

Characterization of staphylococcal communities on healthy and allergic feline skin

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Background – Various *Staphylococcus* species have been demonstrated to play important roles on the skin, including causing disease and protecting the host from pathogens. Although culture-based studies have isolated various *Staphylococcus* spp. from feline skin, very little is known regarding the species-level communities on the host.

Hypothesis/objectives – To describe the species-level staphylococcal communities inhabiting the skin of healthy cats and cats with allergic dermatitis.

Animals – Skin swabs from the ear canal and groin of 11 healthy and 10 allergic (nonlesional) cats were obtained.

Methods and materials – DNA was extracted from the skin swabs and used for next-generation sequencing targeting the V1–3 region of the 16S rRNA gene. Following a standard microbiota analysis of the sequencing data, species-level assignment for the staphylococcal sequences were obtained using a staphylococci-specific database.

Results – *Staphylococcus* spp. had similar relative abundance in healthy and allergic samples. The most abundant staphylococcal species were *S. epidermidis* in healthy samples, and *S. felis* and *S. capitis* in allergic samples. The composition of staphylococcal communities, as well as relative abundance of *Staphylococcus* spp., was variable between body sites and individual cats sampled.

Conclusions and clinical relevance – These results demonstrate that diverse staphylococcal communities inhabit the skin of healthy and allergic cats, and provide a starting point for further research into the importance of *Staphylococcus* spp. in feline allergic skin disease.

Introduction

Staphylococcus spp., although often thought of as pathogens, are known cutaneous commensals. In humans, *S. epidermidis* is the most abundant species on healthy skin, and is outgrown by *S. aureus* on the skin of individuals affected by atopic dermatitis (AD).¹ In AD, *S. aureus* can take advantage of the barrier dysfunction and increase its numbers, gaining deeper access into the skin and resulting in secondary bacterial infections.² Besides the skin barrier and various components of the cutaneous ecosystem that have roles in preventing infection, some microbes, such as *S. epidermidis*, also are important in host defence. These bacteria can prevent overgrowth of *S. aureus* through a variety of mechanisms and can modulate the host immune system.^{3,4} Therefore, the genus *Staphylococcus* is of great importance in allergic

dermatitis. This impact, however, is not strictly limited to humans.

In dogs, *S. pseudintermedius* has been recognized as the predominant staphylococcal species on both healthy and allergic canine skin in both culture-dependent and culture-independent studies.⁵ In one study, *S. pseudintermedius* accounted for 59.4% of the total *Staphylococcus* spp. in all canine samples (healthy and atopic).⁶ In lesions of canine pyoderma secondary to allergic disease, the overall *Staphylococcus* spp. abundance was found to be higher in samples from affected relative to healthy canine samples and *S. pseudintermedius* was the predominant species in both sample types.⁷ Collectively, these results suggest that unlike in human skin, there does not seem to be a difference in the relative abundance of specific *Staphylococcus* species between healthy and allergic skin in dogs.

In feline patients, our knowledge of the cutaneous staphylococcal communities is very limited. Research on cutaneous feline staphylococcal communities has been performed, yet most reports have focused solely on isolates from lesions. Those that have included samples

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from healthy cats have found higher abundances of coagulase-negative as opposed to coagulase-positive staphylococcal species.^{8–10} Studies that have determined the specific coagulase-negative species present have described a predominance of *S. felis* (previously thought to be *S. simulans*).^{10–12} Within the coagulase-positive species identified on healthy skin, *S. pseudintermedius* (previously reported as *S. intermedius*)¹³ seems to be most abundant, followed closely behind by *S. aureus*.^{9,12}

On lesional feline skin, two studies have described higher abundances of coagulase-positive isolates, relative to the numbers found on healthy skin⁸ and relative to the number of coagulase-negative isolates.¹⁴ Many species, including *S. felis*, *S. aureus* and *S. pseudintermedius*,¹⁵ have been isolated from lesions.

These previously reported studies have relied on culture-based methods, which might not offer growth conditions that are equally favourable to all species and therefore may not provide a broad image of the relative abundances of these staphylococcal species. Molecular-based methods are independent of cultivability, allow for species-level identification and can therefore complement data from existing culture-based studies. Although increased *Staphylococcus* spp. on nonlesional allergic feline skin has been described,¹⁶ the importance of specific staphylococcal species in feline allergic skin disease has not been evaluated. In this study, we sought to confirm previous findings of increased *Staphylococcus* spp. on allergic feline skin and describe the species-level composition of staphylococcal communities using next-generation sequencing (NGS).

Methods and materials

Ethical approval

This study was approved by the Texas A&M University Institutional Animal Care and Use Committee and informed written consent was obtained for all cats sampled.

Sample collection

All cats were evaluated by a board-certified dermatologist and only sampled if fitting within the previously described inclusion criteria.¹⁶ Swabs of the ear canal and groin were obtained from 11 healthy and 10 allergic cats (Table S1). Samples were taken by rubbing two Isohelix buccal swabs (Cell Projects Ltd.; Kent, UK) 10 times per side of each swab. Hair was parted with gloved hands to ensure that swabs were applied to the skin and not the fur. The two swabs then were stored in a single MO BIO PowerBead tube (MO BIO Laboratories; Carlsbad, CA, USA) and stored at 4°C (for no longer than seven days) until DNA extraction with the MO BIO PowerSoil DNA Isolation Kit. Along with skin swab samples, DNA was extracted from an empty PowerBead tube and a PowerBead tube containing a sterile swab as controls.

Next-generation sequencing and sequence processing

The DNA was sent to the University of Minnesota Genomics Center for NGS of the V1–3 region of the 16S rRNA gene (V1_27F: AGAGTTTGATCMTGGCTCAG, V3_534R: ATTACCGCGGCTGCTGG). After library preparation with the KAPA Library Amplification Kit (Roche; Basel, Switzerland.), samples were subjected to 2 × 300 bp paired-end sequencing on an Illumina MiSeq (Illumina; San Diego, CA, USA). Data were analysed in MOTHUR v1.39.5,¹⁷ where chimeras were removed with uchime,¹⁸ sequences were aligned to the green-genes(13_8_99) database,¹⁹ and classified with the RDP classifier

(v16).²⁰ Staphylococcal sequences were extracted and aligned to a reference alignment available in a previously published package trimmed to the sequencing region.²¹ Staphylococcal sequences having <99% similarity with sequences in the staphylococcal alignment were considered unclassified to the species level.

