1

Title: Individual Learning Phenotypes Drive Collective Cognition

Authors: Chelsea N. Cook[1*], Natalie J. Lemanski[2], Thiago Mosqueiro[2], Cahit Ozturk[1],

Jürgen Gadau[3], Noa Pinter-Wollman[2◊], Brian H. Smith[1◊]

Affiliations:

[1] School of Life Sciences, Arizona State University, Tempe, USA

[2] Department of Ecology and Evolutionary Biology, University of California Los Angeles,

Los Angeles, USA

[3] Institute for Evolution and Biodiversity, University of Münster, Münster, Germany

[◊]Co-Senior Authors

[*]Corresponding Author

One Sentence Summary: Attentive individuals more strongly influence collective

foraging decisions by focusing on and recruiting to preferred food locations.

ABSTRACT: Collective cognition emerges from individuals responding to local

information to make decisions. However, animals vary in how they learn to pay attention

to important information, which has unknown consequences on collective behavior. We

tested whether honey bee colonies comprised of individuals that differ in their capacity

to focus their attention would choose to continue to visit learned, familiar food locations or

switch to novel food locations. We found that colonies of focused bees preferred familiar

food location, while colonies of less focused bees visited novel and familiar food sites

equally. In mixed colonies, both types of bees preferred the familiar food location.

Attention-focused individuals drive nestmates to their preferred location by recruiting

them more intensely compared to unfocused individuals. Our results reveal that

emergent collective behavior is driven by the attention-focusing abilities of individuals.

Main Text:

Collective cognition allows animal groups to more effectively respond to a rapidly

changing environment compared to their individual counterparts, such as schools of fish

avoiding predators (*1*), flocks of birds migrating across the Earth (*2*), or honey bee

colonies finding and visiting millions of flowers (*3*). Individuals in groups utilize local

information to quickly adjust to ecological changes by implicitly or explicitly

communicating information with group members to form collective behavior (*4–6*).

Collective cognition emerges from interactions between individuals that vary in their

cognitive abilities (*3*, *4*). Variation in the cognitive task of attention can shape critical

individual behaviors, such as effectively cueing in on the correct prey or mate (*7*), and

can have severe consequences on learning and productivity in humans (*8–10*).

However, little is known about how individual variation in attention may influence

emergent collective behavior.

We therefore tested how individual differences in learning to focus attention

scales to shape collective foraging behavior in honey bees by utilizing a learning

behavior called latent inhibition (LI) (*11*). Latent inhibition is a form of non-associative

learning related to the ability to ignore familiar, unrewarding stimuli to pay attention to

novel, important stimuli (*12*). Specifically, after exposure to an odor that is not followed

by reward, some forager bees take longer to learn about this now 'familiar' odor, relative

to a novel odor, when both types of odor are later paired with reward, or "high LI". Other

bees that learn both familiar and novel odors quickly are "low LI". Moreover, differences

in expression of LI correlate to foraging specializations. LI has been mostly studied in

vertebrates (*12–16*). However, honey bees (*Apis meillifera*) also exhibit (*17*, *18*) and

show heritable variation in LI (*11*). Scout bees, who search for novel food sources, show

high LI whereas recruited bees that forage at known food locations show low LI (*19*). To

uncover how individual variation in learning to pay attention impacts collective behavior,

we investigated how an individual's latent inhibition (LI) may scale to influence collective

foraging behavior in honey bee colonies.

The reproductive queens and haploid males (drones) of a honey bee colony

exhibit variation in LI (*11*, *18*). This allowed us to select for distinct high and low LI

phenotypes to generate lines from queens singly inseminated with sperm from like-

performing drones to produce workers that exhibit similar LI to their parents (*20*). We

then created colonies composed of age-matched single cohorts of only low, only high,

50/50 mixed high and low LI workers, as well as age-matched non-selected control

bees. In semi-natural foraging conditions, we counted the number of forager visits, first

visits, and revisits to the familiar or novel food locations. To explore the mechanisms

underlying how individual variation in LI affects collective foraging, we quantified the

round recruitment dance activity in mixed colonies while foraging.

To ensure that selected bees in different social environments exhibited the

predicted heritable LI phenotype, we evaluated the LI score of foragers from selected

lines that spent their adult life in either their natal colony or a control colony. Foragers

retained the expected LI based on the LI of their parents, regardless of whether they

were housed with same or with variable learning phenotypes (GLM: χ^2 = 6.54, df=1,

p=0.011, Fig. 1). We did not detect an effect of the identity of the colony in which the

bees were housed on LI phenotype (χ^2 = 3.766, df=2, p=0.152, Fig. 1).

