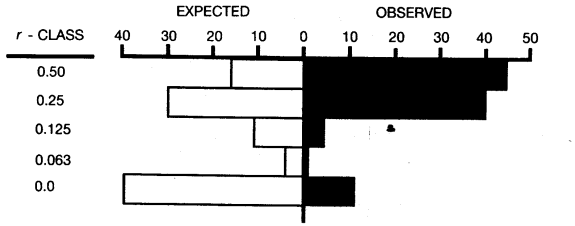
Kin Recognition

Distinguish kin discrimination from kin recognition

Fig. 16.9. Expected and observed frequencies of helping to recipients of various kin-classes in White-fronted Bee-eaters. Expected values show the proportion of recipient nests available belonging to the different kin-classes (*r*). Data include 174 cases of helping and 535 potential recipient nests, all from the 1980–4 breedings of the Baharini population. The null hypothesis of randomly directed helping is rejected, providing strong support for the alternative hypothesis that bee-eaters show kin discrimination in choosing the recipients for their aid (for statistics see the text) (from Emlen and Wrege 1988).



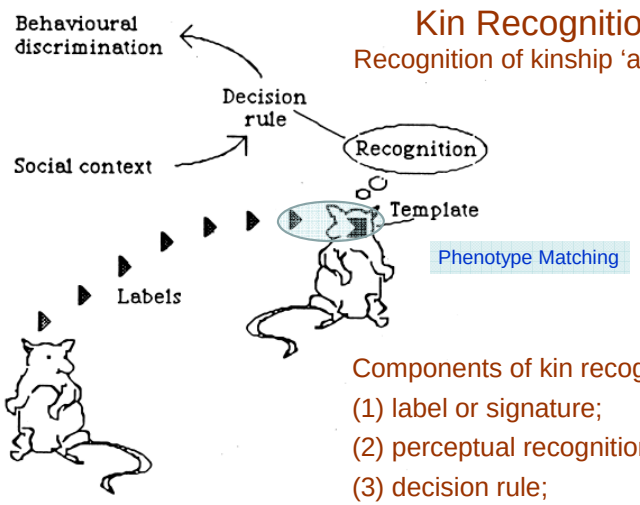
This is kin discrimination, not necessarily kin recognition

Kin discrimination = discriminating kin from non-kin or one kin class from another

Kin recognition = kin discrimination on the basis of cues that reliably predict kinship ("recognizing kinship as such")

Kin recognition usually tested with animals that are unfamiliar or equally familiar

Warren G. Holmes (2004). The early history of Hamiltonian-based research on kin recognition. *Annals of Zoology Fennici* 41: 691-711.



Kin Recognition

Recognition of kinship 'as such'

Phenotype Matching

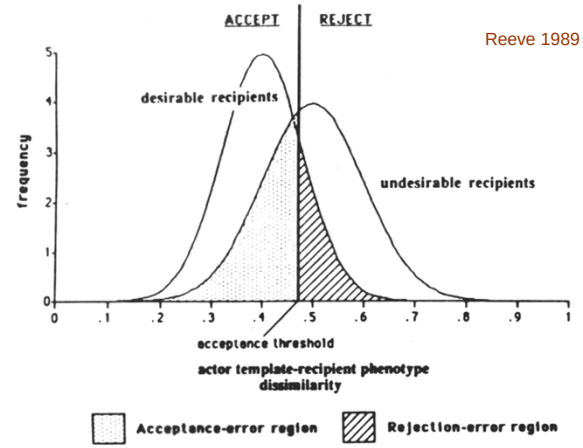
Components of kin recognition:

(1) label or signature;

(2) perceptual recognition;

(3) decision rule;

(4) behavioral discrimination



Reeve 1989

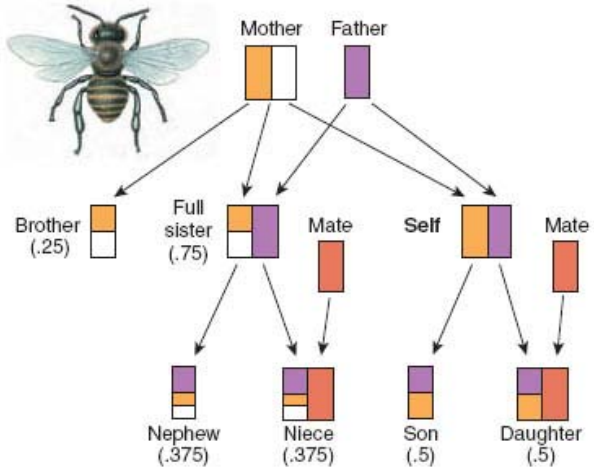
FIG. 1.—Frequency distributions of dissimilarity between the actor template and the recipient phenotype for desirable and undesirable recipients. Also shown are the conspecific-acceptance threshold and the acceptance- and rejection-error regions generated by this threshold.