For diversity analyses, data were rarefied to 15,066 sequences per sample. Alpha diversity was analysed using the observed operational taxonomic units (OTUs), Chao1, Shannon diversity index and Faith's phylogenetic diversity metrics. Beta diversity was analysed using the Bray–Curtis, Jaccard, weighted UniFrac and unweighted UniFrac methods.

Statistical methods

Based on the non-normal distribution of data, as determined with the Shapiro–Wilk test in JMP Pro 14 (SAS Institute Inc.; Cary, NC, USA), alpha diversity and differential taxa relative abundance data were analysed using nonparametric Wilcoxon rank-sum tests in JMP Pro 14. Differential relative abundance of taxa also was analysed using the Linear Discriminant Analyze Effect Size (LEfSe) algorithm on the Huttenhower lab Galaxy (<http://huttenhower.sph.harvard.edu/galaxy/>). Distance matrices for beta diversity were analysed with the analysis of similarities (ANOSIM) test in R/VEGAN.

Results

A total of 1,402,395 sequences (median 33,477) from 42 samples remained after quality filtering. Sequence files are available in the NCBI sequence read archive under BioProject ID PRJNA580000. In terms of composition, this study revealed similar results to what has been described previously in cats,^{16,22} with Proteobacteria (average relative abundance 52.29%), Firmicutes (17.94%), Actinobacteria (13.99%) and Bacteroidetes (11.87%) as the predominant phyla (Figures S1 and S2). Analysis of the bacterial microbiota reveal no differences in diversity between healthy and allergic cats, nor differences when analysing the effect of individual or body site within health groups. When analysing healthy samples based on sex, no differences in diversity were observed, however a few taxa were found to have differential abundance. Two genera, *Rhizobium* spp. ($P = 0.010$) and *Kocuria* spp. ($P = 0.024$), were identified only in male samples with average relative abundances of 1.7% and 0.7%, respectively. Unclassified *Aerococcaceae* (unclassified to the genus level) were not found in any male samples, yet were identified in four female samples with an average relative abundance of 2.1% ($P = 0.040$). Numerous taxa were found to be differentially abundant between healthy and allergic cats (Figure 1). Among the many differentially abundant taxa were *Streptococcus* spp., which were found in higher relative abundances in samples from both body sites of allergic cats (linear discriminant analysis (LDA) = 3.8208, $P = 0.016$), and *Escherichia/Shigella* spp., which also had higher relative abundance in allergic cats, only in the ear canal (LDA = 2.9112, $P = 0.024$). No difference in *Staphylococcus* spp. relative abundance was found between healthy and allergic samples.

Overall, relative abundance of *Staphylococcus* spp. was low, with average relative abundances of 4.34% in healthy and 3.61% in allergic samples (Figure S2). Of the 42 samples analysed, four healthy and three allergic samples had no *Staphylococcus* spp. sequences. Samples with staphylococcal sequences had up to five different species, with an average of two species per sample

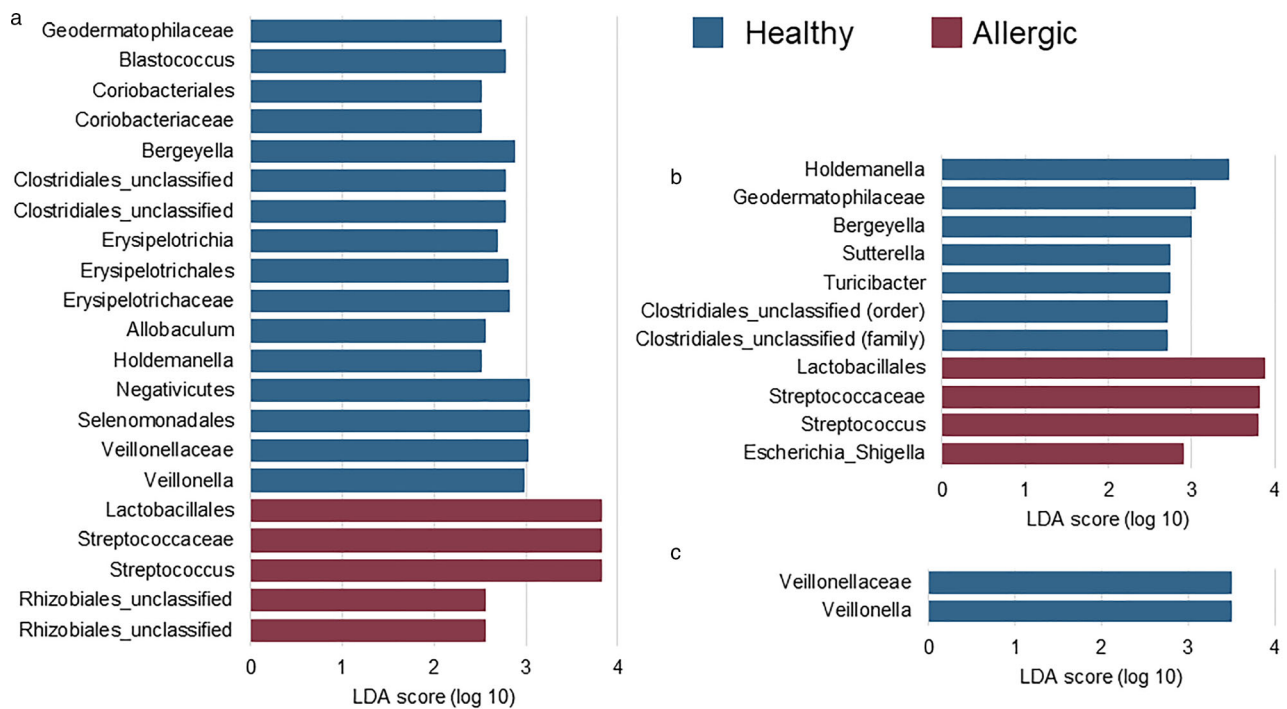


Figure 1. Linear discriminant analysis (LDA) effect size (LEfSe) analysis of bacterial relative abundance between healthy and allergic cat samples. Various taxa were found to be differentially abundant when analysing (a) both body sites, or the (b) ear canal and (c) groin samples only.

(Table S2). When looking at the staphylococcal sequences from all samples, 13 different staphylococcal species could be identified (Figure 2).

