Data Dictionary for Targeted and non-targeted analysis of pesticides and other contaminants in honey bee hive matrices

**Summary of Uploaded Data:**

One data file has been uploaded including a summary of all pesticides detected in honey bee hive matrices. Each hive matrix (DBT=forager bees collected from dead bee traps; IH NB = nurse bees collected from in hive; IH L = larva from uncapped cells in the hive; and IH BB = beebread collected from uncapped cells in the hive) and the corresponding pesticide residues are included. For each hive matrix tab there are identifiers such as apiary location, sampling date, weight of sample and Sample ID. This is followed by a list of pesticides that were detected in that matrix with zeroes, the data have been corrected by mass of each sample to provide ng/g concentrations (mass of sample is provided in column C for each matrix). Within the same tab, scrolling over to the right (everything highlighted yellow) are the same list of pesticides with no zeroes (all the zeroes from the non-highlighted section have been replaced with the minimum value that was quantified in the that pesticide column and then divided by 2 analogous to a method detection limit and used for modeling purposes). The exception to this rule is for the 7 neonicotinoids (dinotefuran, nitenpyram, thiamethoxam, clothianidin, imidacloprid, acetamiprid, and thiacloprid) which were all analyzed by LC-MS/MS, and the LOD was quantified on the blanks by taking [(3\*standard deviation of the blanks for that analyte)/slope of the analyte]. Ten sites represented over 10 sampling times completes the dataset.

Table 1 tab contains a summary of all pesticide residues detected across all matrices as would be displayed in a publication. The pesticides in bold were also identified using GCxGC-ToF/MS.

**Abbreviations**:

DBT = dead bee traps, forager bees collected in traps after death and removal from hive

IH = ‘in hive’, samples collected from inside each hive

NB = nurse bees presumed responsible for making beebread and rearing larvae

L = larvae collected from uncapped cells pre-pupae stages

FP=field pollen

BB = bee bread collected from uncapped cells containing a mixture of corbicular pollen, nectar and nurse bee saliva

GC-MS = gas chromatography coupled with mass spectrometry.

ToF = time of flight

LC-MS/MS = liquid chromatography coupled with mass spectrometry/mass spectrometry.

**Treatment of Data:**

Data were processed using the analytical software control for each instrument. Briefly, for the GCxGC-ToF/MS data, all samples were analyzed with the same data processing method based on LECO’s recommended data interpretation parameters described in de Koning and Gumpendobler (2007). To train the data processing software for the GC-QTOF, a pooled QAQC sample was analyzed through Agilent MassHunter Unknowns Analysis to create a new in-house library for pesticide identification, then all samples were processed in Agilent’s MassHunter Quantitative Analysis (for TOF) using the curated in house library created from the pooled QAQC sample as linked to the method. For LC-MS/MS, manual integration on Xcalibur was used. Following detection, ppb concentrations from the instrument were divided by the mass of sample extracted to result in pesticide residues displayed as ng/g concentrations.