Figure 1: Social environment does not alter expression of genetically selected

latent inhibition. LI scores of individuals from high LI lines that spent their adult life

either in high LI only colonies (red, n=36) or in a control colony with a variety of LI

phenotypes from an open mated queen (red with gray vertical lines, n=18);

individuals from low LI lines that spent their adult life either in low LI only colonies

(yellow, n=52) or in control colonies (yellow with gray vertical lines, n=10). Different

letters above boxes indicate statistically significant differences according GLM

comparison (p<0.05). In this and subsequent figures, the large black dot is the mean,

the white box is the interquartile range (IQR), whiskers extend to 1.5*IQR, and the

small points beyond the whiskers are outliers. Color shaded areas show the

To determine how the learning phenotypes influenced colony-level foraging

behavior, we placed small single-cohort age-matched colonies into a flight cage and

monitored foraging activity to familiar or novel feeders (Fig. 2A). To evaluate the

collective feeder choice, we recorded the number of visits to each feeder by bees from

each selected line according to the color of paint on the bees' thorax. We further

marked bees with a feeder-specific color on their abdomen when they visited the feeder

for the first time to determine if bees revisited that feeder.

Colony learning phenotype strongly influenced overall number of visits to the

food locations (GLM: χ^2 = 1270, df = 3, p < 0.0001, Fig. 2B). Foraging in the high, low,

and control colonies was largely performed by bees revisiting the feeders, while mixed

colonies had more new visitors to the feeders (GLM, χ^2 = 22.32, df =3, p<0.0001, Fig.

2C, table). A colony's LI phenotype composition also determined its preference

between the novel and familiar feeders, with high LI and mixed colonies preferring the

familiar and low and control colonies showing no preference (GLM: Feeder*Colony χ^2

=473.64, df=3, p<0.0001; Fig. 2D). Revisits to feeders drive foraging for all colonies

(Fig. 2E: Colony*Feeder χ^2 =53.67, p<0.0001). However, new foragers in the mixed

colonies that visited the novel feeder were less likely to return to it compared to foragers

who visited the novel feeders in other colonies (Table S6).

Figure 2: Colonies constructed from different genetic lines selected for high or low latent inhibition exhibited differences in collective foraging behavior. *(A) The experimental set up illustrating the location of feeders in relation to the location of the colony (center, white) within the experimental arena (large rectangle) (See table S2 for*

feeder placement and odors) (B) Cumulative number of visits of all bees (bees from

selected lines and controls) to all feeders over time by colony type. Different letters to

the right of the lines indicate statistically significant differences according to a post hoc

test (p<0.05) (See fig S1 for individual visitation). (C) Percent of re-visits out of the total

number of visits to all feeders by colony type. Here and in all following panels, different

letters above boxes indicate statistically significant differences according to a post hoc

test (p<0.05, table S4). (D) Number of all visits to the familiar feeder (solid boxes) and a

novel feeder (hatched boxes) for each type of colony, when both novel and familiar

feeders were presented simultaneously (days 2-4) (for post-hoc results see table S5).

(E) Percent of re-visits out of the total number of visits to either the familiar or the novel

feeder by type of colony when both novel and familiar feeders were presented

simultaneously (days 2-4) (for post-hoc results see table S6). N=24 colonies, 6 colonies

per colony type, 6172 total visits.

To determine why the mixed colonies showed a preference for the familiar feeder

(Fig. 2D), we examined how individual lines visited each feeder (Fig. 3). In 2017, we

tested mixed colonies placed in a flight cage. In 2018, we reselected lines and then

placed mixed colonies into two-frame observation hives to evaluate recruitment dances

along with visitation to the feeders in the flight cages. We found that there was a

significant year effect (table S7), likely due to reselection and different hive placement.

We therefore statistically analyzed each year separately to focus on the within-year

variation between the selected lines.

Low LI and control individuals shift their preference to the familiar feeder when

mixed with high LI bees. In 2017, we found a significant interaction between the

selected line and which feeder foragers visited (GLM: χ^2 =7.79, df=2, p=0.02; Fig. 3A).