In healthy samples (23,440 staphylococcal sequences), 40.3% and 26.9% of the *Staphylococcus* sequences were classified to *S. epidermidis* and *S. pseudintermedius*, respectively (Figure 3). When looking at the

staphylococcal communities in terms of average relative abundance, *S. epidermidis* was the most abundant (average relative abundance 29.4%), followed by *S. capitis* (15.3%) and *S. felis* (6.6%).

In allergic samples (19,139 staphylococcal sequences), *S. capitis* accounted for 30.8% and *S. felis* accounted for 21.2% of sequences. In terms of average relative

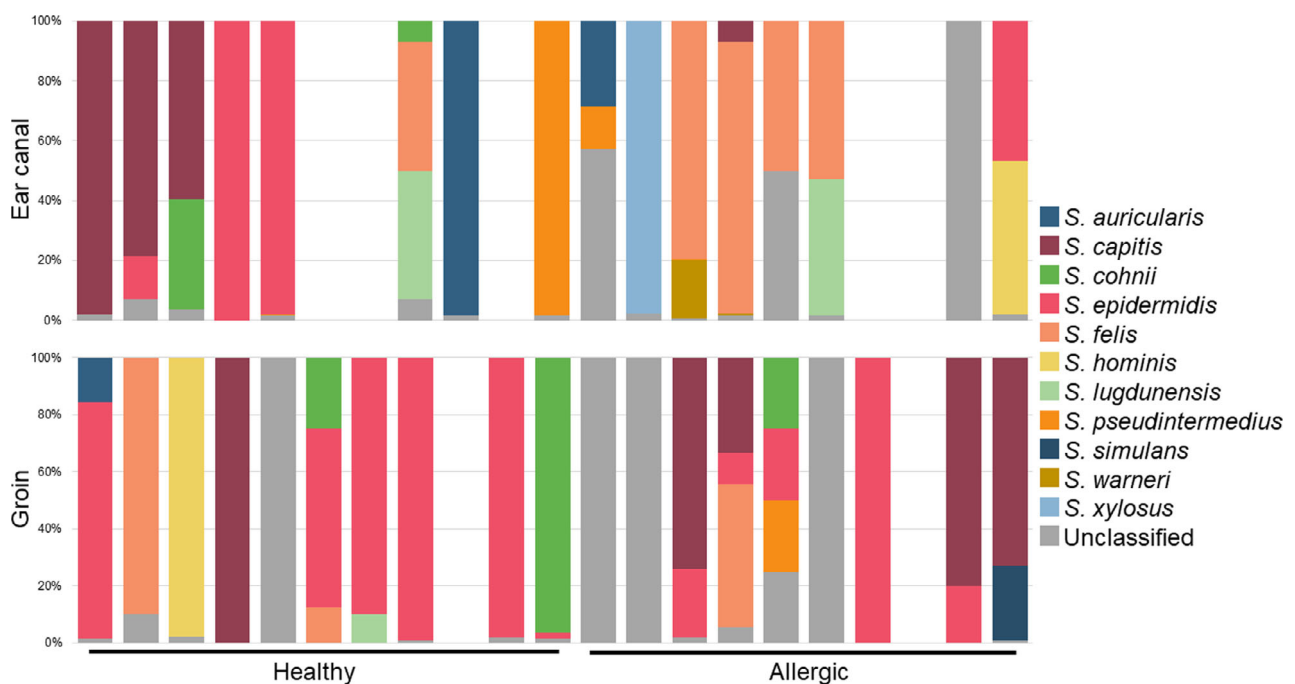


Figure 2. Relative abundance of staphylococcal species in each sample. Staphylococcal community composition was variable across individual cats and body site.

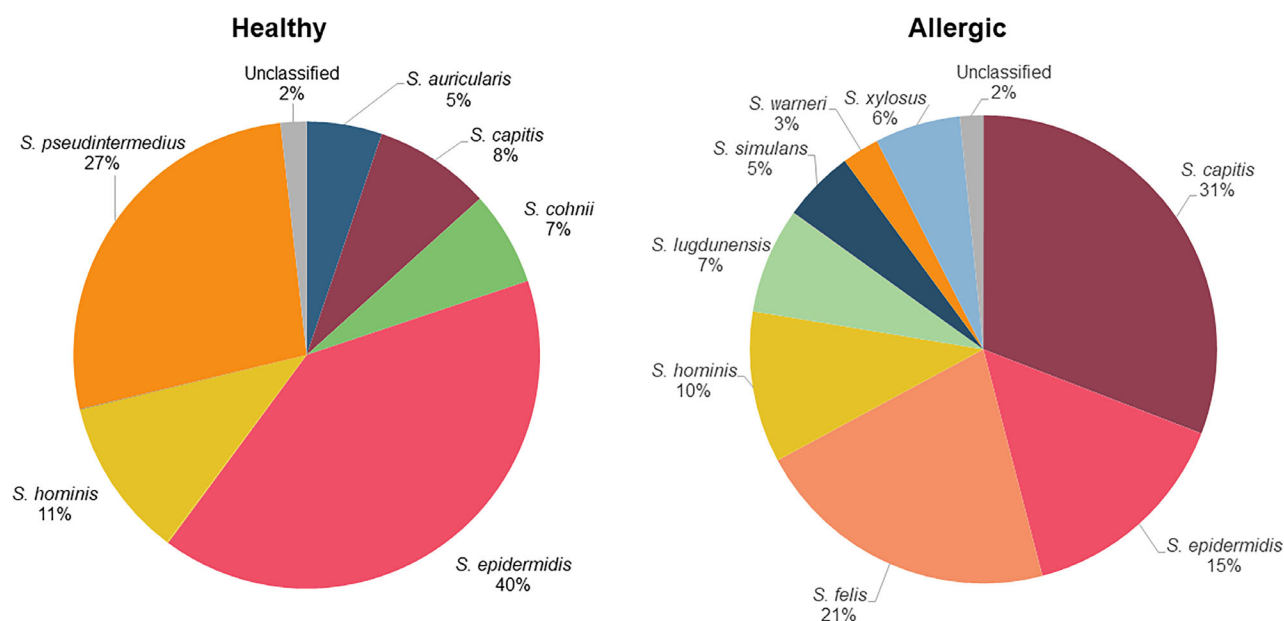


Figure 3. Species-level composition of staphylococcal communities on healthy and allergic feline skin based on the number of sequences per species.

