infecting females with *Wolbachia* or other endosymbionts. Hence firstly we will test the candidate species for the presence of endosymbionts and cure any innate infection to remove possible interferences. Secondly, we will artificially infect them with thelytoky-inducing *Wolbachia* endosymbionts derived from other species and cultivated in vitro in an insect cell line.

10:35 In search for efficient *Trichogramma* application for organic agriculture in Ukraine

Maryna Kaliuzhna (I.I. Schmalhausen Institute of Zoology of National Academy of Sciences of Ukraine, Kyiv, Ukraine, Institute of Organic Agriculture, Agroindustrial group "Arnika", Hlobyne, Ukraine), Andriy Pylypchenko (Institute of Organic Agriculture, Agroindustrial group "Arnika", Hlobyne, Ukraine), Sergiy Sereda (Institute of Organic Agriculture, Agroindustrial group "Arnika", Hlobyne, Ukraine), Valentyn Kulinich (Institute of Organic Agriculture, Agroindustrial group "Arnika", Hlobyne, Ukraine), Svitlana Solokha (Institute of Organic Agriculture, Agroindustrial group "Arnika", Hlobyne, Ukraine), Alla Kulinich (Institute of Organic Agriculture, Agroindustrial group "Arnika", Hlobyne, Ukraine), Oleksiy Zbyranyk (Institute of Organic Agriculture, Agroindustrial group "Arnika", Hlobyne, Ukraine), Oleksandr Vasiliev (LLC "Bioservis Plus", Poltava, Ukraine), Victor Fursov (I.I. Schmalhausen Institute of Zoology of National Academy of Sciences of Ukraine, Kyiv, Ukraine), Alex Gumovsky (I.I. Schmalhausen Institute of Zoology of National Academy of Sciences of Ukraine, Kyiv, Ukraine, Institute of Organic Agriculture, Agroindustrial group "Arnika", Hlobyne, Ukraine)

Abstract

Species of the genus *Trichogramma* are among the most economically important biocontrol agents in Europe, applied against a complex of cutworms and snout moths. *Trichogramma* spp. are widely used against various Lepidoptera pests, mainly against European corn borer (ECB, *Ostrinia nubilalis*) in Ukraine. However, our studies revealed that often the efficacy of *Trichogramma* application was unconvincing, if experimental and control plots (large production fields) are compared. We critically revised *Trichogramma* application practices in Ukraine and conducted series of experiments in attempt to estimate the efficacy of commercially available *Trichogramma* spp. used in organic agriculture in Ukraine, in 2018-2020. Experiments were conducted in the fields and storage facilities of Agroindustrial group "Arnika" (Hlobyne, Ukraine). The main target pest species included ECB on corn, *Helicoverpa armigera* on corn and chickpea, and *Plodia interpunctella* in grain storages. The main problem we dialed with was the mass-replacement of *Trichogramma evanescens*/*T. brassicae*, an established biocontrol agent against ECB in Europe, by *T. pintoi* in laboratory cultures in Ukraine. We compared the efficacy of these species, as well as the characteristics of target crops and pests, application rates and time, and release methods. The results achieved in laboratory conditions often were not repeated on production fields and real storage

conditions. Our preliminary data have not yet confirmed an efficacy of broad-scale use of *Trichogramma* if applied by conventional approaches commonly used in Ukraine. However, some preliminary studies suggest that host-specific strains may affect target hosts more efficiently: *H. armigera*-associated strain of *T. evanescens* is an example.

10:50 Morphological and COI fragment-based identification of *Pauesia* species (Hymenoptera: Braconidae: Aphidiinae) attacking *Eulachnini* aphids (Hemiptera: Aphididae: Lachninae) on coniferous plants in Lithuania

Jekaterina Havelka (Institute of Biosciences, Life Sciences Centre, Vilnius University, Saulėtekio al. 7, LT-10257 Vilnius, Lithuania), Maryna Kaliuzhna (I.I. Schmalhausen Institute of Zoology, NAS of Ukraine, vul. B. Khmelnytskogo, 15, Kyiv, 01030 Ukraine), Jurij Danilov (Institute of Biosciences, Life Sciences Centre, Vilnius University, Saulėtekio al. 7, LT-10257 Vilnius, Lithuania), Rimantas Rakauskas (Institute of Biosciences, Life Sciences Centre, Vilnius University, Saulėtekio al. 7, LT-10257 Vilnius, Lithuania)

