APIMONDIA
SCANDINAVIA 2025
SWEDEN | DENMARK | NORWAY

PP-466 [Bee Biology]

Advancing Genetic Resiliency in Honeybee Populations Through Long-Term Breeding and Matriline Tracking

Eric McEwen[1] and Dustin J. Szumowski[2]

[1] Diggin' Livin' Farm & Apiaries, Cave Junction, Oregon, USA. www.digginlivin.com

[2] Structured-Roots.com

Introduction

Two main aspects of beekeeping are responsible for a large proportion of colony turnover and result in a significant quantity of beekeeper inputs in the form of labor and materials to maintain colony numbers. Foremost is Varroa mites, which parasitize honeybee brood and are the main driver of temperate winter mortality. Secondarily is the maintenance of each colony in a queen-right state, the lack of which is responsible for losses throughout the year.

Thus, the two main activities in managing honeybee colonies in temperate climates are confirming the presence, health, and vitality of the queen in each colony, and the evaluation and mitigation of Varroa infestation levels.

In efforts to increase the frequency of advantageous traits associated with survival, hardiness, and queen longevity, we began a long-term breeding program within our commercial honeybee operation in 2016.

Now, using a newly developed tracking system, we hope to identify matrilines within the operation that demonstrate superior rates of reproductive success and survivorship. We aim to document the matrilines that contribute the greatest amount of genetic material to the maintenance of the total population of colonies, and to then begin investigation into the survivor traits present in these matrilines that contribute to their improved success rates.

Background

Using our small-scale commercial operation based in SW Oregon, USA, as the model system for an interbreeding meta-population (maintained above 260 colonies since the start of the project), we seek to encourage the increase in frequency of multiple survivor traits associated with resistance to Varroa mites, and to increase self-perpetuating habits associated with honeybee queen supersedure and queen longevity in the total population.

We manage our colonies with minimal intervention, using only techniques consistent with organic management practices, seeking only to maintain colony survivorship above minimum levels of economic viability while maintaining selection pressure on the population to evolve toward a greater level of self-reliance and vigor (analogous to a Soft-Bond approach[1]).

To maintain maximal levels of genetic diversity and the preservation of rare alleles associated with survivor traits, we seek to reproduce new colonies from a large sample set within the operation, consisting of roughly 50% of the total colonies each season. This number varies annually based upon needs within the operation for replacement colonies and is dependent upon factors such as mortality rates and the quantity of colonies sold.

We sought to minimize the introduction of any new matrilineal genetics into the operation by discontinuing the introduction of purchased queens from outside the operation and by carrying out rearing and mating of new honeybee queens in isolated locations lacking the presence of other commercial operations.

All new colonies generated in the operation since 2016 are reared either from queen cells originating in the maternal colonies or through inducing the rearing of emergency queens utilizing the walk-away split technique.

Image 1: Lead author and his wife, Joy McEwen, managers and owners of Diggin' Livin' Farm and Apiaries
Image 2: Emergency queen cells used in the production of walk away splits
Image 3: Heritage colonies in the process of removing walk away splits. Note: prepared walkaway splits with additional QR code tags above queen excluders.

Methods

Varroa treatments are applied uniformly across the entire operation at intervals constituting 2–3 times per year as a means of minimizing total colony losses, while also standardizing treatments for statistical purposes.

All colonies are visited twice annually during the months of March–May, which includes the season of natural tendency of colonies to swarm, in order to ascertain the colony size and overall health. If colonies are in a state of vigor roughly above the median level found in the entire operation, a divide is made from the colony in the form of a walk-away split (for details regarding methods used for preparing divides see *Raising Resilient Bees* [2]). The only criteria used to decide if a colony is eligible for a divide is simply the lack of overt disease symptoms and a robust population. It is assumed that forgoing additional selection criteria for reproduction will allow for a suite of resistance mechanisms to increase in frequency in the population simultaneously. Drone source colonies are selected at random from within the operation annually.