Regardless of health status, staphylococcal communities on feline skin are diverse, containing multiple species of substantial abundance. Healthy cats are colonized predominantly by *S. epidermidis* and *S. pseudintermedius*, and *S. capitis* and *S. felis* are the most prevalent staphylococcal species present on allergic cats.

abundance, *S. felis* (16.2%) and *S. capitis* (13.4%) were the most abundant. Only four sequences from all allergic samples were classified as *S. pseudintermedius*. No species was found to be significantly differentially abundant between healthy and allergic cat samples (Figure S1: all samples).

Discussion

This study is the first to describe the species-level staphylococcal communities on feline skin. Previous studies have indicated *S. aureus*, *S. intermedius* (likely *S. pseudintermedius*, which was first described after these studies),²³ *S. felis* and *S. simulans* (likely *S. felis*, which was first described after these studies)¹¹ as some of the most prevalent staphylococci present on healthy feline skin.^{12,13,24} In the results presented here from healthy skin samples, *S. epidermidis* accounted for the majority of sequences and had the highest average relative abundance. Due to the high variability in the abundance of *Staphylococcus* spp. among cats, the definition of a core staphylococcal community on feline skin is still not clear. However, when looking at individual healthy cat samples, *S. epidermidis* was the most abundant species in seven of 22 samples and *S. capitis* was most abundant in four of 22 samples. All other staphylococcal species were only most abundant in at most a single sample. *Staphylococcus aureus* sequences were not found in any sample. A recent study found that *S. aureus* could only be isolated from 4.24% of healthy feline skin samples,¹⁰ so perhaps their low abundance explains why they were not identified in our dataset. Various species have been identified as pathogens in cats, including *S. aureus*, *S. felis*²⁵ and *S. intermedius* (more likely *S. pseudintermedius*).¹⁵ *Staphylococcus capitis* and *S. felis* accounted for the

majority of staphylococcal sequences and were the species with the highest average relative abundance from allergic samples. These results suggest that in addition to *S. felis*, which is typically associated with feline skin, *S. epidermidis* and *S. capitis* also may be important species that previously have not received much attention with respect to feline cutaneous staphylococcal communities. Additionally, our results indicate that the staphylococcal communities inhabiting feline skin are incredibly diverse relative to their human and canine counterparts. Within this study, we were able to identify 13 different staphylococcal species across all samples. Although not all of these had high relative abundance, several species accounted for a substantial percentage of all staphylococcal sequences. This contrasts with data from dogs, where *S. pseudintermedius* accounts for a strong majority of all staphylococci,⁶ and humans, where typically *S. epidermidis* or *S. aureus*, depending on health status and body site, are the predominant staphylococcal species present.²⁶

Given the importance of *Staphylococcus* spp. in human and canine allergic dermatitis, we hypothesized that *Staphylococcus* spp. also may have roles in feline allergic dermatitis. This bacterial genus previously has been demonstrated to be increased in abundance on both allergic human and canine⁶ skin, compared to healthy counterparts. Their relative abundance also has been found to be increased on the skin of allergic cats,¹⁶ particularly in the ear canal and interdigital space. Although not statistically significant, our results indicate there may be differences in the species-level composition of the staphylococcal communities inhabiting healthy and allergic feline skin, including a predominance of *S. epidermidis* in healthy samples. The finding of more *S. epidermidis* sequences in healthy samples is interesting given the importance of

this species on healthy human skin, where it is typically the most abundant bacteria and can convey benefits to the host. This species can produce antimicrobials targeted to more pathogenic bacterial species and secrete compounds that can enhance the host immune system.³ In human atopic patients, *S. aureus* bypasses the protective roles of *S. epidermidis* and becomes highly abundant.⁴ This often leads or contributes to secondary infections during allergic flares. Similar protective roles of *S. epidermidis* and other staphylococcal species have not yet been demonstrated on canine and feline skin, and thus may provide an avenue for therapeutic intervention.

Secondary infections also are known to occur in allergic feline patients, however the true occurrence is unknown and likely underestimated. Although *Staphylococcus* seems to be present on feline skin in similar relative abundances as on canine skin, based on the current and previous study,¹⁶ perhaps the inability of many staphylococcal species to adhere strongly to feline corneocytes^{27,28} is responsible for the seemingly lower occurrence of bacterial skin infection reported in feline patients. However, this potential lack of secondary infections does not negate the importance of this bacteria in feline allergic dermatitis. Perhaps staphylococci are not as important in terms of causing infection in cats than in dogs, and may instead be influential primarily through modulating inflammation.

Interestingly, some of the staphylococcal species observed within these feline samples, such as *S. hominis* and *S. capitis*, are associated with human skin.²⁶ It is uncertain whether these particular staphylococcal species are stable residents of feline skin, or whether they are transient organisms transferred via contact with humans. Although there have been some studies evaluating the microbiome of humans and their pets,^{29–31} the direction and impact of microbiome-sharing between species that cohabit remains unclear.

Besides staphylococci, other bacteria on the skin may contribute to secondary infections in cats with allergic dermatitis. In this study, higher relative abundances of *Streptococcus* spp. and *Escherichia/Shigella* spp. were observed in allergic samples. *Streptococcus* spp. can cause cutaneous bacterial infections, and these infections are rare and typically related to cat bites.³² The finding of higher relative abundance of *Escherichia/Shigella* spp. was limited to the ear canal, which can be a site for secondary *E. coli* infections.³³ The biological significance of the higher relative abundance of *Streptococcus* and *Escherichia/Shigella* spp. in allergic samples is unclear.

Studies describing the staphylococcal communities on lesional skin should be performed to better understand which species may be more relevant during flares of allergic skin disease. Within our own study some staphylococcal species were found to have higher relative abundance in allergic skin, yet these did not reach significance, perhaps as a consequence of the small sample size. Although NGS does allow us to see a broader picture of the entire staphylococcal communities present, like culture-based techniques, it can be biased towards specific species and, given the short length of amplicons, also has the potential for species-level misclassification.

Therefore, the use of other techniques to complement existing studies is desired. When samples from another cohort of healthy and allergic cats were subjected to quantitative PCR targeting *Staphylococcus* spp., the bacteria were detected in only a small number of samples with low abundances (unpublished data). Perhaps other methods would be more beneficial for further describing the staphylococcal communities inhabiting healthy and allergic feline skin.