Abstract

Previously published data concerning *Eulachnini* aphid parasitoids in Lithuania were mostly fragmentary faunistic records reporting three species: *Pauesia* (*Pauesia*) *unilachni*, *P.* (*Paraphidius*) *cupressobii* and *P.* (*Paraphidius*) *jezoensis*. During 2018-2019, ten species of the genus *Pauesia* (Hymenoptera: Braconidae: Aphidiinae) reared from 14 out of 27 *Eulachnini* species (Hemiptera: Aphididae: Lachninae) were identified by morphological characters. Seven *Pauesia* species were recorded in Lithuania for the first time. Parasitoids for *Cinara* (*Cinara*) *hyperophila* and *C.* (*C.*) *piniphila* were detected for the first time. New parasitoid species were recorded for aphid host species *C.* (*C.*) *brauni*, *C.* (*C.*) *neubergi*, *C.* (*C.*) *pinea*, *C.* (*C.*) *pini* and *C.* (*C.*) *pruinosa*. Partial sequences of mitochondrial COI for 98 parasitoid individuals were analyzed. This enabled identification of specimens that appeared problematic to identify by morphological characters - males and females with intermediate character states or with some parts broken or lacking. DNA-based species delimitation by means of Automatic Barcode Gap Discovery (ABGD), Generalised Mixed Yule-Coalescent (GMYC) model, Poisson Tree Processes (PTP) model and statistical parsimony network analysis (TCS) gave number of candidate species ranging from 11 to 15. The values of match ratio for each method were from 0.67 for PTP to 0.93 for GMYC. Sequence divergences (*p*-distances, %) between the parasitoid species *Pauesia jezoensis*, *P. pinicollis*, *P. cupressobii* and *P. goidanichi* were on the intraspecific level (0.62 – 1.14 %). Molecular species delimitation methods indicate possible existence of three species new for science.

11:20 Enhancing pollinator biodiversity in agricultural landscapes

F.J. Peris-Felipo (Syngenta Crop Protection), L. Aguado-Martín (Andrena Iniciativas y Estudios Medioambientales S.L.), M. Schade (Syngenta Crop Protection), L. Miranda-Barroso (Agricultura Sostenible Syngenta España), G. Swart (Syngenta Crop Protection)

Abstract

Starting in the 1950ies, agricultural production has been remarkably intensified, resulting in the modern management systems, providing higher yields and increasing yield security, but at the same time leading to a substitution of heterogeneous agricultural landscapes by homogeneous ones with poor crop diversity, short crop rotations, and thanks to the high efficacy of modern herbicides, also to minimum in-crop diversity. A severe increase in plot size led to an elimination of edges and other ecologically valuable structural elements that had formerly provided floral resources, nesting sites and shelter for our fauna. „The resulting habitat loss caused dramatic changes in the natural communities of birds, insects and mammals. In addition, the intensification has also been compromising soil health, increasing the risk of losing the most valuable agricultural resource. „The phenomenon called “Insect

Declines” has been among the top headlines in the daily news and the European Commission for the Conservation of the Environment identified an urgent need to promote research on the conservation of insects in general and specifically pollinators in agriculture. As an approach to enhancing biodiversity in agricultural landscapes, Syngenta had proactively introduced international programmes to increase biodiversity promoting pollinators and other beneficial arthropods in the crops. „In this presentation, results obtained from different biodiversity projects carried out in different monoculture crops such as alfalfa, apple, soybean, stone fruits or vineyards are provided to show how biodiversity and modern agriculture can coexist.,

11:35 Using modern insect taxonomy to revise the morphologically variable ants *Camponotus* subgenus *Myrmosaga* (Hymenoptera: Formicidae) from the Malagasy region

Jean Claude Rakotonirina (Madagascar Biodiversity Center), Brian Fisher (California Academy of Sciences)

Abstract

Addressing how species are to be delimited is scientifically challenging for the taxonomy of species rich and morphologically variable ant genus *Camponotus*. . In the Malagasy region, knowledge of species is important to answer questions in ecosystem development and conservation planning, in evolutionary biology and biogeography. Rigorous species delineation can be obtained by applying integrative complementary methods. In my revision, I analyzed qualitatively the variation of morphological characters of worker caste of the *Camponotus* (*Myrmosaga*) group and proposed hypothetical species. These hypotheses were tested using multivariate statistical analysis of quantitative morphology, the specimen distributional data and biology, the results from DNA barcoding. In total, 32 species are recognized, of which 16 are newly discovered. Because of geographical variation of morphological characters, qualitative morphology-based analysis alone failed to accurately define the species and overestimated the number of species. The additional taxonomic approaches have facilitated the delimitation of the species and raised our level of confidence in species hypotheses. Included in this revision will be an illustrated species identification key, taxonomic discussions, images, and distribution maps for each species.