Greenberg: Genetic component of bee odor in kin recognition. *Science* 1979

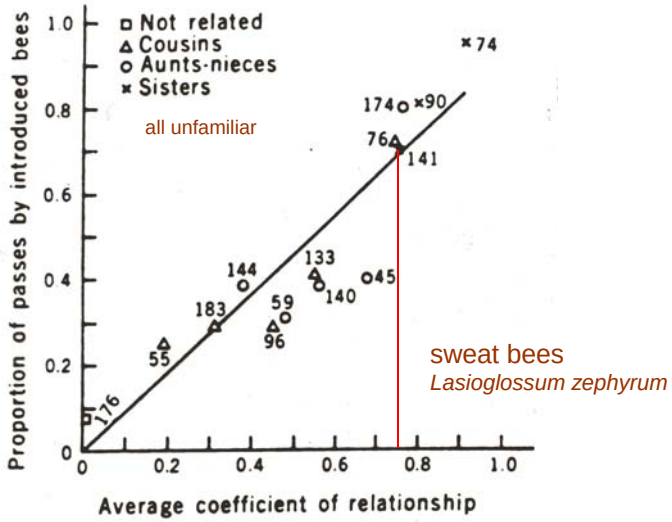
Neotropical sweat bee *Megalopta genalis* in its tunnel nest, with one wall of the tunnel removed.

http://footage.shutterstock.com/clip-1642849-stock-footage-amazonian-sweat-bees-at-entrance-of-nest.html

Haplodiploidy in Hymenopterans (bees, wasps and ants)



Greenberg: Genetic component of bee odor in kin recognition. *Science* 1979



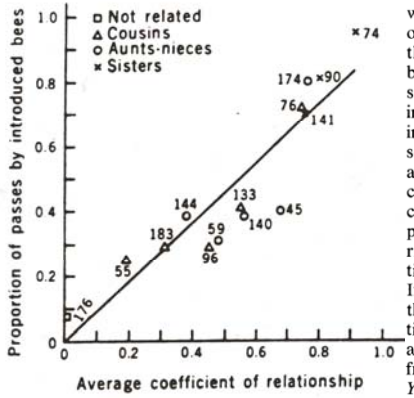
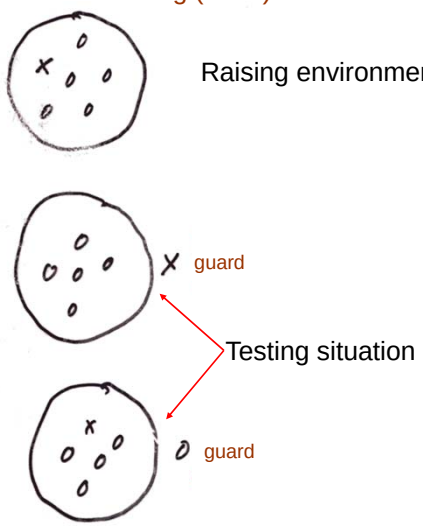
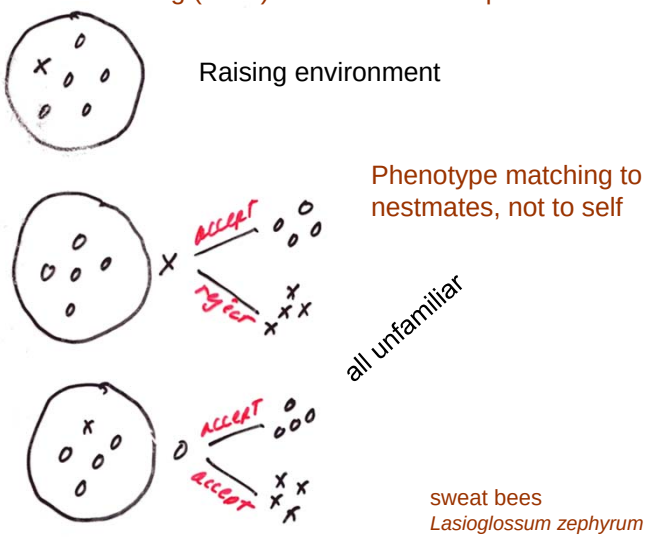