The other main means of genetic conversion of maternal genetics within the operation, aside from generation of new colonies, results from the remedy of hopelessly queenless colonies found during apiary inspections. In addition to tracking the maternal origin of germplasm for divides, we likewise track the maternal origin of any germplasm used to fix or re-start a hopelessly queenless colony, and the subsequent success of queen rearing in these instances is likewise recorded.

When a colony is found to lack a queen or the means of rearing a queen, and a suitable amount of time has lapsed to ensure that queen rearing is not in process (aka. the presence of a virgin or newly mated queen), and a colony is found to have sufficient strength to attend to queen rearing, it is designated as a Restart. Brood of a known maternal origin is inserted and subsequently inspected to ascertain the success of queen rearing. If a colony is lacking the vigor to maintain colony functions, it is terminated in the database and a new queen-right colony may be inserted to return the colony to queen-right status.

A tracking system was developed, and a prototype implemented in 2024 to record the maternal origin of the germplasm used to originate new colonies and to measure the relative reproductive success and lifespan of each matriline within the operation. 511 colonies living at the time of the origination of the database were designated as Heritage Colonies. Furthermore, all matrilines are recorded as terminated if the colony fails to maintain a queen-right state. To aid in comparison of reproductive success of each colony and its maternal relatives, a series of simple computations is conducted periodically to aid in identification of matrilines with superior levels of survivorship.

Scoring Metrics

Each colony is scored for the following metrics:

- Mother score = # of living daughters × (# living daughters ÷ total number of daughter colonies originated)
- Sister score = # of living sister colonies × (# living sisters ÷ total number of sister colonies originated)
- Legacy score = # of living descendants × (# living descendants ÷ total number of descendants originated)

Daughter colonies are defined as colonies which reared a new queen from germplasm that originated as eggs laid by a given mother colony. Sister colonies are defined as colonies originating from germplasm obtained from the same maternal colony. Descendent colonies are defined as daughters of a given colony as well as daughters from any colony derived from a given maternal colony (daughters of daughters, and daughters of daughters of daughters etc.).

Results

Eighteen months of data for colony survivorship and relative reproductive success have been recorded, and initial analyses are presented here. After 18 months of colony management the composition of colonies changed significantly from the onset of the data tracking component of this project. Of the original 511 Heritage Colonies, 205 have maintained intact queen lines in their hives without beekeeper intervention. While this number is lower than anticipated, the 2024 season included multiple stochastic events that had deleterious effects on successful supersedure events, resulting in high levels of summer mortality not common in this operation.

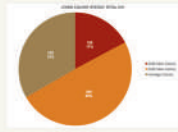

Fig. 1. Living Colonies by Colony Type (Aug 24, 2025)

Investigating this matter further, we see in Fig. 2 that the main month of mortality recorded is February of 2025, when colonies were inspected upon the initiation of brood-rearing. Colonies were terminated if they failed to maintain suitable cluster size sufficient for pollination grading or to build up suitable brood area prior to colony rental. Varroa parasitization is likely the driving factor behind failing colonies, though termination was only coded as Parasitic Mite Syndrome if actual brood infestation symptoms were noted, including hygienic behavior, irregular brood patterns, malformed larvae, and mite feces.

The subsequent peaks noted in the months of April and May coincide with the investigation of new colonies initiated to rear new queens, and represent the failed attempts at walk-away splits conducted in March and April. The high levels of mortality reported for the month of August reflect a summation of summer mortality driven by queen failure and are indicative of queen-less colonies being left alone in the months of June and July to ensure they were hopelessly queen-less. The August peak also reflects that data entry was delayed due to a busy season of apiary tasks in the months preceding.

Fig. 2. Mortality by month 2025

In summary of our 2025 mating season, we present that a total of 286 colonies were used to prepare walk-away splits, of which ()% were Heritage Colonies. Additionally, in 2025, new colonies previously generated in 2024 comprised 30% of reproductive colonies and represent a continuation of the increase in the representation of individual matrilines that were reproductive in 2024.