11:50 Effects of climate, host plant, and parasitoids on hornworm distributions

Emelia Obodum Kusi, Dr. Karen Kester, Dr. Catherine Hulshof - (Virginia Commonwealth University)

Abstract

Ecology is increasingly quantitative and predictive. My research is characterized by both. I use ecological models to study insect distribution as a factor of host plant distribution, and abiotic and biotic interactions (such as the distribution of parasitoids). The model system of the study include two congeneric insect herbivores, in the order Lepidoptera and family Sphingidae - *Manduca sexta*(L.) (“tobacco hornworm”) and *Manduca quinquemaculata*(Haworth) (“tomato hornworm”), their primary host plant, and the only shared parasitic wasp -*Cotesia congregata*(Say) in the order Hymenoptera and family Braconidae. The larvae of tobacco hornworm and tomato hornworm feed exclusively on various plants in the family Solanaceae, particularly on cultivated tobacco (*Nicotiana tabacum* L.) and tomato (*Lycopersicon esculentum*_Mill) by defoliating their leaves. The tobacco hornworm has been recognized as the most common and destructive pest of tobacco in the United States since 1850. *Cotesia congregata*, deposit eggs into the hornworm, and the larval wasps develop, feeding on nutrients in the host hemolymph. Mature larvae bite through the host cuticle and spin small, white, silken cocoons. Adults emerge from the still-living caterpillar while the host dies to starvation. My goal is to move beyond the traditional species distribution model approach (SDM) by incorporating population dynamics and spatial and temporal variation in abiotic and

biotic factors. Doing so will provide an important assessment of the potential effects of climate change and the susceptibility of these two Lepidoptera species to ecosystem change. Because these two species feed on major agricultural crops (tobacco, tomato), understanding their distributions and population dynamics has major economic implications.

12:05 A rare genus calls into question the morphological monotony of Trissolcus Ashmead

Cristina Vasilița (Research Group in Invertebrate Diversity and Phylogenetics, Faculty of Biology, University „Alexandru Ioan Cuza” in Iași), Ovidiu Alin Popovici (Research Group in Invertebrate Diversity and Phylogenetics, Faculty of Biology, University „Alexandru Ioan Cuza” in Iași), Elijah Talamas (Florida State Collection of Arthropods, Division of Plant Industry, Florida Department of Agriculture and Consumer Services), Norman Johnson (Department of Entomology, The Ohio State University), Lubomir Masner (Agriculture and Agri-Food Canada), Francesco Tortorici (Dipartimento di Scienze Agrarie, Forestali e Alimentari (DISAFA), Entomologia Generale e Applicata, University of Torino), Lucian Fusu (Research Group in Invertebrate Diversity and Phylogenetics, Faculty of Biology, University „Alexandru Ioan Cuza” in Iași)

Abstract

The monotypic genus *Latonius* Kononova, 1982 (Platygastroidea: Scelionidae) was described from a singleton female specimen collected in southern Ukraine. It somewhat resembles *Trissolcus* Ashmead, but has a very distinct claval formula. The only species in the genus, *Latonius planus*, is lacking any details regarding biology, sexual dimorphism, intraspecific variability, or distribution. Due to a lack of material, further investigation was not possible until August 2018, when five fresh specimens of *L. planus* were collected in southern France. The present study defines the position of *Latonius* within the Telenominae, provides a comprehensive description accompanied by high quality images, and compares *Latonius* and *Trissolcus*. Five molecular markers were amplified; sequences of *L. planus* were included and analyzed within the data set on the molecular phylogeny of Telenominae (Taekul et al., 2014) as well as the molecular phylogeny of *Trissolcus* (Talamas et al., 2019). We dissected the metasoma, tarsi, antennae, and ovipositor and performed SEM imaging. With the means of molecular tools combined with punctilious morphological investigation, we tried to debunk *Latonius* and shed some light on this seemingly abandoned, but peculiar genus from Telenominae.

12:35 The Perils of Platygaster

Jessica Awad (State Museum of Natural History Stuttgart), Elijah Talamas (Florida State Collection of Arthropods), Lars Krogmann (State Museum of Natural History Stuttgart)

Abstract

Platygaster is the type genus for Platygastroidea, and includes approximately 10% of the described species in the superfamily. Despite its taxonomic importance, its large size and lack of organization are serious barriers to revisionary work. Mounting evidence suggests that *Platygaster* is not a natural group, but sometimes the only way forward is to go back. To that end, we review the history of *Platygaster*: a tale of questionable decisions, linguistic confusion, and mysterious missing specimens.