Although low LI and control colonies did not show a preference to a novel or familiar

feeder when they had a uniform colony composition (Fig. 2E), when mixed with high LI

individuals, low LI and control individuals exhibited a preference to the familiar feeder

(Fig. 3A, table S8). High LI individuals showed a preference to familiar feeders just as

colonies comprised of only high LI individuals did (Fig. 2E). We found a significant

interaction between selected line and feeder again in 2018 (GLM: χ^2 =85.27, df=2,

p<0.0001; Fig. 3B), with low LI and control individuals showing preference to the familiar

feeder over the novel feeder (Fig. 3B, table S9) similar to high LI individuals preferring

the familiar feeders.

Figure 3: Visits of individuals from different genetically selected lines when in a mixed colony. Daily visits to the familiar and novel feeders by individual bees in mixed colonies from low LI parents (yellow), high LI parents (red) or open mated queens (grey) in (A) 2017, N=6 mixed colonies, 2347 overall visits and (B) in mixed colonies from lines that were re-selected in 2018, N=6 colonies, 6272 overall visits. In both years, low LI and control bees switched to prefer the familiar feeder.

To uncover the behavioral mechanisms that underlie why low LI and control bees

switch feeder preference when housed with high LI bees, we evaluated how each line

performed the round dance, the modified waggle dance used for recruitment to food at

short distances (*21*). Individuals from the lines differed in their likelihood to perform a

round dance (Chi-square test: χ^2=26.61, df=2, p<0.0001; Fig. 4B). Low LI individuals

were significantly more likely to perform a dance compared to high Li individuals

(pairwise chi-square test: p=0.0001) and controls (pairwise chi-squared test: p=0.004).

High LI individuals were just as likely to perform a dance as controls (p=0.36).

Individuals differed in their likelihood to follow a dance based on their selected line (Chi-

square test: χ^2=28.26, df=2, p<0.0001; Fig. 4B). Low LI individuals were significantly

more likely to follow a dance compared to high LI bees (pairwise chi-square test:

p<0.0001) and controls (p<0.003). High LI and control individuals were equally likely to

follow a dance (p=0.240).

Although the high LI individuals danced less often, high LI dances had

significantly more followers compared to low and control bees (Chi-square test: χ^2=

13.93, df=2, p<0.001; Fig. 4C). Low LI bees performed more dances that had no

followers compared to high LI and control dances. Low LI individuals spent more time

dancing; however, they attracted fewer followers than high and control dancers,

indicated by the significant interaction between the LI of the dancer and dance duration

when predicting the number of followers (GLMM: χ^2= 6.42, df=2, p=0.04; Fig. 4E). The

relative attraction of dances of high LI bees could be due to the intensity of the dance.

High LI bees performed more turns per second during their dances (ANOVA: χ^2=12.8,

df=2, p=0.002; Fig. 4F).

Figure 4: Recruitment dances facilitate integration of information from different genetically selected lines. (A) The experimental set up illustrating the location of feeders in relation to the location of the colony entrance (top right, white) within the experimental arena (large rectangle). (See SI Table 2 for feeder placement and odors) (B) Proportion of dances (N=667) or follows (N=1201) across 6 colonies performed by bees from each line, relative to their abundance in the mixed colony (350 high, 350 low, 700 control). We accounted for the difference in abundance of each selected line by dividing the number of observed control dancers by 2 before calculating these proportions. (C) Proportion of dances performed per LI line type that were either followed by at least one individual (colored) or not followed by any other bees (black). (D) Proportion of dances by LI line type that were followed (from panel B) broken down by LI of the follower. (E) Relationship between number of followers and duration of a dance by line. Point and line colors indicate LI of dancer. Best fit line represents the GLM, shaded area represents the 95% confidence interval. (F) Rate of turns per second in a dance by line.

By combining techniques from experimental psychology and behavioral ecology, we have developed a system for investigating how variation in individual learning behavior drives collective cognition. We demonstrate that a laboratory-selected heritable learning behavior with natural individual variation scales to shape the collective performance of honey bee colonies on quasi-natural foraging tasks. In the lab, high LI

bees learn to ignore familiar odors that they experienced without reinforcement, while

readily learning novel odors.