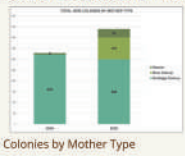

Fig.3 Total New Colonies by Mother Type

Since the start of the 2024 season of increase, we have made a total of 802 new colonies from a total of 384 mother colonies, (see Fig. 4). Amongst reproductive colonies, there was a mean of 2.09 colonies generated per mother colony. This mean value represents another measure of the slow conversion of the genetic composition of the meta-population towards a greater representation of the matrilineal genetics of colonies with a presumed greater level of fitness. As well, many individual mother colonies made much larger contributions to the total population composition, with as many as 8 daughter colonies.

Fig. 4. Daughter Colonies Per Mother Colony

Results continued

Two previously mentioned activities within the meta-population management result in changes in maternal genetic representation. First, and of greatest significance, is the origination of new colonies generated from either queen cells or emergency queen rearing in response to a walk-away split action. In 2025 we initiated a total of 390 walk-away splits from 286 colonies. At the time of writing, 64%, or 250 new colonies, were alive and present within the operation's apiaries. Combined with the 5% of colonies that were sold, we see that a total success rate of 69% was achieved in 2025 using this method of queen rearing.

Additionally, we present the success rate of initiating a Restart of hopelessly queenless colonies. Figure 6 presents our success in initiating queen rearing in colonies lacking the ability to rear a new queen from existing germplasm. The results demonstrate that this technique is less successful as a means of generating new queens than properly constructed walk-away splits. Complexities such as the palletized format of colonies in this season and the presence of laying workers may contribute to the lower success rates observed.

Fig. 5. 2025 Walk-Away Split Outcome

Fig. 6. 2025 Restart Outcome

In preliminary investigation of the metrics of our first two years of genealogical tracking, we have documented significant variation in levels of reproductivity amongst mother colonies. Colonies ranged from non-reproductive, with zero daughter colonies generated, to highly reproductive, with as many as 8 daughter colonies generated. As well colonies have been documented with large variability in reproductive success, ranging from 0 living daughter colonies to as many as 5 living daughter colonies.

Discusssion

Looking at the metrics for individual colonies within the operation is provocative. It is apparent that our lineage tracking system is already elucidating useful information on the relative rate and success of reproduction with the meta-population comprised as our commercial operation. Despite stochastic events, we see that certain individual colonies have reproductive patterns that are anomalies that distinguish them as worthy of further investigation. Interestingly, we see in Fig. 7, that despite Colony 1678 being robust and presumably found to be above the average state of vigor on all visits during swarm season in both 2024 and 2025, and a total of 8 daughter colonies originating from it, none of the daughter colonies are alive today. One could infer that either the colony is failing to impart any significant level of fitness to its daughter colonies, or the daughter colonies have all been very unlucky.

Fig. 7. Metrics for Colony 1678

Fig. 8. Metrics for Colony 1715

Note: Lineage Score is defined here as the Legacy Score of a colony's Mother Colony. It shows how large of a 'family' of living colonies the colony is part of, compared with how many descendants it has of its own. Of greater interest, and the first example of data this project was designed to produce, are the metrics for Colony 1715. Colony 1715 has a Mother Score of 3.57 and a Mother Score Percentile of 98%, due to the fact that 7 daughter colonies have been generated from it and 5 are still living within the operation. With a Legacy Score of 6.25, this colony already has 10 living descendants, showing that several of its daughters have gone on to generate living colonies of their own.

Another example of the relationship between Mother Score, Daughter Score and Legacy Score is seen in Colony 1185 and one of its living daughters. Colony 1185 scores a Mother Score of 5, and a Mother Score Percentile of 100%, signifying it is the highest Mother Score in the operation, as it has generated 5 daughter colonies, all of which are still alive. Furthermore, it has a Legacy Score of 10, denoting that all 10 of its descendants remain alive in the operation.

