Initial Statistical Exploration of Xenofelinoid Genetics*

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***Abstract*—Xenofelinoids, the fascinating feline-like creatures of Colony TF*6290193 (Felisfire), are a popular subject of study and breeding. However, scientific understanding of their complex genetics remains limited. This study provides baseline statistical data on xenofelinoid inheritance patterns. Using a controlled breeding protocol with two distinct lineages over five generations, we meticulously tracked the frequency of markings, analyzed dominant and recessive traits, and documented any novel genetic combinations. Our findings contribute to a more systematic approach to xenofelinoid breeding, enhancing predictability and informed genetic experimentation within the Felisfire community.**

***Index Terms*—statistics, genetics, xenobiology, breeding**

I. Introduction

Since the inception of the colony by the crew of the U.T.V. Optimism, Humanity has been inundated with interest and inquiry about the lifeforms on Colony TF*6290193 "*Felisfire*". Plenty of research has been done on the main object of fascination, the *Xenofelinoids* [1]. But publicized records are sparse and information is collected informally in the form of guides distributed amongst the colony [2]

This paper aims to provide baseline statistical data for more informed breeding of xenofelinoids. We aim to enhance reproducibility in this popular Felisfirian pastime [3].

II. Methods

A. Specimens

We start with 8 progenitor felidae specimens, divided into 2 identical lineages. Each lineage was established with 2 mating pairs engineered with distinctive markings that serve as visual identifiers. These identifiers were unique within each lineage, allowing us to clearly differentiate and track the progeny's genealogical origins.

The two lineages, though visually distinct due to their coat colors, were designed to be genetically identical apart from select sections of the exome, serving as mirrors of each other. This strategic design ensured that the genetic makeup of both groups remained diverse enough to prevent inbreeding [1]. The setup thus created a balanced environment, allowing us to study hereditary patterns and mitigate any unwanted consequences of close breeding.

This meticulous setup enabled us to control the breeding process, fostering a controlled environment where the risks of inbreeding were significantly mitigated. The distinctive markings acted as a telltale sign of each cat's lineage, offering an at-a-glance understanding of their genetic heritage.

Since the main goal is to track the marking distribution amongst each generation, the marking colors have been kept with similar values but have been allowed to be in different positions of the genome. The base coat, nose, and eye colors are flipped between the lineages to allow for easy distinction.

Fig. 1: Lineage 1

(a) L1FBY (b) L1MBY (c) L1FRG (d) L1MRG

Fig. 2: Lineage 2

(a) L2FBY (b) L2MBY (c) L2FRG (d) L2MRG

B. Breeding

Each lineage began with four freshly hatched xenofelinoids. To promote diverse genetic combinations, we employed a structured breeding approach. Initially, we used love potions[tm] to artificially increase interaction scores to facilitate breeding when natural interactions had not yet reached the optimal range (95-100) [1].

Within each lineage, we implemented a round-robin breeding system. This involved systematically pairing each female with each male to maximize genetic diversity and avoid immediate inbreeding [insert citation for round-robin breeding

techniques, if applicable]. After this initial round, we introduced selected specimens from the opposite lineage into the breeding pool. A second, cross-lineage round-robin breeding cycle followed, further diversifying the genetic makeup of each group [4]. This process continued through five generations, allowing us to track inheritance patterns effectively.

We meticulously recorded the frequency of marking inheritance, instances of dominant or recessive traits, and the emergence of any novel markings or combinations.

TABLE I: Gen 1 Mating Table

Specimens	L1FBY	L1FRG	L2FBY	L2FRG
L1MBY	N/A	N/A	N/A	N/A
L1MRG	N/A	N/A	N/A	N/A
L2MBY	N/A	N/A	N/A	N/A
L2MRG	N/A	N/A	N/A	N/A

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