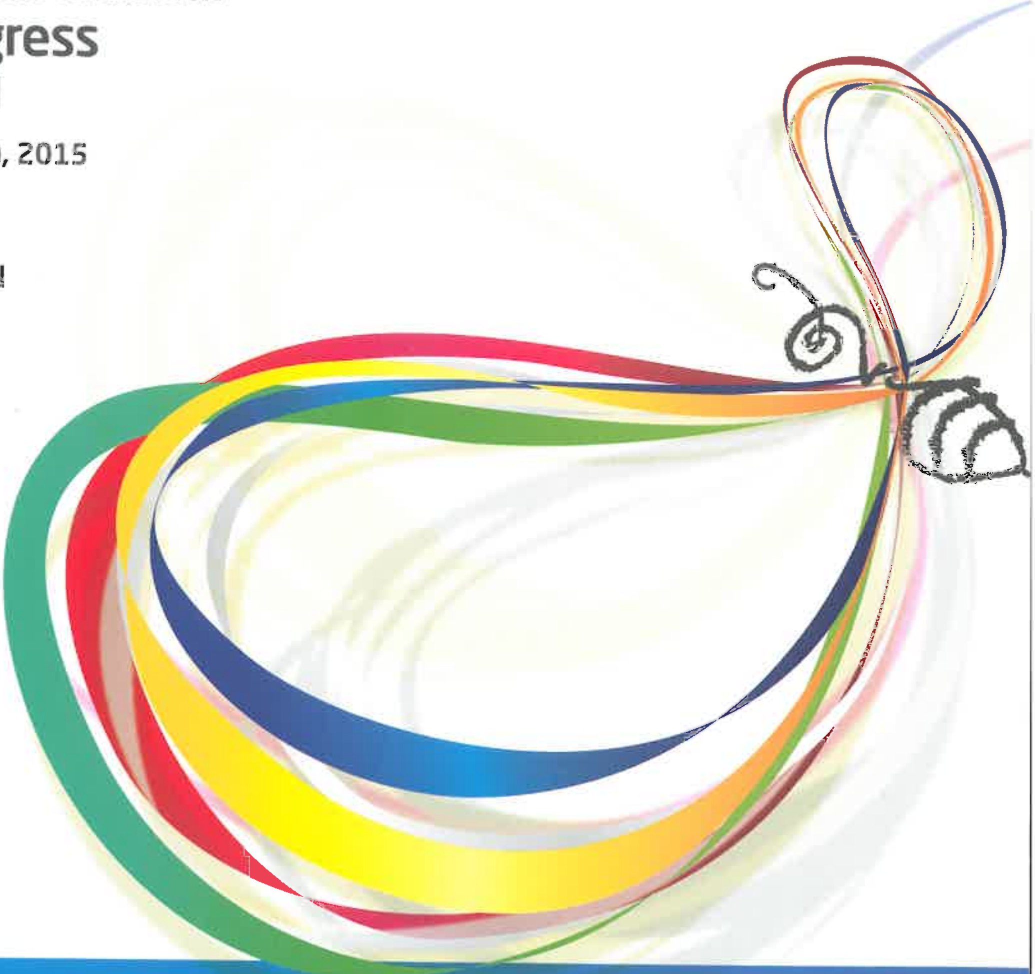
APIMONDIA 2015
Daejeon, Korea

Scientific Program Abstracts

대전세계양봉대회 초록집

44th
APIMONDIA International
Apicultural Congress
제44회 2015세계양봉대회

September 15(Tue) - 19(Sat), 2015
Daejeon Convention Center
2015년 9월 15일(화) – 19일(토)
대전컨벤션센터 및 대전무역전시관 일원



- Hosted by **APIMONDIA**
- Organized by **Apimondia Congress 2015 Local Organizing Committee**

developmental characteristics of B. ignitus queens, the most favorable diapause treatment was CT-1M-CO2. A combination method of CO2–narcosis and cold temperature treatment yielded better results than that of single CO2–narcosis or cold temperature treatment on the colony development of diapause-broken B. ignitus queens. In the case of B. terrestris queens, we concluded that a combination method of CO2 and cold temperature treatment yielded better results than that of a single cold- temperature (up to 2 months) treatment. In conclusion, the findings of the present study indicated that the combined application of CO2 and cold temperature was a favorable method for the colony development of diapause-broken B. ignitus and B. terrestris queens compared with only CO2–narcosis or cold temperature treatments. A combination method of CO2 and cold treatment reduced the side effect of CO2–narcosis and shortened the duration of cold treatment by at least 1 month.