One interpretation of reduced learning to a familiar, unrewarding, stimulus is that

pre-exposure reduces attention to, and thus associability of, that stimulus (*22, 23*). In

this interpretaiton, latent inhibition allows animals to focus attention on important

information (*15, 24, 25*). Our observations of field behavior of low and high LI individuals

and colonies are consistent with this interpretation, whereby high LI individuals have

stronger attention capacities to food compared to low LI individuals. Once high LI

individuals have found a food location, they continue to revisit it, 'attending' more

strongly to reinforced feeders over new ones. The increased impact of the resource on

these bees could translate into stronger, more vigorous dances. In contrast, low LI

individuals learn and visit both known and new feeders equally, dividing their attention

across resources and acting more like generalist foragers. In mixed colonies, this

broadened attention by low LI individuals may therefore make them the perfect

audience for the high LI dancers, driving them to prefer feeders that high LI individuals

preferentially visit. Under natural conditions, where queens mate with many different

drones, most colonies would possess both types of learners, perhaps more closely

resembling our mixed colonies (*26*). We propose that this diversity of 'attention' aspect

of individual cognitive phenotypes may enhance the overall efficacy with which a colony

finds and exploits resources (*27*). In summary, our work indicates that individual

cognition scales to shape the collective cognition of animals solving critical ecologically

relevant tasks.

REFERENCES AND NOTES

1. A. J. W. Ward, J. E. Herbert-Read, D. J. T. Sumpter, J. Krause, Fast and accurate decisions through collective vigilance in fish shoals. *Proc. Natl. Acad. Sci.* **108**, 2312–2315 (2011).

2. T. Sasaki, D. Biro, Cumulative culture can emerge from collective intelligence in animal groups. *Nat. Commun.* **8**, 15049 (2017).

3. I. D. Couzin, Collective cognition in animal groups. *Trends Cogn. Sci.* **13**, 36–43 (2009).

4. D. J. Sumpter, *Collective animal behavior* (Princeton University Press, 2010).

5. S. Camazine, J.-L. Deneubourg, N. R. Franks, J. Sneyd, E. Bonabeau, G. Theraula, *Self-organization in biological systems* (Princeton university press, 2003).

6. I. D. Couzin, J. Krause, in *Advances in the Study of Behavior* (Elsevier, 2003; https://linkinghub.elsevier.com/retrieve/pii/S0065345403010015), vol. 32, pp. 1–75.

7. R. Dukas, Behavioural and ecological consequences of limited attention. *Philos. Trans. R. Soc. Lond. B. Biol. Sci.* **357**, 1539–1547 (2002).

8. R. Schachar, G. D. Logan, P. Robaey, S. Chen, A. Ickowicz, C. Barr, Restraint and Cancellation: Multiple Inhibition Deficits in Attention Deficit Hyperactivity Disorder. *J. Abnorm. Child Psychol.* **35**, 229–238 (2007).

9. P. Dayan, S. Kakade, P. R. Montague, Learning and selective attention. *Nat. Neurosci.* **3**, 1218–1223 (2000).

10. C. J. Mitchell, M. E. Le Pelley, *Attention and associative learning: From brain to behaviour* (Oxford University Press, USA, 2010).

11. S. B. C. Chandra, J. S. Hosler, B. H. Smith, Heritable variation for latent inhibition and its correlation with reversal learning in honeybees (Apis mellifera). *J. Comp. Psychol.* **114**, 86–97 (2000).

12. R. E. Lubow, Latent inhibition. *Psychol. Bull.* **79**, 398 (1973).

13. M. D. Mitchell, M. I. McCormick, M. C. O. Ferrari, D. P. Chivers, Friend or foe? The role of latent inhibition in predator and non-predator labelling by coral reef fishes. *Anim. Cogn.* **14**, 707–714 (2011).

14. M. C. O. Ferrari, D. P. Chivers, Latent inhibition of predator recognition by embryonic amphibians. *Biol. Lett.* **5**, 160–162 (2009).

15. R. E. Lubow, Latent inhibition as a measure of learned inattention: some problems and solutions. *Behav. Brain Res.* **88**, 75–83 (1997).

16. R. E. Lubow, Latent inhibition: Effects of frequency of nonreinforced pre-exposure
of the CS. *J. Comp. Physiol. Psychol.* **60**, 454–457 (1965).

17. C. I. Abramson, M. E. Bitterman, Latent inhibition in honeybees. *Anim. Learing
Behav.* **14**, 184–189 (1986).

18. H. J. Ferguson, S. Cobey, B. H. Smith, Sensitivity to a change in reward is heritable
in the honeybee, Apis mellifera. *Anim. Behav.* **61**, 527–534 (2001).

19. C. N. Cook, T. Mosqueiro, C. S. Brent, C. Ozturk, J. Gadau, N. Pinter-Wollman, B.
H. Smith, Individual differences in learning and biogenic amine levels influence the
behavioural division between foraging honeybee scouts and recruits. *J. Anim. Ecol.*
88, 236–246 (2018).

