



## Heterologue Skin Microbiota Transplantation for Treatment of Sarcoptic Manges in Two Dogs with Zoonotic Transmission

Kerem URAL<sup>1</sup>, Hasan ERDOĞAN<sup>1</sup>, Songül ERDOĞAN<sup>1</sup>

<sup>1</sup>Department of Internal Medicine, Faculty of Veterinary Medicine, Aydın Adnan Menderes University, Aydın/TURKEY

◆ Geliş Tarihi/Received: 21.11.2022

◆ Kabul Tarihi/Accepted: 13.12.2022

◆ Yayın Tarihi/Published: 30.12.2022

**Bu makaleye atıfta bulunmak için/To cite this article:**

Ural K, Erdogan H, Erdoğan S. Heterologue Skin Microbiota Transplantation for Treatment of Sarcoptic Manges in Two Dogs with Zoonotic Transmission. Bozok Vet Sci (2022) 3, (2): 52-56.

**Abstract:** In the present case report, the authors inspected the feasibility of transferring unenriched (however moistured and pre-biotic treated) skin microbiota communities between two heterologous hosts, namely heterologue skin microbiota transplantation (hSmT), [from apparently healthy donor to other relevant and diseased dogs, with scabies, separately]. Two cross-bred, client-owned dogs (belonging to the same owners) with a diagnosis of scabies and intense pruritus were enrolled. Nivea Clear Up Strips were attached in a total of 3 various apparently healthy integumentary tissue of another donor dog and allowed to dry for 10-12 minutes. This was followed by peeling off, all 3 strips were then transferred to diseased skin tissue (laterolateral area in 2 dogs with scabies, separately) which were also irrigated with isotonic and allowed to attach for at least 12-15 minutes. Finally, all 3 strips were removed. Both in case I and II, Vas pruritus scores were decreased significantly beginning on day 0 (initial hSmT day) to days 21. Vas pruritus score ranged between 8-10 and 7-9, in case I and II, respectively, prior to hSmT [days -14 to day 0]. Prior to hSmT all skin scrape positivity were deemed available on days -14 to 0, whereas after day 2 of hSmT, all 2 dogs gave negative skin scraping results till the end of the study. It should not be unwise to draw preliminary conclusion that transfer of unenriched skin microbiota from a healthy donor to the diseased dogs with scabies, should have helped hastening clinical and parasitological recovery by manipulation of cutaneous microenvironment.

**Keywords:** Dog, Microbiome manipulation, Microbiome modulation, Skin microbiota transplantation

## Zoonotik Bulaşı olan İki Sarkoptik Uyuzlu Köpeğin Sağaltımında Heterojen Deri Mikrobiyota Transplantasyonu

**Özet:** Bu vaka raporunda yazarlar, iki heterolog konakçı arasında (görünüşe göre sağlıklı donörden diğer uyuzlu hasta köpeklere ayrı ayrı) zenginleştirilmemiş (ancak nemlendirilen ve probiyotik uygulanan) deri mikrobiyota topluluklarının transferinin (hDmT) uygulanabilirliğini inceledi. Uyuz tanısı konulan ve yoğun kaşıntısı bulunan sahipli (aynı hasta sahibine ait olan), melez ırkı 2 köpek çalışmaya dahil edildi. Nivea t bölgesi burun bantları, başka donör bir köpeğin görünüşte sağlıklı toplamda 3 farklı integümenter dokusuna yapıştırıldı ve 10-12 dakika kurumaya bırakıldı. Akabinde bantlar alınarak her 3 bant izotonik ile irriga edilen hasta deri dokusuna (her iki uyuzlu köpekte ayrı ayrı laterolateral bölgelere) yapıştırıldı en az 12-15 dakika yapışmasına izin verildi. Sonunda 3 bantta uzaklaştırıldı. Vas pruritus skorları, hem vaka I hem de II'de, 0. günden (hDmT başlangıç günü) 21. güne kadar önemli ölçüde azaldı. hDmT'den önce [-14. -(0.) günler] Vas kaşıntı skoru vaka I' de 8-10, vaka II' de 7-9 arasında değişmekteydi. hDmT'den önce, deri kazıntıları -14 ila 0. günlerde pozitif iken, hDmT'nin 2. gününden sonra, her iki köpekte çalışmanın sonuna kadar negatif elde edildi. Zenginleştirilmemiş deri mikrobiyotasının sağlıklı bir donörden hasta uyuzlu köpeklere aktarılmasının, deri mikroekolojisinin manipülasyonu ile klinik ve parazitolojik iyileşmeyi hızlandırmış olması gerektiği gibi bir ön yargıya varmak yanlış olmayacaktır.

