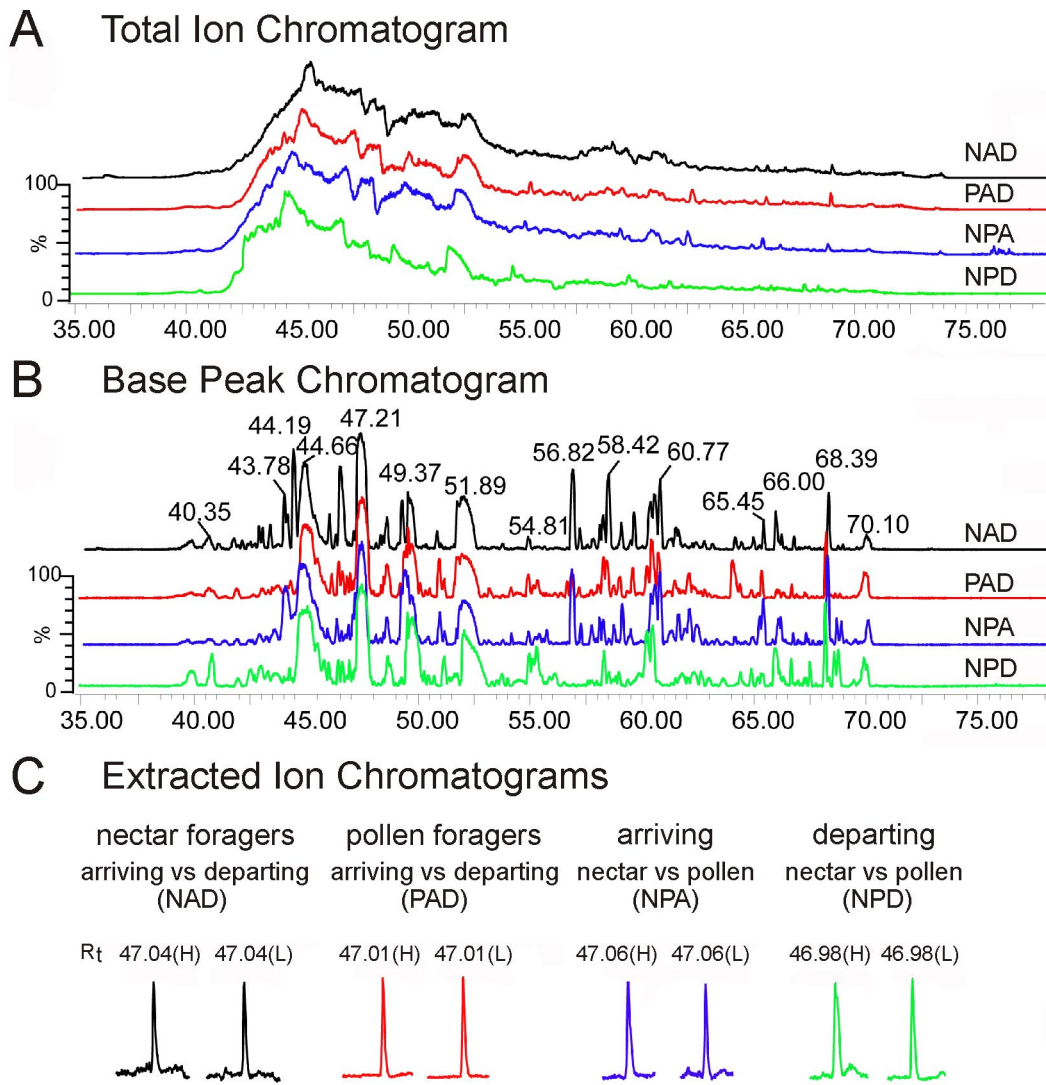
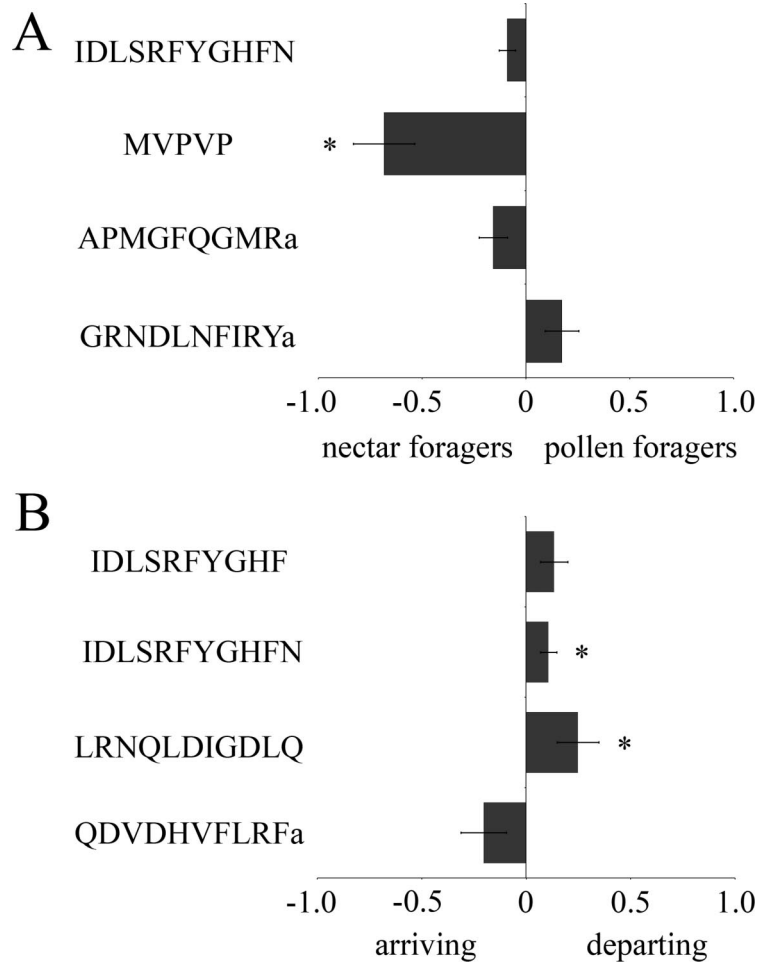


# Supporting Information

Brockmann et al. 10.1073/pnas.0813021106



**Fig. S1.** Peptide extraction and analysis demonstrating consistent chromatograms across samples. Brain peptides were labeled and separated as described in *Materials and Methods*. Representative total ion chromatograms (A) and base peak chromatograms (B) for the 4 different sample comparisons from one colony (NAD, arriving versus departing nectar foragers; PAD, arriving versus departing pollen foragers; NPA, arriving nectar versus arriving pollen foragers; NPD, departing nectar versus departing pollen foragers). After the separation, brain peptide samples were directly analyzed by using an electrospray ionization quadrupole time-of-flight (ESI-QTOF) mass spectrometer. (C) Extracted ion chromatogram peaks for the heavy (H) and light (L) isotope labeled tachykinin peptide APMGFQGMRA from the 4 different samples for one colony.  $R_t$ , retention time.



**Fig. S2.** Relative differences in brain peptide abundances between (A) nectar and pollen foragers independent of arriving and departing and (B) arriving and departing foragers independent of collected food. Indicated significance levels (Student's *t* test): \*, *P* < 0.05.