Fig. 1. Linear regression of frequencies with which introduced bees passed guarding bees on the average coefficient of relationship of the tested bees. Each data point was weighted by the number of interactions for that relationship, shown next to each point. A total of 593 introduced bees was used to obtain the 1586 interactions shown. The regression line is described by the equation $Y = 0.07 + 0.924\ X$ and the Pearson product-moment correlation coefficient for the data = .93. The regression coefficient is significant at $P \ll .001$. The data points were also analyzed with a nonparametric test, Kendall's coefficient of rank correlation, and found to be significant at $P < .001$. If one assumes worker-produced males and therefore cousin matings, the regression equation becomes $Y = 0.02 + 0.941\ X$, significant at $P \ll .001$. If the sister data are excluded from the regression analysis, the equation is $Y = 0.03 + 0.821\ X$, signficant at $P < .001$. For the latter, Kendall's coefficient of rank correlation is significant at $P < .001$. The data points show a better fit to a power function, but there are not enough points to show that it is significantly better.

Buckle & Greenberg (1982) – the 'odd bee' experiment



Buckle & Greenberg (1982) – the 'odd bee' experiment



Mechanisms of Kin recognition

Major Histocompatibility Complex (MHC)

A series of closely-linked genes (called HLA and on chromosome 6 in humans, called H-2 and on chromosome 17 in mice) that determine the major histocompatibility factors, i.e., surface antigens or receptors that are responsible for the recognition and elimination of foreign tissues.

Got its name from its relation to tissue transplants – donor and recipient should have similar HLA types (be 'histocompatible'), otherwise tissue is recognized as foreign and is attacked and rejected by recipient's immune cells (lymphocytes) – these immune cells normally play a key role in fighting disease.

Major Histocompatibility Complex (MHC)

At least some of the MHC genes are extremely mutable – hence many alleles exist at each of these loci – so that it is highly unlikely that 2 unrelated individual will be identical at this locus, and why organ donors must come from within the family.

Lewis Thomas (President, Sloan-Kettering Cancer Center, NY, and noted science writer, e.g., "Lives of a Cell", "The Youngest Science"): hypothesized that MHC could code for a signal of individual identity that might be involved in social interactions (Thomas 1974).

First evidence for hypothesis derived independently by researchers at Sloan-Kettering (Yamazaki et al 1976)" with **congenic** mice (= strains of mice that are genetically identical except for 1 small genetic region): house male with female of same congenic strain and one of different congenic strain: he will preferentially mate, nest with the unlike female.

CONTROL OF MATING PREFERENCES IN MICE BY GENES IN THE MAJOR HISTOCOMPATIBILITY COMPLEX*

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(From the Memorial Sloan-Kettering Cancer Center, New York 10021)

While observing AKR and AKR backcross mice being bred to produce an AKR-$H\text{-}2^b$ congenic mouse strain, one of us (J. B.) noticed that homozygous $H\text{-}2^b$ ♂♂ were more attracted to heterozygous $H\text{-}2^b$:$H\text{-}2^k$ ♀♀ than to $H\text{-}2^b$ homozygous ♀♀. Meanwhile another of us (L. T.), unaware of these observations, arrived at the theoretical conclusion that histocompatibility antigens might act as olfactory self-markers distinguishing different members of a population from one another (1).

This article is an account of our study of *H-2*-associated "mating preference." By *"H-2"* we imply the chromosomal region including *H-2* which differentiates congenic stocks from their partner strains. We used a straightforward experimental design: A ♂ mouse (e.g., **"bb"**) was caged with two *H-2* congenic ♀♀ (e.g., **"bb"** and **"kk"**), in estrus, and the trio was observed continuously until the ♂ successfully mated with one of the ♀♀.

Journal of Experimental Medicine (1976) 144, 1324-1335.