20. J. S. Latshaw, B. H. Smith, Heritable variation in learning performance affects
foraging preferences in the honey bee (Apis mellifera). *Behav. Ecol. Sociobiol.* **58**,
200–207 (2005).

21. K. D. Waddington, Honey bee foraging profitability and round dance correlates. *J.
Comp. Physiol.* **148**, 297–301 (1982).

22. P. I. Pavlov, Conditioned reflexes: an investigation of the physiological activity of
the cerebral cortex. *Ann. Neurosci.* **17**, 136 (1927).

23. R. E. Lubow, I. Weiner, P. Schnur, in *The Psychology of Learning and Motivation:
Advances in Research and Theory.* (Academic Press, New York, 1981;
http://site.ebrary.com/id/10244511), vol. 15, pp. 1–49.

24. S. J. Gershman, D. M. Blei, Y. Niv, Context, learning, and extinction. *Psychol. Rev.*
117, 197–209 (2010).

25. R. E. Lubow, *Latent inhibition and conditioned attention theory* (Cambridge
University Press, 1989), vol. 9.

26. H. R. Mattila, K. M. Burke, T. D. Seeley, Genetic diversity within honeybee colonies
increases signal production by waggle-dancing foragers. *Proc. R. Soc. B Biol. Sci.*
275, 809–816 (2008).

27. T. T. Hills, P. M. Todd, D. Lazer, A. D. Redish, I. D. Couzin, Exploration versus
exploitation in space, mind, and society. *Trends Cogn. Sci.* **19**, 46–54 (2015).

28. S. B. C. Chandra, J. S. Hosler, B. H. Smith, Heritable variation for latent inhibition
and its correlation with reversal learning in honeybees (Apis mellifera). *J. Comp.
Psychol.* **114**, 86–97 (2000).

29. C. N. Cook, T. Mosqueiro, C. S. Brent, C. Ozturk, J. Gadau, N. Pinter-Wollman, B.
H. Smith, Individual differences in learning and biogenic amine levels influence the

behavioural division between foraging honeybee scouts and recruits. *J. Anim. Ecol.*
88, 236–246 (2018).

30. S. W. Cobey, D. R. Tarpy, J. Woyke, Standard methods for instrumental
insemination of *Apis mellifera* queens. *J. Apic. Res.* **52**, 1–18 (2013).

31. J. R. Harbo, in *Bee Breeding and Genetics,* (Academic Press, Inc, Rinderer T.E.,
1986), pp. 361–389.

32. Z. S. Liang, T. Nguyen, H. R. Mattila, S. L. Rodriguez-Zas, T. D. Seeley, G. E.
Robinson, Molecular Determinants of Scouting Behavior in Honey Bees. *Science*.
335, 1225–1228 (2012).

33. B. Ripley, B. Venables, D. M. Bates, K. Hornik, A. Gebhardt, D. Firth, M. B. Ripley,
Package 'mass.' *Cran R* (2013).

34. D. Bates, M. Maechler, B. Bolker, S. Walker, lme4: Linear mixed-effects models
using Eigen and S4. *R Package Version*. **1**, 1–23 (2014).

35. R. Lenth, M. R. Lenth, Package 'lsmeans.' *Am. Stat.* **34**, 216–221 (2018).

36. R. C. Team, R: A language and environment for statistical computing (2018).

Acknowledgements: We thank S. Ohrt, E Sezen, N Kulkarni, and A Phillips for help

with data collection. We thank C. Kwapich and D. Charbonneau for comments on

drafts of this manuscript. **Funding**: This grant was funded by NIH NIGMS

R01GM113967 to BHS, JG, & NPW, and NIH NIGMS F32GM126728 to CNC.

Author Contributions: CNC, TM, JG, NPW, BHS conceived of and helped design

the study. CNC, NJL, and TM analyzed the data. CNC and CO created the

genetically selected lines and CO maintained them. CNC carried out data collection

and wrote the first draft of the manuscript. CNC, TM, NJL, NPW, BHS discussed

results. All authors commented on the manuscript. **Competing Interests:** The

authors declare no competing financial interests **Data Availability:** Data will be

available on FigShare and code will be available on Github upon publication.

SUPPLEMENTAL MATERIALS

Materials and Methods

Tables S1-S9

Fig. S1

References 28-36