12:50 Taxonomic revision of the Malagasy Camponotus Subgenus Mayria (Hymenoptera: Formicidae) through morphological, morphometric and molecular analyses

Nicole Rasoamanana (Madagascar Biodiversity Center), Brian L. Fisher (California Academy of Sciences)

Abstract

The taxonomy of the *Camponotus* Subgenus *Mayria* (Hymenoptera: Formicidae) is being revised in the Malagasy region. We provide a comprehensive taxonomic review of this subgenus, integrating multiple lines of evidence including qualitative morphology, quantitative morphometrics and molecular analysis. An integrative taxonomic approach supports the existence of 36 species which are arranged in 9 species groups: *alamaina*-group, *antsaraingy*-group, *darwinii*-group, *edmondi*-group, *efitra*-group, *elliotti*-group, *madagascarensis*-group, *repens*-group, *robustus*-group. Eleven species are described, five species are redescribed and one species is raised to species. Twenty two species previously described are transferred to this Subgenus. A comprehensive reinterpretation of this subgenus is included. This revision of *Mayria* includes a classification, a key to species group and an updated key to species based on minor worker caste, descriptions and images of workers, information on geographic distribution are provided.

13:05 Ancient amber meets modern methods: Using micro-CT scanning to describe new species of *Spalangiopelta* from Baltic amber

Marina Moser (Department of Entomology, State Museum of Natural History Stuttgart and Institute of Biology, Systematic Entomology), Roger A. Burks (Department of Entomology, University of California Riverside), Jonah M. Ulmer (Department of Entomology, State Museum of Natural History Stuttgart and Institute of Biology, Systematic Entomology), John M. Heraty (Department of Entomology, University of California Riverside), Thomas van de Kamp (Institute for Photon Science and Synchrotron Radiation (IPS) and Laboratory for Applications of Synchrotron Radiation, Karlsruhe Institute of Technology (KIT)), Lars Krogmann (Department of Entomology, State Museum of Natural History Stuttgart and Institute of Biology, Systematic Entomology),,,

Abstract

Spalangiopelta (Hymenoptera: Pteromalidae) is a small genus of chalcid wasps that has received little attention despite the widespread distribution of its extant species. The fossil record of the genus is restricted to a single species from Miocene Dominican amber. We described two new species of *Spalangiopelta* from Baltic amber. 3D models were reconstructed from X-ray μ CT scans. The models assisted in the descriptions, the determination of character states and the construction of an identification key for the females of all currently known *Spalangiopelta* species. Phylogenetic and functional relevance of two wing characters, admarginal setae and the hyaline break, are discussed. The newly described Baltic amber fossils significantly extend the minimum age of *Spalangiopelta* to the Upper Eocene.

13:20 Molecular and morphological diversity of *Torymus sinensis* Kamijo (Hymenoptera, Torymidae) in France

I.M. Viciriu (Research Group in Invertebrate Diversity and Phylogenetics, Faculty of Biology, Al. I. Cuza University, bd Carol I no. 11, 700506 Iasi, Romania), L. Fusu (Research Group in Invertebrate Diversity and Phylogenetics, Faculty of Biology, Al. I. Cuza University, bd Carol I no. 11, 700506 Iasi, Romania), M. Thaon (Sophia Agrobiotech Institute, UMR INRAE-CNRS-Université Côte d'Azur, 400 route des Chappes, BP167, 06903 Sophia Antipolis, France), S. Moriya (National Agriculture and Food Research Organization, Tsukuba, Japan), S. Warot (Sophia Agrobiotech Institute, UMR INRAE-CNRS-Université Côte d'Azur, 400 route des Chappes, BP167, 06903 Sophia Antipolis, France), J. Zhang (MoA-CABI Joint Laboratory for Biosafety, Chinese Academy of Agricultural Sciences, Beijing, China), A. Aebi (Laboratory of Soil Biodiversity, University of Neuchâtel, Emile-Argand 11, 2000 Neuchâtel, Switzerland), N. Ris (Sophia Agrobiotech Institute, UMR INRAE-CNRS-Université Côte d'Azur, 400 route des Chappes, BP167, 06903 Sophia Antipolis, France), N. Borowiec (Sophia Agrobiotech Institute,

UMR INRAE-CNRS-Université Côte d'Azur, 400 route des Chappes, BP167, 06903 Sophia Antipolis, France)