Fig. 9. Metrics for Colony 1185 (mother of Colony 1406)

Fig. 10. Metrics for Colony 1406 (daughter of Colony 1185)

This provides early evidence for the existence of inheritable traits contributing to survivorship. While these scores will likely be diluted by stochastic events over time, the metrics appear robust enough to give a clear signal that can help identify colonies with enhanced survivorship characteristics.

Summary

As preliminary data for a long-term breeding and tracking project, we are pleased to report on the observed variability within our meta-population. With additional years of data, our tracking system will offer greater resolution of the matrilines responsible for increases in genetic representation within our operation.

Coupled with genetic sampling, this system of observation will allow documentation of gene introgression into a quasi-natural population. We hope that this project will serve as a model of honeybee reproduction that may be repeated, in part as a response to myopic attempts to select 'superior' breeding lines under narrow criteria, which may result in the loss of rare alleles associated with latent or unobservable selection pressures.

References:

1. John Kefuss et al., "Varroa Tolerance in France of Intermissa Bees from Tunisia and Their Naturally Mated Descendants: 1993–2004," *American Bee Journal* 144, no. 7 (July 2004): 564, https://www.researchgate.net/publication/288620065_Varroa_tolerance_in_France_of_Intermissa_bees_from_Tunisia_and_their_naturally_mated_descendants_1993-2004.
2. Eric McEwen and Joy McEwen, *Raising Resilient Bees: Heritage Techniques to Mitigate Mites, Preserve Locally Adapted Genetics, and Grow Your Apiary*, Chelsea Green Publishing, 2023.

PP-466 [Bee Biology]
Advancing Genetic Resiliency in Honeybee Populations through Long-Term Breeding and Population Tracking

Eric Mcewen
Diggin' Livin' Farm & Apiaries, commercial beekeeping operation, Oregon, USA

Background/PURPOSE:
The increasing decline of honeybee populations, largely due to disease susceptibility and genetic bottlenecks, threatens global pollination services and food security. Traditional breeding programs often focus on accelerating resistance traits in a way that reduces genetic diversity, leading to unintended consequences such as diminished colony adaptability. This study aims to develop a long-term breeding program that enhances Varroa resistance, queen longevity, and genetic resiliency while maintaining intra-population diversity. Our research focuses on utilizing population-level tracking and genetic fingerprinting to establish a robust honeybee breeding methodology.

Problem Description:
One of the greatest challenges in modern beekeeping is the lack of stable, inheritable resistance traits in commercially available honeybees. Many known resistance mechanisms (e.g., VSH, SMR) appear recessive, resulting in weakened expression over generations. Additionally, queen failure rates are at an all-time high, increasing costs for beekeepers and reducing colony sustainability. This study investigates whether maintaining an inbred meta-population under natural selection pressures can stabilize resistance traits without reducing genetic diversity, ensuring that beneficial alleles persist in future generations.

METHODOLOGY:
Since 2016, Diggin' Livin' Apiaries has maintained a closed breeding population exceeding 250 colonies, with no introduction of new matrilineal genetics. We employ: Walk-away splits in isolated mating yards to encourage natural queen selection. Minimal Varroa treatments (1-2 oxalic acid applications annually) to allow for the expression of natural resistance traits. QR code tracking & genetic fingerprinting to evaluate parentage, longevity, and Varroa resistance over multiple generations. Comparative analysis of allele frequencies in Varroa-resistant colonies and surrounding feral populations.

Results & CONCLUSION: Preliminary data suggest that resistance traits can be stabilized over time while maintaining genetic diversity. Early results from Unhealthy Brood Odor (UBO) testing indicate an above-average presence of hygienic behaviors linked to Varroa resistance. Additionally, QR code tracking has provided insights into queen longevity and reproductive success, key factors in colony sustainability.

Practical Implications for Beekeepers:
Demonstrates a sustainable, closed breeding approach that allows natural selection to improve colony vigor.
Provides a scalable model for genetic tracking, allowing beekeepers to monitor lineage performance and enhance selection.
Addresses queen longevity issues, offering insight into breeding for extended reproductive viability.