**Anahtar Kelimeler:** Köpek, Mikrobiyom manipülasyonu, Mikrobiyom modülasyonu, Deri mikrobiyota transferi

### 1.Introduction

Resident skin microbiota is requisited for archetypal skin functioning, influencing the innate immune respond with prevention of colonization against probable pathogenic microorganisms (1). In several skin conditions, it has to be clearly elucidated whether if changes in the cutaneous microbiome are causative or a result of the cutaneous disorder itself (2).

Prior investigations regarding the influence of sarcoptic mange on the skin microbiome revealed decreased levels of microbial diversity, altered relative abundance along with elevated *Staphylococcus* spp. (3) with similar findings in humans, domestic/wildlife animals with scabies (4-7) and in dogs and humans with allergy (8-11). All aforementioned data confirmed disruption of microbial ecology might participate a major role within the pathogenesis of scabies. Given relevant data, this prompted us to perform this case series of 2 dogs with scabies with zoonotic transmission, in

which both dogs and owners were unresponsive to traditional treatment prior to referral, by veterinary surgeons on the field. Therefore in the present case report, the researchers investigated the feasibility of transferring unenriched skin microbiota communities between two heterologous hosts [from apparently healthy donor to other relevant and diseased dogs, with scabies, separately].

Apart from the purpose of our study, readers should fully inform about hSmT. The skin microbiota could be beneficially altered by several mechanisms. The foremost methodology is hSmT. During hSmT, cutaneous microbiome belonging to a healthy person is transmitted to washed/ disinfected cutaneous location of another person in an attempt to modulate dermatological condition of the latter. This methodology has both advantages and disadvantages [cutaneous microecology is transmitted with its natural environment vs. solely a few bacteria could be collected from an individual skin] (12).

## 2. Case Presentation

Written owner consent was deemed available for all participant dogs. Day 0 was defined as initial day for heterolog skin microbiota transplantation (hSmT) and it was repeated twice (second application was on day 5). Prior values were analyzed by the help of responsible veterinary surgeon at field conditions (day -14 to day 0 analytes).



**Figure 1:** Clear up test strips were used as hSmT vehicle at this study.

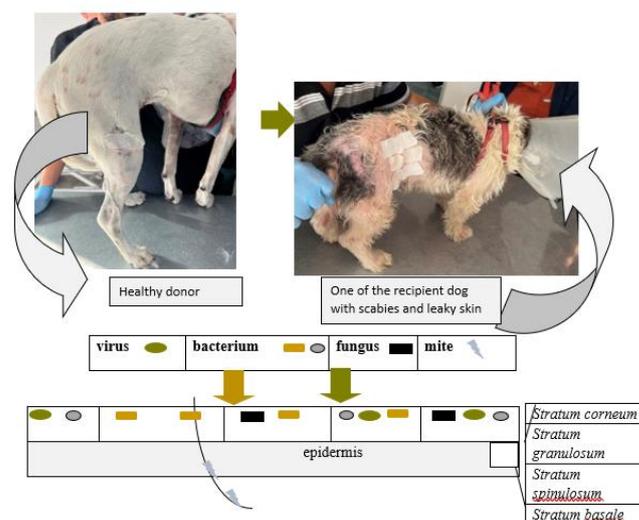
### 2.1. Demographic data

Two cross-bred (n=2) client-owned dogs (belonging to the same owners) living at the center of Aydin Municipality) at the age of 2.5 and 4 years old, of both sexes and various sizes with a diagnosis of scabies on referral to Aydin Adnan Menderes University, Faculty of Veterinary, Department of Internal Medicine Clinics. Two dogs, with intense pruritus for several days, beginning from the starting point of housing process, were lived in the same closure. Clinical signs compatible with scabies involved regional/local alopecia, severe erythema, crusts, and scaling localized widely in one of the dogs and mildly involved the other one.

Diagnosis of scabies was mainly based on i) rule out of other relevant skin conditions, ii) cytology, skin scraping, [superficial skin scrapings were withdrawn to those of lesional areas in which exhibited the occurrence of numerous live *S. scabiei* mites in two of the dogs) and iii dermatoscopic analytes. Other relevant supportive analytes involved Vas pruritus score, pruritus triage (field version), skin scrape positivity.