Staphylococcus spp. have low relative abundance on feline skin, yet they may have an important role in skin homeostasis and during flares in feline allergic skin disease. Although statistically significant differences were not demonstrated in the present study, there are appreciable differences in the species-level composition of these communities between healthy and allergic cats, and between individual cats. Unlike their canine counterparts, and more similar to the dynamic communities on human skin, there was not a single predominant species in all samples, regardless of health status. Further research of the staphylococcal communities inhabiting lesional feline skin may identify species that are associated with disease, which could represent new targets for therapy.

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Supporting Information

Additional Supporting Information may be found in the online version of this article.

Figure S1. Relative abundance of bacteria taxa across individual samples of cat skin.

Figure S2. Average relative abundance of taxa found on cat skin.

Table S1. Signalment of sample cohort.

Table S2. Relative abundance of staphylococcal species and number of unique species identified (excluding unclassified staphylococcal sequences) in each sample.

Résumé

Contexte – Plusieurs espèces de *Staphylococcus* ont montré un rôle important dans la peau, dont la cause de maladies ou la protection de l'hôte des pathogènes. Bien que les études basées sur les cultures aient permis d'isoler le nombreuses *Staphylococcus* spp. de la peau de chat, on en sait très peu sur les niveaux d'espèces de communautés de l'hôte.

Hypothèses/Objectifs – Décrire les communautés staphylococciques de niveau d'espèce occupant la peau de chats sains et de chats avec dermatites allergiques.

Sujets – Des écouvillons cutanés des conduits auriculaires et du nez de 11 chats sains et 10 chats allergiques (non lésionnels) ont été obtenus.

Matériels et méthodes – L'ADN a été extrait d'écouvillons cutanés et utilisés pour le séquençage de dernière génération ciblant la région V1-3 du gène ARNr 16s. Suivant une analyse de microbiote standard des données de séquençage, la désignation des niveaux d'espèce pour les séquences staphylococciques ont été obtenues à l'aide de données spécifiques de staphylocoques.

Résultats – *Staphylococcus* spp. était présent en quantité relative similaire pour les échantillons sains et allergiques. Les espèces de staphylocoques les plus abondantes étaient *S. epidermidis* dans les échantillons sains, et *S. felis* et *S. capitis* dans les échantillons allergiques. La composition des communautés de staphylocoques, ainsi que la quantité relative de *Staphylococcus* spp., était variable entre les sites corporels et entre les chats prélevés.

Conclusion et importance clinique – Ces résultats démontrent que les communautés de staphylocoques diverses occupent la peau de chat sain et allergique et fournit un point de départ pour des recherches supplémentaires sur l'importance de *Staphylococcus* spp. dans les dermatoses allergiques félines.

RESUMEN

Introducción – se ha demostrado que varias especies de *Staphylococcus* desempeñan papeles importantes en la piel, incluyendo causar enfermedades y proteger al huésped de los patógenos. Aunque los estudios basados en cultivos han aislado varios *Staphylococcus spp.* de piel felina, se sabe muy poco sobre las comunidades a nivel de especie en el hospedador felino.

Hipótesis/objetivos – describir las comunidades estafilocócicas a nivel de especie que habitan la piel de gatos sanos y gatos con dermatitis alérgica.

Animales – se obtuvieron hisopos de piel del canal auditivo y de la ingle de 11 gatos sanos y 10 gatos alérgicos (sin lesiones).

Métodos y materiales – se extrajo el DNA de hisopos de la piel y se usó en secuenciación de próxima generación dirigida a la región V1-3 del gen 16s rRNA. Después de un análisis estándar de microbiota de los datos de secuenciación, se obtuvo la asignación a nivel de especie para las secuencias estafilocócicas utilizando una base de datos específica de estafilococos.

Resultados – *Staphylococcus spp.* tuvo abundancia relativa similar en muestras sanas y alérgicas. Las especies de estafilococos más abundantes fueron *S. epidermidis* en muestras sanas y *S. felis* y *S. capitis* en muestras alérgicas. La composición de las comunidades de estafilococos, así como la abundancia relativa de *Staphylococcus spp.*, fue variable entre las zonas del cuerpo y en los gatos individuales muestreados.

Conclusiones y relevancia clínica – estos resultados demuestran que diversas comunidades de estafilococos habitan en la piel de gatos sanos y alérgicos, y proporcionan un punto de partida para futuras investigaciones sobre la importancia de *Staphylococcus spp.* en la enfermedad cutánea alérgica felina.

Zusammenfassung

Hintergrund – Es konnte gezeigt werden, dass verschiedene *Staphylococcus* Spezies eine wichtige Rolle auf der Haut spielen, so verursachen sie auch Erkrankungen und schützen den Wirt vor Krankheitserregern. Obwohl mittels Kultur-basierten Studien verschiedene *Staphylococcus spp.* von Katzenhaut isoliert werden konnten, ist sehr wenig bekannt über die Spezies-Level Arten auf dem Wirt.

Hypothese/Ziele – Die Beschreibung der Staphylokokken Spezies-Level Arten, die die Haut gesunder Katzen und die Haut von Katzen mit allergischer Dermatitis bewohnen.

Tiere – Es wurden Hauttupfer aus dem Ohrkanal und der Inguinalgegend von 11 gesunden und 10 allergischen (nicht-läsionalen) Katzen genommen.

Methoden und Materialien – Es wurde DNA von den Hauttupfern extrahiert und für die Next-Generation Sequenzierung verwendet, welche auf die V1-3 Region des 16s rRNA Gens abzielte. Nach einer Standard Mikrobiota Analyse der Sequenzierungsdaten wurden Spezies-Level Zuordnungen der Staphylokokken Sequenzen mittels einer Staphylokokken-spezifischen Datenbank erzielt.

Ergebnisse – *Staphylococcus spp.* zeigte eine ähnliche relative Häufigkeit bei gesunden wie auch bei allergischen Proben. Die am häufigsten vorkommende Staphylokokken Spezies waren *S. epidermidis* bei gesunden Proben und *S. felis* und *S. capitis* bei allergischen Proben. Die Zusammensetzung der Staphylokokken Arten sowie die relative Menge an *Staphylococcus spp.* war zwischen den verschiedenen Körperstellen und den individuellen Katzen, von denen Proben entnommen wurden, unterschiedlich.