BBP-011

De novo assembly and comparative genomic analysis of *Lactobacillus kunkeei* isolated from the gut of a Chilean honey bee

Freddy Asenjo[1], Juan Ugalde[2], Nicole Trombert[2]

[1] *Universidad Nacional Andrés Bello*

[2] *Universidad Mayor, Chile*

The honey bee (*Apis mellifera*) is the most important pollinator in agriculture worldwide, playing a key role in the human food supply by providing pollination services for diverse crops. One of the most common species present in the honey bee gut microbiota is Lactobacillus kunkeei. We previously isolated a L. kunkeei strain (denominated as MP2) from the gut of a Chilean honey bee. The genome of this strain was sequenced using the Illumina MiSeq platform, which resulted in a draft genome of 44 contigs, for a total genome size of 1,581,395 bp, and 826 well-annotated protein coding-genes. The nature of the short-reads used for this assembly, did not allowed to resolve the complete genome without gaps, and complicated the analysis as multiple repetitions, such as the presence of multiple copies of the ribosomal operon, could not be resolved in this draft genome. To overcome this limitations, we performed a resequencing of the L. kunkeei MP2 genome, using single molecule sequencing with the Pacific Biosciences platform. This de novo assembly, resulted in one single contig compromising the complete genome of L. kunkeei MP2 in a single 1,614,522 chromosome. This allowed us to perform comparative genomic analysis of our isolated of Lactobacillus kunkeei against others strains of Lactobacillus, with bioinformatic tools, showing a cluster of unique genes in our isolate.

BBP-012

Honeybee preservatin centers in Western Europe: an innovative strategy using sustainable beekeeping to reduce honeybee decline

Miguel Vilas Boas[1], Alice Pinto[1], Lionel Garnery[2], Hélène Legout[2],
Vincent Douarre[3], Sylvie Houte[3], Jean-François Odoux[4], Andone Estonba[5],

Irati Miguel[5], Iratxe Montes[5], Noel Mallet[6], Claude Grenier[6], Jean-Charles Labat[6], Luc Champin[6], Jonathan Colombet[7], Samuel Guyot[7], Telesphore Sime-Ngando[7], Frédéric Delbac[7], David G. Biron[7]

[1] *Polytechnic Institute of Braganca, Portugal*

[2] *EGCE, UMR CNRS 9191, PARIS, France*

[3] *Centre d'Etudes Biologiques de Chizé - approved ILTER - UPR CNRS 1934, France*

[4] *Centre INRA Poitou-Charentes, France*

[5] *University of the Basque Country, Spain*

[6] *Lycée Professionnel Agricole / Centre Régional de formation d'Apprentis, St-Gervais, France*

[7] *LMGE, UMR CNRS 6023, Aubière, France*

Apis mellifera is subdivided into at least 26 physiologically, behaviourally and morphologically distinct subspecies. As an agronomical species of interest, the natural distribution of honeybee subspecies has been disturbed for many decades by beekeeping activities, particularly because of international trade of honeybees. These movements were particularly amplified this last decade due to livestock rebuilding to counter the effects of colony losses. An interesting assumption is that current honeybee declines observed in European apiaries can be caused by commercial and European trades of honeybees by (i) the introduction (for their apicultural traits) of non- adapted and artificially maintained colonies, and (ii) the spread of allochtone and invasive pathogens carried by allochtones bees. Genetic surveys have demonstrated that some populations of honeybee subspecies are adapted to local climate and flora. Those populations thus constitute particularly interesting populations to study and preserve in a context of sustainable beekeeping. BEEHOPE, our BioDIVERSA ERANET funded project, is to set up, according to a North/South gradient, genetic conservatories of original naturally distributed honeybee populations. These honeybee conservation areas will have as missions: (i) to characterize the genetic and eco-ethologic diversity of honeybees from the West-Mediterranean lineage, (ii) to preserve the genetic diversity of those populations, (iii) to constitute a reserve of diversity usable by the honeybee industry and by beekeepers, (iv) to study the impact of the domesticated honeybee in the maintenance of local floristic diversity, and (v) to be able to use the honeybee as a bio-collector and as a biological indicator of environmental quality.

BBP-013

Desmometopa sordida (Fallén), a freeloader fly (Milichiidae, Diptera), found kleptoparasitic on a dead honeybee in Korea

Hyon Chong (Hyun Jung) Choe[1], Heung Sik Lee[2]

[2] *Quarantine Inspection Agency, Republic of Korea*

Freeloader flies (Family Milichiidae) have been occasionally noted as kleptoparasites of various insects including honey bee. *Desmometopa sordida* (Fallén) that has not been reported from Korea was found on a dead honey bee, in Seoul, recently. Kleptoparasitic behaviors of this species have been repeatedly recorded that they possibly ride on predatory arthropds and sarcophagous on the hunted prey. Distribution of the fly has been reported from temperate regions in northern hemisphere, including many European countries, Asia (Mongolia and Japan) and North America (U.S. and Canada).