### 2.2. Skin microbiota transplantation by use of Nivea Clear Up Strips

Nivea Clear Up Strips were unboxed from its original version which was followed by separation of each different strip. In a total of 3 various apparently healthy integumentary tissue with evidence of hair growth [without any skin lesions], the strips were located at moistened skin (Bepanthol Sensiderm Cream, Bayer, Turkey) and allowed to dry for 10-12 minutes. Healthy donor was participated due to its well-recognized history, clinical findings and health status. This was followed by peeling off, all 3 strips were then transferred to diseased skin tissue laterolateral area in 2 dogs with scabies, separately) which were also irrigated with isotonic and allowed to attach for at least 2-15 minutes (Fig 2.). At last step all 3 strips were removed. There were no side effects were noticed in 2 dogs were subjected to hSmT.



**Figure 2:** Skin microbiota transplantation (heterologue in origin as defined by apparently healthy donor to diseased one) from the donor to the recipient, as involved at this study. Schematic representation was adopted and transformed from (22). Self-photos belong to the first authors' archive of this study. Days 0 and 5 were the selected timeline for hSmT, which meant the application was available for twice.

### 2.3. Parasitological and clinical cure

Parasitological and clinical cure were detected by biomarkers of composite analytes involving skin scraping

results, Vas pruritus scores and triage coloring. Interestingly owners were also cured following treatment of both dogs, despite previous therapeutical drug applications (medical doctors for owners, referring veterinary surgeon for dogs) without success.



**Figure 3:** Case I at referral (prior to hSmT) on day 0 (a), 5 (b) and 10 (c), respectively thereafter hSmT. No more pruritus was evident.



**Figure 4:** Two dogs enrolled at this study and subjected to hSmT with photographic records obtained on days a) 0 and b) 10. There was no more pruritus, which was one of the criteria for treatment success.

#### 2.4. Composite analytes

Biomarkers as selected, in an attempt to supportive diagnosis, were composed of Vas pruritus scores, skin scrape results and triage levels of pruritus. Both in case I and II, Vas pruritus scores were diminished beginning on day 0 (initial hSmT day) to days 21. Vas pruritus score ranged between 8-10 and 7-9, in case I and II, respectively, prior to hSmT [days -14 to day 0]. Triage levels of pruritus altered from black code to green code in respond to hSmT application. Skin scraping results were deemed negative after day 2 in each case (Fig 5) as shown below. Prior to hSmT all skin scrape positivity were dammed available on days -14 to 0 (Fig 5).

Days	-14	-10	-5	-3	0	2	5	10	21
Case I-Vas pruritus scores	10	10	9	8	9	2	0	0	0
Skin scrape positivity	+	+	+	+	+	+	-	-	-
Triage level of pruritus	Black	Black	Black	Red	Black	Green	Green	Green	Green
Case II-Vas pruritus scores	8	7	9	8	8	1	0	0	0
Skin scrape positivity	+	+	+	+	+	+	-	-	-
Triage level of pruritus	Black	Red	Black	Black	Black	Green	Green	Green	Green

**Figure 5:** Showing Vas pruritus scores, skin scrape positivity and triage level of pruritus among 2 dogs with zoonotic *S. scabiei* invasion.

### 3. Discussion and Conclusion

Considering interaction among microbes and mange, diminished microbial variation and elevated pathogenic abundance is compatible with people invased with *S. scabiei* var. *hominis* (13, 14), pigs exploratory infected with *S. scabiei* var. *suis* (3) and dogs/humans presenting allergic integumentary diseases (8, 10, 11, 15). Hence determination of opportunistic pathogens could alter due to host, *Staphylococcus* spp. and *Streptococcus* spp. were frequently encountered. Host existence of mite, ease secondary bacterial invasion via secretion of proteins hindering complement system, that is well recognized as critical participant within the immune respond against mite/bacterial infection (16-18). Mite scrape, in which primary/secondary dermatological signs could thus offer absolute environmental factors for proliferation of opportunistic pathogens. In a prior study analyzing the interaction among mites and microbes to those of 3 different canid species with *S. scabiei* invasion, the principal microbial taxa in relationship with mange exhibited *S. pseudintermedius* and *Corynebacterium* spp., along with *S. agalactiae* [with relevant *Staphylococcus* spp.] significantly altered in abundance. *S. scabiei* invasion in human and pigs demonstrated elevated abundance of *S. aureus* (3, 13). In the present study although cutaneous microbiota was not analyzed (no financial support) hSmT could have helped hastening clinical recovery by probable amelioration of pathogenic bacteria evolved within scabies on to the lesional area.