Abstract

The Asian chestnut gall wasp *Dryocosmus kuriphilus* Yasumatsu, (Hymenoptera, Cynipidae) accidentally introduced in several countries on three continents became the most severe insect pest of chestnuts. To reduce the negative impact on the chestnut industry, *Torymus sinensis* Kamijo (Hymenoptera, Torymidae) was introduced, firstly from China to Japan and then from Japan to other countries. During the first translocation, *T. sinensis* was suspected of interspecific hybridizations with *T. beneficus* Yasumatsu and Kamijo. Reproductive compatibilities were observed in controlled conditions or inferred from field-collected hybrids. The males of this species are hardly distinguishable morphologically and only the length of the ovipositor seems to discriminate *T. sinensis* females from *T. beneficus*. Based on the success in other countries, a classical biological control program has been implemented in France since 2011 using the Italian stock of *T. sinensis* and he was successfully established. Our results evidenced for the first time that the European stock of *T. sinensis* has some rare molecular signatures of historical hybridization that took place in Japan. Our morphometric study also shows that European and Japanese *T. sinensis* are morphologically intermediate between the two species that hybridized. *T. beneficus* is morphologically very close to *T. sinensis*, and the interspecific distance on COI, though large, is comparable with the larger intraspecific variability found in other Chalcidoidea species. The AMOVA test results show the lack of genetic differentiation between French populations, but this was expected because the introduced individuals of *T. sinensis* are part of the same stock (Italian).

- 13:35 The Waterston's Organ of Ceraphronidae: A morphological barcode to a cryptic taxon**
Jonah M. Ulmer (SMNS), István Mikó (UNH), Andrew R. Deans (PSUC), Lars Krogmann (SMNS)

Abstract

The parasitoid wasp family Ceraphronidae is a small cosmopolitan group consisting of roughly 300 species separated into 16 genera with over 90% of the described species belonging to two genera, Ceraphron and Aphanogmus. Species and generic level separation within the group has been a long standing issue with few discrete characters many of which are sexually dimorphic, preventing the development of complete species concepts with even generic delimitation uncertain in many cases. Of the 16 genera, nine are monotypic with only a single sex described, often females, and even in the species rich genera over half are known only from females. Recent morphological efforts have shown male genitalia to be an incredibly efficient character for species delimitation however it still lacks the ability to confidently match sexes. The Waterston's organ is a putative exocrine gland located on the 6th metasomal segment in all ceraphronids. The associated cuticular modification provides a suite of characters which not only provide confirmation of generic and species level classifications but provide a unique monomorphic character which allows for the matching of males and females within the family. Characterization of the structure and its taxonomic significance will be discussed along with its impact on the surrounding organs, including a novel modification of the dorsal vessel within Hymenoptera.

Americas Session (all times in UTC -6)

10:05 Genomic architecture of endogenous polydnviruses revealed by whole genome sequencing of ichneumonid wasps

Bernardo F. Santos (National Museum of Natural History), Fabrice Legeai (Institut national de la recherche agronomique), Stephanie Robin (Institut national de la recherche agronomique), Rebecca Dikow (National Museum of Natural History), Seán G. Brady (National Museum of Natural History), Anne-Nathalie Volkoff (Institut national de la recherche agronomique)

Abstract

Polydnviruses (PDVs) are mutualistic endogenous viruses associated with some lineages of parasitoid wasps that allow successful development of the wasps within their hosts. PDVs are unusual viruses in that their relatively large genomes are divided into separate, circular DNA molecules. Furthermore, their genomes are fully incorporated into the wasp genomes and comprise two major elements: (1) virulence genes located on proviral segments that are packaged into the viral particle, and (2) genes involved in the production of the viral particles, which are found in the wasp genome but not encapsidated. Elucidating how viral insertions are organized in the wasp genomes is fundamental to understand the process of “domestication” of viruses in parasitic wasps. However, the genomic architecture of PDVs found in ichneumonid wasps remains poorly understood. We describe the first whole genomes of ichneumonid wasps, enclosing viral elements that derive from the integration of an ancestral virus into the wasp genome. Assemblies with long scaffold size allowed mapping of the integrated ichtnovirus sequences against the wasp genome. We found that proviral segments are widely dispersed across the wasp genome, with their position widely variable between the two wasp species. Conversely, the replication genes in both species were grouped in clusters harboring a conserved organization in terms of gene content and gene order. This distinction is consistent with the biological properties of these two viral elements: proviral segments need to be fine-tuned to the host physiology, while viral architecture genes should have largely conserved biological function.