Schlussfolgerungen und klinische Bedeutung – Diese Ergebnisse zeigen, dass diverse Staphylokokkenarten die Haut gesunder und allergischer Katzen bewohnen und stellen einen Ansatz für die weitere Forschung über die Wichtigkeit der *Staphylococcus spp.* bei Katzen mit allergischer Hauterkrankung dar.

要約

背景 – 様々なブドウ球菌種が、疾患の発生や病原体からの宿主の保護など、皮膚に重要な役割を果たすことが実証されている。培養ベースの研究は、猫の皮膚から様々なブドウ球菌属を分離しているが、宿主における種レベルのコミュニティについてはほとんど知られていない。

仮説/目的 – 本研究の目的は、健康猫およびアレルギー性皮膚炎の猫の皮膚に生息する種レベルのブドウ球菌コミュニティについて説明することであった。

供試動物 – 健康猫11頭およびアレルギー（非病変部位）猫11頭の外耳道および鼠径部の皮膚スワブを採取した。

材料と方法 – 皮膚スワブからDNAを抽出し、16s rRNA遺伝子のV1-3領域をターゲットとした次世代シーケンシングを使用した。シーケンスデータの標準的な微生物叢解析に続いて、ブドウ球菌固有のデータベースを使用し、ブドウ球菌シーケンスに対する種レベルの割当を取得した。

結果 – ブドウ球菌属は健康およびアレルギーサンプルで同様の相対量を有していた。最も豊富なブドウ球菌種は、健康サンプルでは*S. epidermidis*、アレルギーサンプルでは*S. felis*および*S. capitis*であった。ブドウ球菌コミュニティの組成およびブドウ球菌属の相対量は、身体部位および採取した個々の猫間で変動した。

結論と臨床的関連性 – 本研究結果は、様々なブドウ球菌コミュニティが健康およびアレルギー猫の皮膚に生息していることを示しており、猫のアレルギー性皮膚疾患におけるブドウ球菌属の重要性に関する

さらなる研究の出発点を提供している。

摘要

背景 — 已证实各种葡萄球菌在皮肤上发挥重要作用，包括引起疾病和保护宿主免受病原体的影响。尽管从猫皮肤分离培养的研究发现了各种葡萄球菌，但对该宿主身上菌种水平的群落仍知之甚少。

假设/目的 — 常驻在健康猫和过敏性皮炎猫皮肤上的葡萄球菌，对其菌种水平上的群落进行描述。

动物 — 对11只健康猫和10只过敏（无病变）猫的耳道和腹股沟皮肤棉签采样。

方法和材料 — 从皮肤棉签样本中提取DNA，使用针对16s rRNA基因V1-3区的新一代测序。对测序数据进行标准微生物群分析后，利用葡萄球菌特异性数据库，获得菌种水平上的葡萄球菌序列。

结果 — 健康和过敏猫的葡萄球菌相对丰度很相似。在健康样本的葡萄球菌中，丰度最高的菌种为表皮葡萄球菌，过敏样本中为猫链球菌和头葡萄球菌。葡萄球菌的群落组成，以及葡萄球菌的相对丰度，在不同采样的身体部位和个体猫之间存在差异。

结论和临床相关性 — 这些结果表明，健康和过敏猫皮肤上存在不同的葡萄球菌群落，并为猫过敏性皮肤病中的葡萄球菌，对其进一步研究的重要性提供了起点。

Resumo

Contexto — Várias espécies de *Staphylococcus* têm demonstrado desempenhar papéis importantes na pele, incluindo causar doenças e proteger o hospedeiro de patógenos. Embora estudos baseados em cultura tenham isolado diversos *Staphylococcus* spp. da pele de felinos, muito pouco se sabe sobre as comunidades em nível de espécie no hospedeiro.

Hipótese/objetivos — Descrever as comunidades estafilocócicas em nível de espécie que habitam a pele de gatos saudáveis e gatos com dermatite alérgica.

Animais — Foram obtidos swabs de pele do conduto auditivo e virilha de 11 gatos saudáveis e 10 alérgicos (alesionais).