Previous researches investigating the influence of sarcoptic mange on the skin microbiota, experimental *S. scabiei* var. *suis* invasion of pigs exhibited diminished levels of microbial diversity, changed relative abundance along with elevated *Staphylococcus* spp. (3). Equivalent findings were also detected in humans, domestic/wildlife animals with scabies (4-7) and in dogs and humans with allergic skin conditions [i.e. atopic dermatitis] (8-11). This evidence

suggests that disrupted microbial communities may play a key role in the pathogenesis of sarcoptic mange. In the present study treatment respond with hSmT could be capable of reversing disruption of cutaneous microenvironment by transplantation of beneficial bacteria from healthy donor to the recipient dogs with scabies.

Regarding this context, this case control study asks whether if moving superficial cutaneous microbial communities from a healthy donor to diseased dogs with scabies is feasible or not. This briefly clinical design relied on leaky skin among 2 dogs with scabies and the topographical differences of skin microbiota in each host. We selected sites with a contrasting microbial composition, the hindfeet vs. forefeet, or stifle vs. elbow., as reported previously for human (19). Treatment efficacy was based on negative skin scraping, pruritus triage alterations (color changes as was based on Vas pruritus scores).

In parallel line with therapeutical approach for digestive system disorders with bacterial communities, therapy of integumentary system disorders with microbial transplantation is exhibiting evolution and able to bestow an encouraging approach for therapeutical armamentarium against skin disorders (20, 21). The malodor-causing microbiota was detached via antibacterial compounds and substituted with a cutaneous micro-ecologic niche withdrawn from a non-odorous donor (22). It should be kept in mind that it is unclear that the transplanted bacteria could be capable of stably colonizing the skin. Briefly hSmT could be inadequate for colonization (23) thus, expanded transplantation practices might be warranted (22).

Someone might criticize our study as because of hSmT with an unenriched microbiota substituted lesional areas in 2 dogs with scabies. First of all sometimes the clinician is in a hurry up position due to animal owner attitude and extraordinary behavior. The vast majority of owners lost their time, patient and respect due to economic burden and time wasting treatment trials of prior referrals. For instance, the animal owner involved and participated in each clinical session were presenting sleep disturbance due to itching behavior by themselves. This prompted us to seek for a quick response, in which first author of the study [K.U. (has planned, applied)]. This was due to zoonotic transmission, at the same time, prior to hSmT performed by ourselves (experience of the authors of this manuscript) and several treatment applications were evident (medical doctors for owners and responsible veterinary surgeons for dogs enrolled herein) without evidence of satisfactory results. As was shown in fig. 5. prior to hSmT (days -14 to day 0) triage colors, Vas pruritus scores were remained exactly at the same level, indicating unsatisfactory therapeutical interventions. Hence skin scraping results were all deemed positive from day -14 to day 0. Contrarily with the beginning and application of hSmT parasitological and

clinical cure were both evident. This treatment modality would be a substitute for several old therapeutical interventions. Our competing interest should be warranted with further studies.