10:20 Progress toward an inventory of the ants (Formicidae) of Santa Barbara County, California

Zach Brown (Mississippi Entomological Museum, Mississippi State University, Starkville, Mississippi), Elaine Tan (Graduate Assistant, John Longino Lab, School of Biological Sciences, University of Utah, Salt Lake City, Utah), Katja C. Seltmann (Katherine Esau Director, Cheadle Center for Biodiversity and Ecological Restoration, University of California, Santa Barbara, Santa Barbara, California)

Abstract

California is a hotbed of floral and faunal species diversity. Santa Barbara County is a 4000 square mile area on the central California coast. It has four distinct ecoregions: Southern California Coast, Southern California Mountains and Valleys, Central California Coast, and Central Valley Coast which include chaparral and coastal sage scrub habitats. Santa Barbara County also includes four of the eight Channel Islands, which has a similar assemblage of habitats as the mainland, and a recent history of invasive ant eradication projects. In 2018, we began to compile an inventory of ant species that occur in the county, obtaining records from online digitized collections including AntWeb, GBIF, Symbiota Collections of Arthropods Network, Ecdysis, and iNaturalist. We included our own sampling from North Campus Open Space (NCOS), a recent coastal saltmarsh restoration site, and the Coal Oil Point Reserve (COPR), part of the UC Natural Reserve System. From this effort we found 66 species across 27 genera within Santa Barbara County including new records from our sampling sites. This checklist was built using Symbiota’s built-in check-list creation software. The coastal restoration sites proved to be less diverse and contain more invasive species than other areas within Santa Barbara County. In conclusion, the ongoing 2-year data collection from NCOS and COPR is a small part of a larger effort to expand the known ant species of Santa Barbara

County. To provide a more comprehensive picture of the regional ant diversity, more targeted ant sampling in each ecoregion is needed.

10:35 One Hundred and Sixty Years of Taxonomic Confusion Resolved: *Belonocnema* Mayr (Hymenoptera: Cynipidae, Cynipini) Gall Wasps Associated with Live Oaks in the USA

Y. Miles Zhang (Systematic Entomology Laboratory, USDA-ARS, c/o National Museum of Natural History, Washington, DC, USA), Scott P. Egan (Department of Biosciences, Rice University, Houston, TX, USA), Amanda L. Driscoe (Department of Biology, Population and Conservation Biology Program, Texas State University, San Marcos, TX, USA, 78666), James R. Ott (Department of Biology, Population and Conservation Biology Program, Texas State University, San Marcos, TX, USA, 78666)

Abstract

Gall wasps (Hymenoptera: Cynipidae) in the genus *Belonocnema* Mayr induce galls on live oaks (*Quercus* L. series *Virentes*), forming multilocular potato-like root galls in the sexual generation and unilocular pea-like leaf galls in the asexual generation. The taxonomy of *Belonocnema* has remained convoluted for over 160 years. Using morphological characters, host records, museum specimens, flight propensity, and phylogenetic analysis of published COI and multilocus nuclear SNP data, we resolve the long-standing taxonomic confusion within *Belonocnema* and recognize three distinct species that are distributed throughout the southern and southeastern USA: *B. fossoria* Weld comb. nov., *B. kinseyi* Weld comb. nov., and *B. treatae* Mayr. The presence of mitonuclear discordance results in the failure of a mitochondrial DNA barcode region to distinguish between *B. fossoria* and *B. treatae* while recognizing *B. kinseyi*, despite the three species being clearly separated based on morphology and phylogenetic analysis of multilocus nuclear data. All three species exhibit heterogony and we provide (re)descriptions and an updated dichotomous key for both asexual and sexual generations of these widespread species. Finally, as *Belonocnema* has emerged as a model organism for ecological and evolutionary studies we clarify the species examined in published studies to date.

11:05 Native bees from the Oklahoma City Zoo

Jose Montalva (Department of Biology, East Central University, 146 Physical and Environmental Sciences Building, Ada, Oklahoma. and Department of Geography and Environmental Sustainability, University of Oklahoma, 100 East Boyd St, SEC 684, Oklahoma),

Abstract

Bees (Anthophila) are very important pollinators. They pollinate commercial crops (most of our food) and plants in the wild (including in your national parks, preserves, prairies, forests, deserts, etc.). However, we know very little about bee diversity and abundance within Oklahoma, especially compared to neighboring states (Texas, Kansas, Missouri). Here, I describe several native bees and results from a survey conducted March to October 2020 at the Oklahoma City Zoo and Botanical Garden. We found a high diversity of native species, approximately 60 species in total were collected. This included accounts of endangered bumble bee species and new state records. Making cadastres and taking frequent censuses allows us to better understand the position and role our unique bees play in the environment and thus help mitigate human-caused threats to their stability. We will also be gathering information for OKC Zoo's planned prairie habitat restoration project, located in the future Girl Scouts' Camp Trivera. Our goal is to see how ecological restoration can provide higher quality habitats and increase the diversity of pollinators.