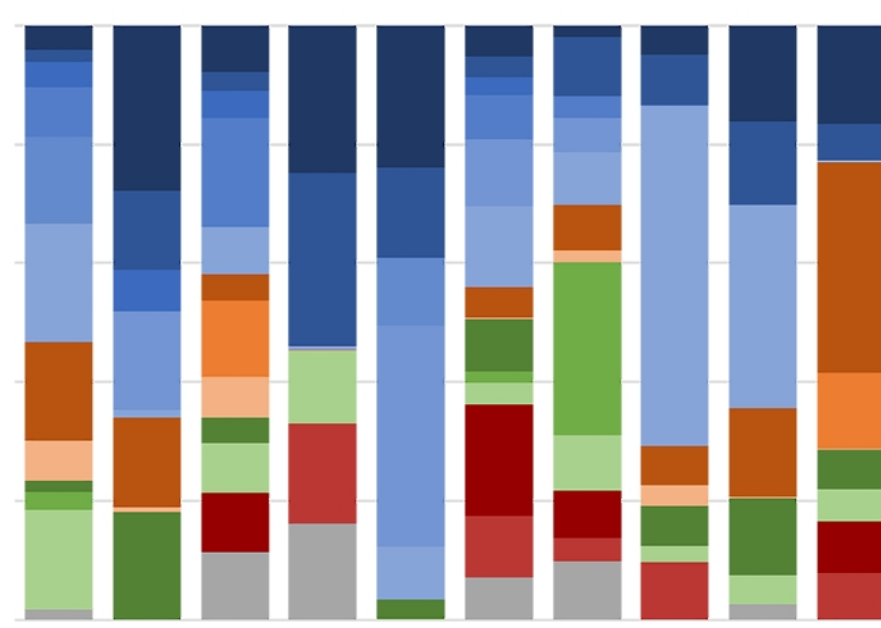
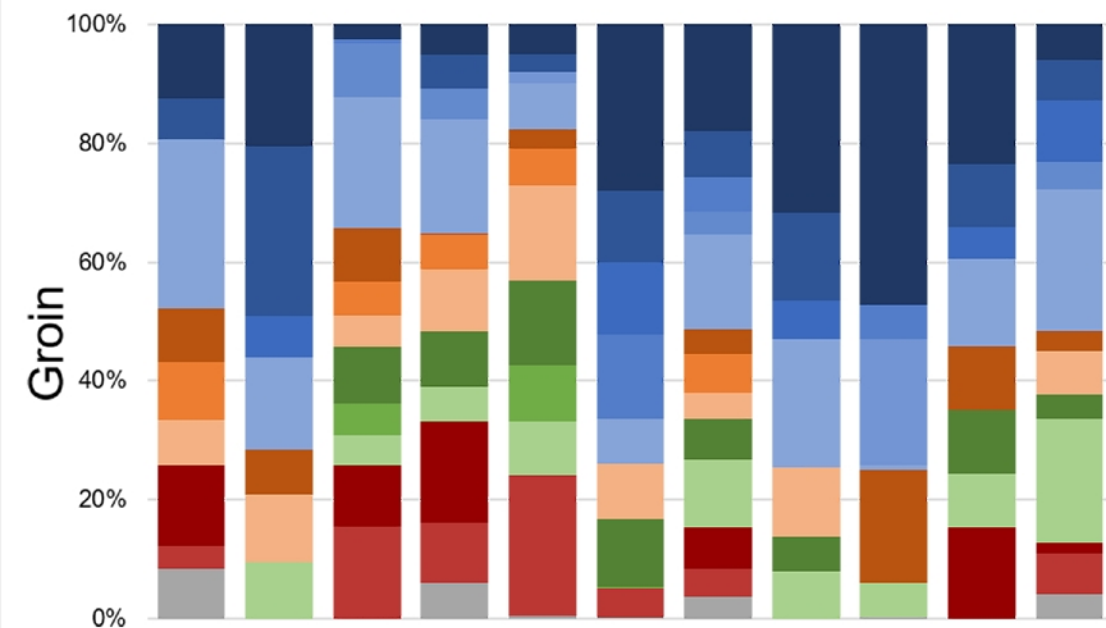
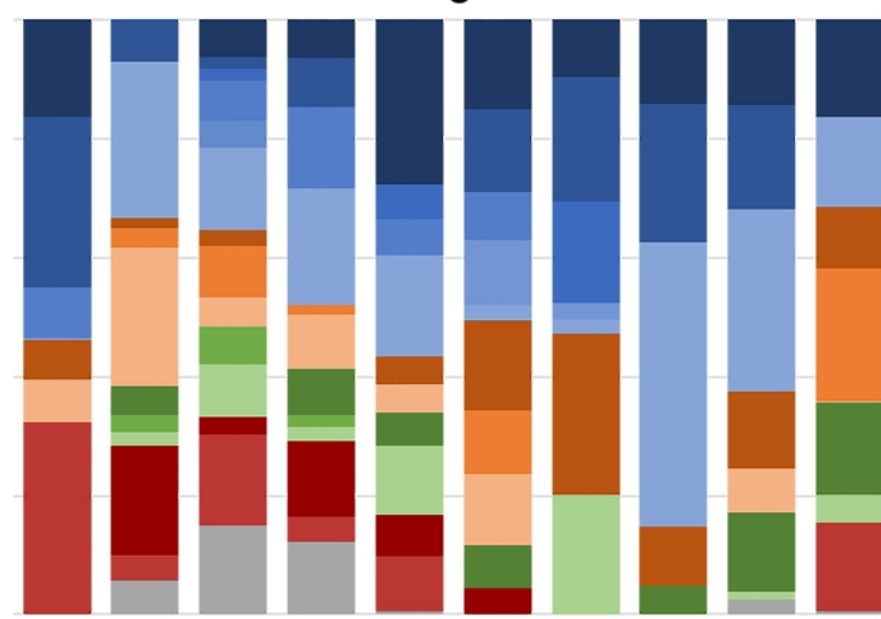
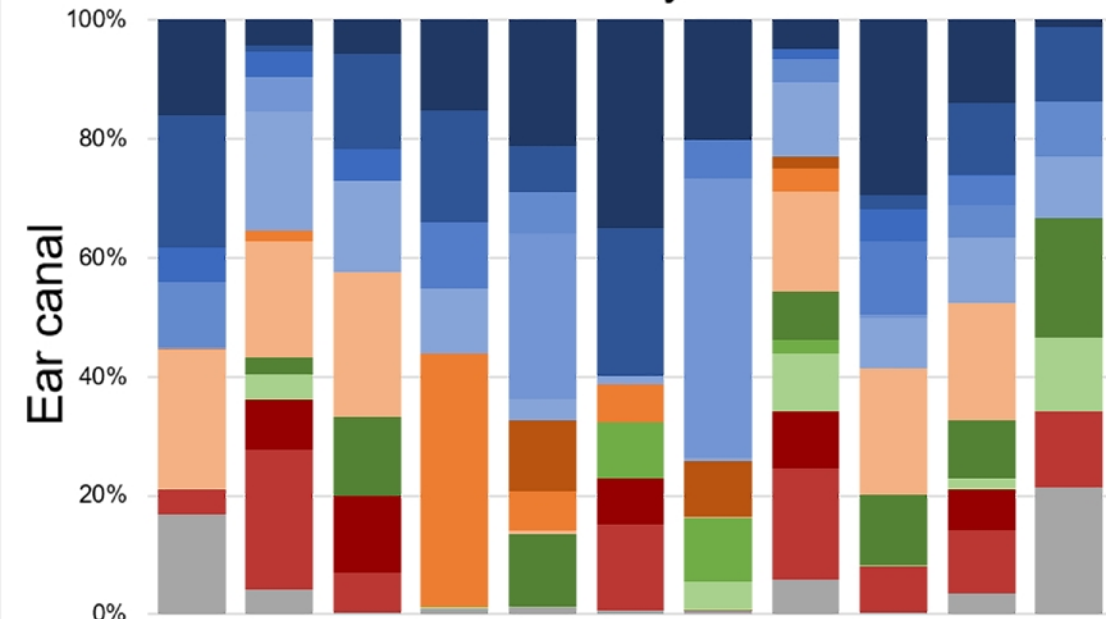
Métodos e materiais — O DNA foi extraído dos swabs de pele e utilizado para o sequenciamento de nova geração da região V1-3 do gene 16S rRNA. A partir uma análise de dados de microbiota padronizada para dados de sequenciamento, a atribuição em nível de espécie para as sequências estafilocócicas foi obtida usando um banco de dados específico para estafilococos.

