ESA2019 LOUISVILLE

# 85: A method for identifying pollen resources for brood development in cavity-nesting native bees

**Wednesday, August 14, 2019**
**04:30 PM - 06:30 PM**
*Kentucky International Convention Center - Exhibit Hall*

**Background/Question/Methods**

Native bees' critical role in ecosystem function and agriculture has given rise to a variety of efforts to support their communities. This has resulted in widespread cultivation of wild plants (companion plantings) to improve their foraging resources, and deployment of artificial nesting habitats (bee hotels) to serve as breeding grounds. However, there is little information regarding the types of pollens gathered by native bees for provisioning brood within these bee hotels. To better understand the benefit of these practices, a method for identifying the pollen resources used in brood development would help define the interaction between nesting and foraging resources. The present study used a two-loci, single PCR, DNA-based identification of pollen grains taken from sampled native bee brood cells. Brood cells were obtained from a bee hotel deployed spring to early fall 2018. Pollen load from a single brood cell was collected, suspended in water and randomly sampled. Single pollen grains were stained with aniline blue, isolated under a microscope and transferred to a 25-µL PCR tube containing two sets of primers; (ITS2, *trnH-psbA*), Phire™ Plant Direct PCR Master Mix, and nuclease free water. Amplification was carried out at an annealing temperature of 62°C for thirty-five cycles.

**Results/Conclusions**

Amplification of two regions of DNA in a single PCR reaction can generate multiple amplicons for sequencing from a single source. The use of two loci in plant identification by DNA barcoding helps to improve the discriminatory power of these regions when identifying the species of pollen within the GenBank® database. Preliminary PCR experiments demonstrated that two loci could be amplified directly from an individual pollen grain taken from a brood cell. The *trnH-psbA* amplicon showed less success in amplification as evidenced by the lack of bands produced during electrophoresis relative to ITS on-agarose gel. This suggests an easier PCR amplification of the nuclear locus compared to the plastid locus, possibly due to copy number variation. Preliminary sequencing results from amplified ITS2 region revealed mixed pollens from a variety of flowering plants including; *Vicia amoena, Pstium sativa, & Trifolium repens.* A comprehensive understanding of seasonal pairings between local plant and cavity nesting bee species, specifically brood resources, would allow selective plantings to promote the specific native bee that is likely to inhabit man-made habitat. Furthermore, this type of information could be particularly useful in an agricultural setting where interactions between nesting preferences, foraging preferences and crop pollination might be established.

## Authors

**Zachary Thuotte**
*Massasoit Community College*

Matthew R. Healy
*Massasoit Community College*

Adam Germaine
*Massasoit Community College*

Andrew Oguma
*Massasoit Community College*

Prisca Sanon
*Massasoit Community College*

Michael Bankson
*Massasoit Community College*

Folusho Ajayi
*Massasoit Community College*

Find Similar

## View Related Events

**Day:** Wednesday, August 14, 2019