11:20 Using Diachasma wasps to measure mutation accumulation as a consequence of asexual reproduction

Benjamin Trendle, Eric S. Tvedte, PhD (University of Maryland School of Medicine)

Abstract

Why are asexual organisms less prevalent than sexual organisms? Asexual lineages lack the genetic recombination of sexuals and are predicted to be unable to prevent the accumulation of deleterious mutations. These asexuals are predicted to be pushed into extinction by this unstopped and irreversible accumulation of mutations, called Muller's ratchet. In this presentation, I will present the evidence for increased mutation accumulation in the asexual parasitoid wasp, *Diachasma muliebre* through genomic comparisons with its close, sexually-reproducing relatives. From the *Diachasma* genomes, pairwise distance, nucleotide substitutions rates, and maximum likelihood phylogenies were all calculated to detect increased mutation accumulation in the asexual *D. muliebre*. From all of our genomic comparisons, we were able to detect increased mutation accumulation in the asexual *D. muliebre*.

11:35 Mitochondrial evolution in the subfamilies of the parasitoid wasps family Braconidae (Hymenoptera: Ichneumonoidea)

Jovana M. Jasso-Martínez (Colección Nacional de Insectos, Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad de México, Mexico), Donald L. J. Quicke (Integrative Ecology Laboratory, Department of Biology, Faculty of Science, Chulalongkorn University, Pathumwan, Bangkok, Thailand), Sergey A. Belokobylskij (Zoological Institute, Russian Academy of Sciences, St Petersburg 199034, Russia, Museum and Institute of Zoology Polish Academy of Sciences, Warszawa 00-679, Poland), Bernardo F. Santos (Department of Entomology, National Museum of Natural History, Smithsonian Institution, 10th Street & Constitution NW, Washington, 20560, DC, USA), Robert R. Kula (Department of Entomology, National Museum of Natural History, Smithsonian Institution, 10th Street & Constitution NW, Washington, 20560, DC, USA), José L. Fernández-Triana (Department of Integrative Biology and the Biodiversity Institute of Ontario, University of Guelph, Guelph, ON, Canada, Canadian National Collection of Insects, Ottawa, ON, Canada), Alejandro Zaldívar-Riverón (Colección Nacional de Insectos, Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad de México, Mexico),

Abstract

Braconidae is one of largest radiations of hymenopterans with ca. 21,000 described species. Most members of this family are either endo- or ectoparasitoids, koino- or idiobionts (i.e. allowing or not the further development of host, respectively), though few species of Mesostoinae, Braconinae and Doryctinae are phytophagous. Classification within Braconidae has been challenging mainly due to the presence of high levels of morphological convergence, rapid ancestral radiations, as well as by the limited taxon sampling in previous phylogenetic studies performed for the group. The molecular information provided by the mitochondrial DNA has been one of the most used and successful tools for inferring the evolution of species and populations. In particular, the use of complete mitochondrial genomes has showed good resolution for investigating evolutionary relationships at different taxonomic levels. Mitochondrial genomes have been previously used to reconstruct the evolutionary relationships among the braconid subfamilies, though in these studies the taxon sampling was considerably limited, with most of the subfamilies being only represented by one species. Here we show the preliminary results of an ongoing study that seeks to characterize more than 100 mitochondrial genomes from braconid species belonging to several cyclostome and non-cyclostome subfamilies, including some rare, enigmatic taxa (e.g. Apozyginae, Telengainae). We explore the use of mitochondrial gene rearrangements as a potential source for the

classification within the Braconidae at various taxonomic levels. We will also extract DNA sequences data from the protein coding genes to reconstruct the phylogenetic relationships of this family.