Resultados — *Staphylococcus* spp. teve abundância relativa semelhante em amostras de gatos saudáveis e de alérgicos. As espécies estafilocócicas mais abundantes foram *S. epidermidis* em amostras de saudáveis e *S. felis* e *S. capitis* em amostras de alérgicos. A composição das comunidades estafilocócicas, bem como a abundância relativa de *Staphylococcus* spp., foi variável entre os locais do corpo e individualmente entre os gatos amostrados.

Conclusões e relevância clínica — Esses resultados demonstram que diversas comunidades estafilocócicas habitam a pele de gatos saudáveis e alérgicos e fornecem um ponto de partida para pesquisas futuras sobre a importância de *Staphylococcus* spp. na dermatite alérgica felina.

Healthy

Allergic



- Proteobacteria
- Bradyrhizobium*
 - Ralstonia*
 - Sphingomonas*
 - Pseudomonas*
 - Actinobacillus*
 - Delftia*
 - Other Proteobacteria
- Firmicutes
- Streptococcus*
 - Staphylococcus*
 - Other Firmicutes
- Actinobacteria
- Propionibacterium*
 - Corynebacterium*
 - Other Actinobacteria
- Bacteroidetes
- Porphyromonas*
 - Other Bacteroidetes
- Other bacteria

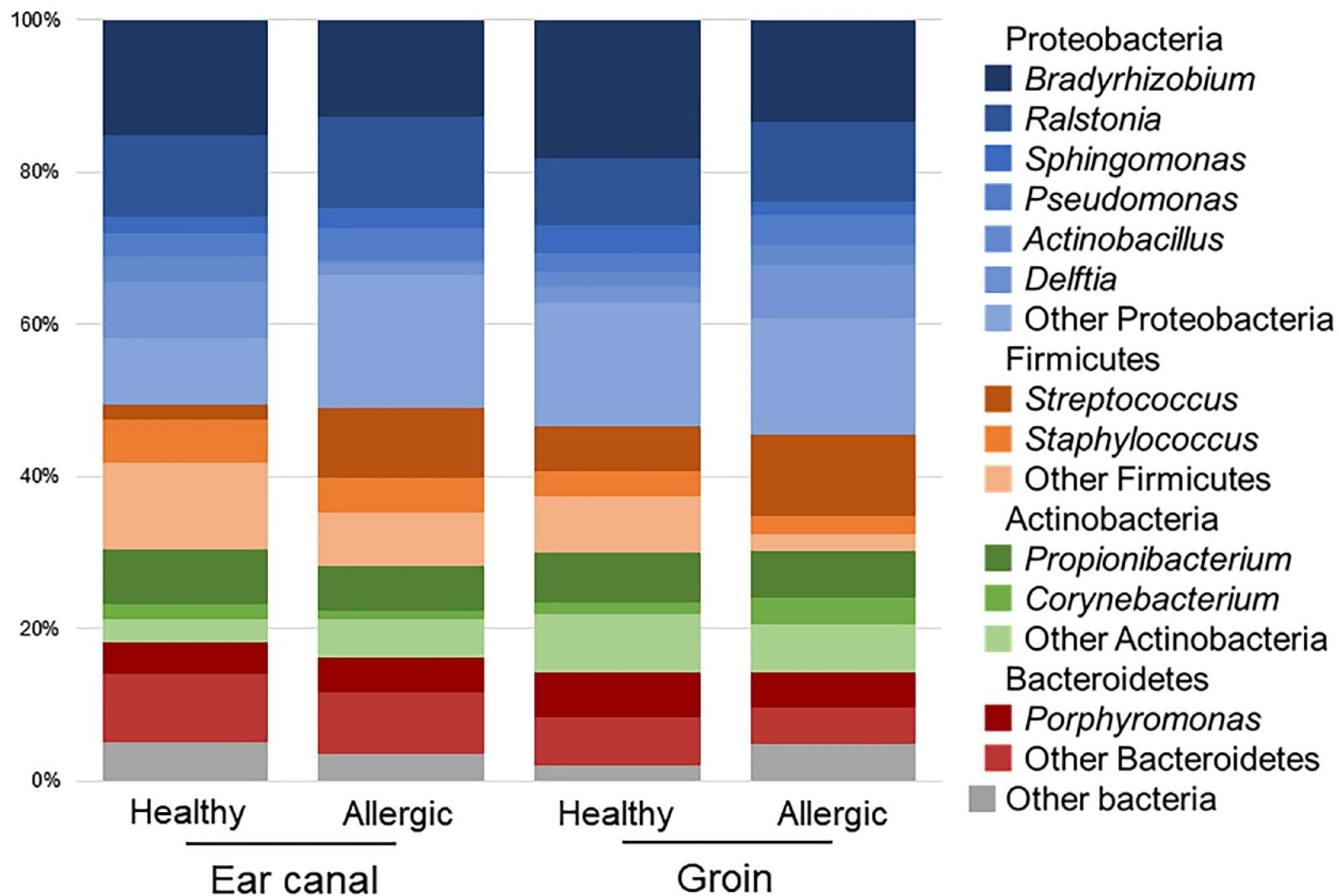


Table S1: Signalment of sample cohort.

Cat	Breed	Sex	Age	Indoor/Outdoor	Status
INC3	DSH	M	1y 4m	100/0	Healthy
INC4	DSH	M	10y	100/0	Healthy
INC5	DSH	F	3y	100/0	Healthy
INC6	DMH	F	6y	95/5	Healthy
INC7	DSH	CM	3y	100/0	Healthy
INC8	DSH	SF	9y	100/0	Healthy
INC9	DSH	SF	11y	98/2	Healthy
INC10	DSH	F	12y	100/0	Healthy
INC11	DSH	M	13y	100/0	Healthy
INC12	DSH	SF	3y	100/0	Healthy
INC13	DMH	CM	5y	100/0	Healthy
F12	DSH	CM	9y	100/0	Allergic
F13	Siamese	CM	8y	100/0	Allergic
F14	DSH	CM	11y	95/5	Allergic
F15	Siamese	SF	9y	100/0	Allergic
F16	DSH	SF	5y	60/40	Allergic
F17	DSH	SF	9y	100/0	Allergic
F18	Persian	CM	4y	100/0	Allergic
F19	DSH	SF	11y	95/5	Allergic
F20	DSH	SF	7y	100/0	Allergic
F21	DSH	SF	8y	95/5	Allergic