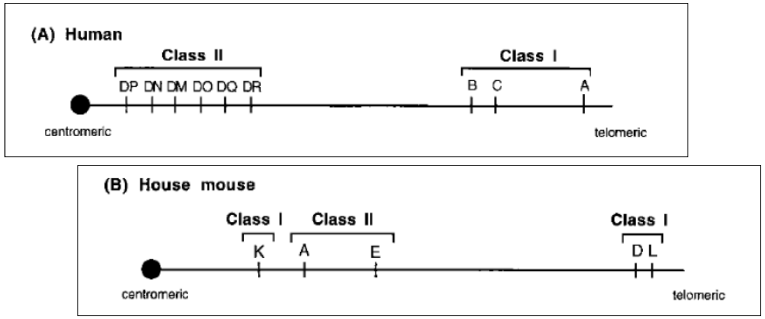

Figure 1: The MHC is a large chromosomal region (around 2,000 kb in mice and 3,500 kb in humans) containing over 200 coding loci that control the immune system, growth, and reproduction. The term "MHC genes" usually refers to the highly polymorphic "classical" loci that encode class I and II antigen-binding molecules. Class I and II MHC genes arose by tandem duplication events and are inherited as a unit (haplotype) since they are closely linked in many species. *A*, Human MHC encodes six antigen-presenting molecules, and the polymorphism, which is still incompletely characterized, varies from one to 179 alleles per locus (41 on average; Parham and Ohta 1996). *B*, In house mice, there are five antigen-presenting molecules with over 100 alleles per locus in local populations (Duncan et al. 1979; Klein 1986).

From Penn & Potts 1999

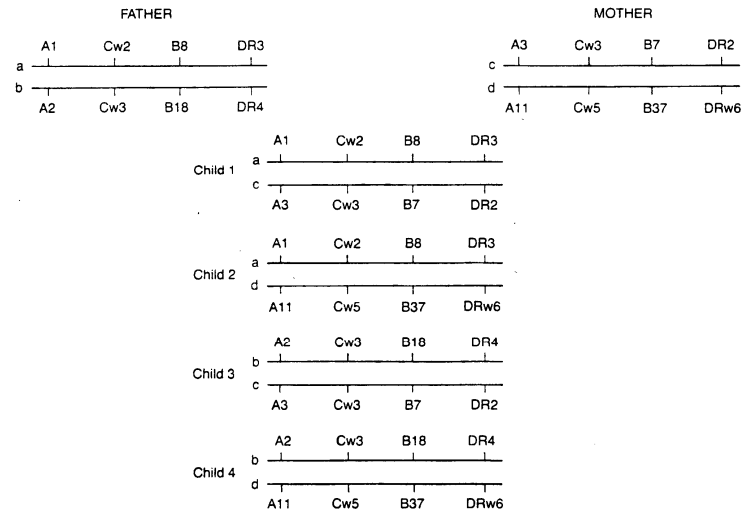

Figure 22-3. Schematic representation of the HLA loci on the short arm of chromosome 6. (From Miller, WV and Rodey, G: *HLA without Tears*. American Society of Clinical Pathologists, Chicago, 1981, p 10, with permission.)

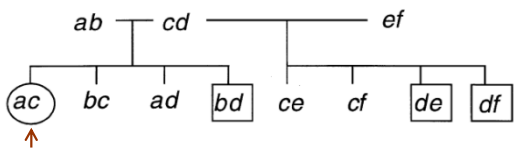

Figure 4. Examining the MHC genotypes of closely related mice reveals that self-inspection would not provide a particularly effective mechanism for avoiding kin matings (this pedigree is typical for house mice in the wild, as most individuals are heterozygous at MHC loci because these genes are highly polymorphic). For example, if female *ac* uses self-inspection, then she will risk mating with one-fourth of her siblings (*bd*) and one-half of her half-siblings (*de* and *df*). Familial imprinting, in contrast, would provide a more effective inbreeding avoidance mechanism. If female *ac* uses familial imprinting, then she can effectively avoid mating with her kin, including all full siblings (*ab*, *bc*, *ad*, *bd*), all half-siblings (*ce*, *cf*, *de*, *df*), and half of all cousins. As house mice are often reared in communal nests and nursed by their aunts (Wilkinson & Baker 1988; Manning *et al.* 1992*b*, 1995), familial imprinting may enable females to avoid mating with all close cousins.

Inbreeding avoidance

Self matching would lead to errors with p=1/4 for full sibs and p=1/2 for half sibs

From Penn & Potts 1998

Nature 1992

Communal nesting patterns in mice implicate MHC genes in kin recognition

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