## References

1. Wanke I, Steffen H, Christ C, Krismer B, Götz F, Peschel A, Schitteck B. Skin commensals amplify the innate immune response to pathogens by activation of distinct signaling pathways. *Journal of Investigative Dermatology* 2011; 131(2): 382-390. doi:10.1038/jid.2010.328.
2. Zeeuwen PL, Boekhorst J, van den Bogaard EH, de Koning HD, van de Kerkhof P, Saulnier DM, Timmerman HM. Microbiome dynamics of human epidermis following skin barrier disruption. *Genome Biology* 2012; 13(11): 1-18. doi:10.1186/gb-2012-13-11-r101.
3. Swe PM, Zakrzewski M, Kelly A, Krause L, Fischer K. Scabies mites alter the skin microbiome and promote growth of opportunistic pathogens in a porcine model. *PLOS Neglected Tropical Diseases* 2014; 8: e2897. doi:10.1371/journal.pntd.0002897.
4. Walton SF, Holt DC, Currie BJ, Kemp DJ. Scabies: new future for a neglected disease. *Advances in Parasitology* 2004; 57(57): 309-76.
5. Hengge UR, Currie BJ, Jäger G, Lupi O, Schwartz RA. Scabies: a ubiquitous neglected skin disease. *The Lancet Infectious Diseases* 2006; 6(12): 769-779.
6. Almberg ES, Cross PC, Dobson AP, Smith DW, Hudson PJ. Parasite invasion following host reintroduction: a case study of Yellowstone's wolves. *Philosophical Transactions of the Royal Society B: Biological Sciences* 2012; 367(1604): 2840-2851. doi:10.1098/rstb.2011.0369.
7. Fraser TA, Charleston M, Martin A, Polkinghorne A, Carver S. The emergence of sarcoptic mange in Australian wildlife: an unresolved debate. *Parasites & Vectors* 2016; 9(1): 1-11.
8. Kong HH, Oh J, Deming C, Conlan S, Grice EA, Beatson MA, Segre JA. Temporal shifts in the skin microbiome associated with disease flares and treatment in children with atopic dermatitis. *Genome Research* 2012; 22(5): 850-859. doi: 10.1101/gr.131029.111.
9. Rodrigues Hoffmann A, Patterson AP, Diesel A, Lawhon SD, Ly HJ, Stephenson CE, Suchodolski JS. The skin microbiome in healthy and allergic dogs. *PloS One*, 2014; 9(1): e83197. doi:10.1371/journal.pone.0083197.
10. Williams MR, Gallo RL. The role of the skin microbiome in atopic dermatitis. *Current Allergy AND Asthma Reports* 2015; 15(11): 1-10. doi:10.1007/s11882-015-0567-4.
11. Bradley CW, Morris DO, Rankin SC, Cain CL, Mistic AM, Houser T, Grice EA. Longitudinal evaluation of the skin microbiome and association with microenvironment and treatment in canine atopic dermatitis. *Journal of Investigative Dermatology* 2016; 136(6): 1182-1190. doi: 10.1016/j.jid.2016.01.023.
12. Callewaert C, Knödseder N, Karoglan A, Güell M, Paetzold B. Skin microbiome transplantation and manipulation: Current state of the art. *Computational and Structural Biotechnology Journal* 2021; 19: 624-631. doi:10.1016/j.csbj.2021.01.001.
13. Whitehall J, Kuzulugil D, Sheldrick K, Wood A. Burden of paediatric pyoderma and scabies in North West Queensland. *Journal of Paediatrics and Child Health* 2013; 49(2): 141-143. doi:10.1111/jpc.12095.

14. McCarthy JS, Kemp DJ, Walton SF, Currie BJ. Scabies: more than just an irritation. *Postgraduate Medical Journal* 2004; 80(945): 382-387.
15. Wolina U, Hipler UC, Nenoff P. Trichobacteriosis, erythrasma and pitted keratolysis—the spectrum of non-diphtheroid *Corynebacteria*. *Romanian Journal of Clinical and Experimental Dermatology*, 2017; 4(2):64-67.
16. Swe PM, Fischer K. A scabies mite serpin interferes with complement-mediated neutrophil functions and promotes staphylococcal growth. *PLoS Neglected Tropical Diseases* 2014; 8(6): e2928. doi:10.1371/journal.pntd.0002928.
17. Mika A, Reynolds SL, Pickering D, McMillan D, Sriprakash KS, Kemp DJ, Fischer K. Complement inhibitors from scabies mites promote streptococcal growth—a novel mechanism in infected epidermis?. *PLoS neglected Tropical Diseases* 2012; 6(7): e1563. doi:10.1371/journal.pntd.0001563.
18. Bergström FC, Reynolds S, Johnstone M, Pike RN, Buckle AM, Kemp DJ, Blom AM. Scabies mite inactivated serine protease paralogs inhibit the human complement system. *The Journal of Immunology* 2009; 182(12): 7809-7817. doi:10.4049/jimmunol.0804205.
19. Grice EA, Kong HH, Conlan S, Deming CB, Davis J, Young AC, Segre JA. Topographical and temporal diversity of the human skin microbiome. *Science* 2009; 324(5931): 1190-1192. doi: 10.1126/science.117170.
20. Myles IA, Earland NJ, Anderson ED, Moore IN, Kieh MD, Williams KW, Datta SK. First-in-human topical microbiome transplantation with *Roseomonas mucosa* for atopic dermatitis. *JCI Insight* 2018; 3(9). doi: 10.1172/jci.insight.120608.
21. Paetzold B, Willis JR, Pereira de Lima J, Knödlseher N, Brüggemann H, Quist S. R, Güell M. Skin microbiome modulation induced by probiotic solutions. *Microbiome* 2019; 7(1), 1-9. doi:10.1186/s40168-019-0709-3.
22. Ito Y, Amagai M. Controlling skin microbiome as a new bacteriotherapy for inflammatory skin diseases. *Inflammation and Regeneration* 2022; 42(1): 1-13. doi: 10.1186/s41232-022-00212y.
23. Perin B, Addetia A, Qin X. Transfer of skin microbiota between two dissimilar autologous microenvironments: A pilot study. *PLoS One* 2019; 14(12): e0226857. doi:10.1371/journal.pone.0226857.