11:50 Systematics and evolution of different phytophagous strategies in Allorhogas (Braconidae: Doryctinae) and other gall-associated related genera

Ernesto Samacá-Sáenz (Instituto de Biología, Universidad Nacional Autónoma de México, CDMX, México), Bernardo F. Santos (Department of Entomology, National Museum of Natural History, Washington, DC, USA), Scott P. Egan (Department of BioSciences, Rice University, Houston, TX, USA), Juan José Martínez (Departamento de Ciencias Biológicas, Facultad de Ciencias Exactas y Naturales, Universidad Nacional de La Pampa, La Pampa, Argentina), Paul E. Hanson (Escuela de Biología, Universidad de Costa Rica, San Pedro de Montes de Oca, Costa Rica), Scott R. Shaw (Department of Ecosystem Science and Management, University of Wyoming, Laramie, WY, USA), Alejandro Zaldívar-Riverón (Instituto de Biología, Universidad Nacional Autónoma de México, CDMX, México)

Abstract

The subfamily Doryctinae is a group of braconid wasps mainly represented by ectoparasitoid species. However, within this cosmopolitan subfamily there is a group of mainly Neotropical genera whose species are strictly associated to galls of various plant families. Previous studies based on few DNA sequence markers have consistently recovered the monophyly of this group and have supported its origin of phytophagy from parasitoidism. Nevertheless, various relationships and the number of transitions to phytophagy are still unclear, particularly in Allorhogas, which is by far its most speciose genus. Here, we show the results of an ongoing phylogenetic study among the gall-associated doryctine genera based on ultraconserved element data (UCEs). We have generated UCEs for 70 species belonging to ten gall-associated genera, with an emphasis on Allorhogas (44 species). Our phylogenetic analyses yielded robust topologies that are partially congruent with the previous estimates of phylogeny based on few gene markers, with *Percnobracon* recovered as sister to the remaining genera. Allorhogas was confirmed as polyphyletic, though most of its members were recovered within a major clade composed of species with different phytophagous strategies in different host plant families including gall formation, seed predation and inquilineism.

CONVERSION OF START SESSIONS FOR VARIOUS TIME ZONES

Australasia session (Start Time: 10:00 JST (UTC +9) i.e. 01:00 GMT)

Tokyo (Japan)	Thursday, 12 November 2020, 10:00:00	JST
Adelaide (Australia - South Australia)	Thursday, 12 November 2020, 11:30:00	ACDT
New Delhi (India - Delhi)	Thursday, 12 November 2020, 06:30:00	IST
Dolgoprudny (Russia - Moscow)	Thursday, 12 November 2020, 04:00:00	MSK
Stuttgart (Germany - Baden-Württemberg)	Thursday, 12 November 2020, 02:00:00	CET
New York (USA - New York)	Wednesday, 11 November 2020, 20:00:00	EST
Mexico City (Mexico - Ciudad de México)	Wednesday, 11 November 2020, 19:00:00	CST
Los Angeles (USA - California)	Wednesday, 11 November 2020, 17:00:00	PST
Corresponding UTC (GMT)	Thursday, 12 November 2020, 01:00:00	

Europe, Middle East, Africa Session (Start Time: 10:00 CET (UTC+1) i.e. GMT 09:00)

Brussels (Belgium - Brussels)	Thursday, 12 November 2020, 10:00:00	CET
Adelaide (Australia - South Australia)	Thursday, 12 November 2020, 19:30:00	ACDT
New Delhi (India - Delhi)	Thursday, 12 November 2020, 14:30:00	IST
Dolgoprudny (Russia - Moscow)	Thursday, 12 November 2020, 12:00:00	MSK
Stuttgart (Germany - Baden-Württemberg)	Thursday, 12 November 2020, 10:00:00	CET
New York (USA - New York)	Thursday, 12 November 2020, 04:00:00	EST
Mexico City (Mexico - Ciudad de México)	Thursday, 12 November 2020, 03:00:00	CST
Los Angeles (USA - California)	Thursday, 12 November 2020, 01:00:00	PST
Corresponding UTC (GMT)	Thursday, 12 November 2020, 09:00:00	

Americas Session (Start Time: 10:00 CST (UTC-6) i.e. GMT 16:00)

Mexico City (Mexico - Ciudad de México)	Thursday, 12 November 2020, 10:00:00	CST
Adelaide (Australia - South Australia)	Friday, 13 November 2020, 02:30:00	ACDT
New Delhi (India - Delhi)	Thursday, 12 November 2020, 21:30:00	IST
Dolgoprudny (Russia - Moscow)	Thursday, 12 November 2020, 19:00:00	MSK
Stuttgart (Germany - Baden-Württemberg)	Thursday, 12 November 2020, 17:00:00	CET
New York (USA - New York)	Thursday, 12 November 2020, 11:00:00	EST
Los Angeles (USA - California)	Thursday, 12 November 2020, 08:00:00	PST
Corresponding UTC (GMT)	Thursday, 12 November 2020, 16:00:00	
