

Supplementary Materials

Spatiotemporal dynamics of the microbial diversity on salt-preserved goatskins assessed by culturing and 16S rRNA gene amplicon sequencing

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Table S1 Comparison results of 45 protease-producing strains in EzBioCloud database

Strains	Genera	The most similar bacterium	Highest similarity	GenBank numbers
L1	<i>Bacillus</i>	<i>Bacillus seohaeanensis</i> BH724 ^T	99.86%	MT516442
L2	<i>Chryseobacterium</i>	<i>Chryseobacterium indologenes</i> RH542 ^T	99.00%	MT516454
L3	<i>Salinicola</i>	<i>Salinicola lusitanus</i> CR50 ^T	99.45%	MN099427
L4	<i>Aeromonas</i>	<i>Aeromonas bestiarum</i> CECT 4227 ^T	100.00%	MT516456
L5	<i>Halomonas</i>	<i>Halomonas saliphila</i> CGMCC 1.15818 ^T	98.83%	MN099429
L6	<i>Halobacillus</i>	<i>Halobacillus dabanensis</i> D-8 ^T	99.58%	MT516457
L7	<i>Virgibacillus</i>	<i>Virgibacillus salarius</i> SA-Vb1 ^T	99.86%	MT516474
L8	<i>Virgibacillus</i>	<i>Virgibacillus halodenitrificans</i> LMG 9818 ^T	99.86%	MT516475
L9	<i>Ornithinibacillus</i>	<i>Oceanobacillus limi</i> H9B ^T	98.22%	MN577409
L10	<i>Staphylococcus</i>	<i>Staphylococcus lentus</i> ATCC 29070 ^T	99.93%	MT516467
L11	<i>Staphylococcus</i>	<i>Staphylococcus sciuri</i> DSM 20345 ^T	99.93%	MT516468
L12	<i>Piscibacillus</i>	<i>Piscibacillus halophilus</i> HS224 ^T	99.79%	MT516465
L13	<i>Bacillus</i>	<i>Bacillus marisflavi</i> JCM 11544 ^T	99.79%	MT516443
L14	<i>Kocuria</i>	<i>Kocuria rosea</i> DSM 20447 ^T	99.57%	MT516480
L15	<i>Virgibacillus</i>	<i>Virgibacillus marismortui</i> 123 ^T	99.32%	MT516476
L16	<i>Halobacillus</i>	<i>Halobacillus litoralis</i> SL-4 ^T	99.44%	MT516458
L17	<i>Staphylococcus</i>	<i>Staphylococcus pseudoxylus</i> S04009 ^T	99.93%	MT516471
L18	<i>Bacillus</i>	<i>Bacillus paranthracis</i> Mn5 ^T	99.30%	MT516451
L19	<i>Bacillus</i>	<i>Bacillus atrophaeus</i> JCM 9070 ^T	99.58%	No data
L20	<i>Citricoccus</i>	<i>Citricoccus nitrophenolicus</i> PNP1 ^T	99.50%	MT516479
L21	<i>Bacillus</i>	<i>Bacillus siamensis</i> KCTC 13613 ^T	99.93%	MT516448
L22	<i>Bacillus</i>	<i>Bacillus atrophaeus</i> JCM 9070 ^T	99.86%	MT516444
L23	<i>Bacillus</i>	<i>Bacillus paralicheniformis</i> KJ-16 ^T	100.00%	MT516447
L24	<i>Oceanobacillus</i>	<i>Oceanobacillus limi</i> H9B ^T	100.00%	MT516464
L25	<i>Halobacillus</i>	<i>Halobacillus sediminis</i> NGS-3 ^T	99.31%	MT516460
L26	<i>Halobacillus</i>	<i>Halobacillus sediminis</i> NGS-2 ^T	99.65%	MT516459
L27	<i>Bacillus</i>	<i>Bacillus aryabhatai</i> B8W22 ^T	99.51%	MT516449
L28	<i>Bacillus</i>	<i>Bacillus zanthoxyli</i> 1433 ^T	99.65%	MT516450
L29	<i>Comamonas</i>	<i>Comamonas testosteroni</i> ATCC 11996 ^T	99.71%	MT516453
L31	<i>Oceanobacillus</i>	<i>Oceanobacillus jeddahense</i> S5 ^T	99.24%	MT516461

L32	<i>Virgibacillus</i>	<i>Virgibacillus halodenitrificans</i> LMG 9818 ^T	100.00%	MT516477
L33	<i>Arthrobacter</i>	<i>Arthrobacter pascens</i> DSM 20545 ^T	99.64%	MT516441
L34	<i>Erwinia</i>	<i>Erwinia tasmaniensis</i> Et1/99 ^T	98.87%	MT516455
L35	<i>Bacillus</i>	<i>Bacillus velezensis</i> CR-502 ^T	99.35%	MT516452
L36	<i>Bacillus</i>	<i>Bacillus tequilensis</i> KCTC 13622 ^T	99.72%	No data
L38	<i>Oceanobacillus</i>	<i>Oceanobacillus picture</i> LMG 19492 ^T	99.24%	MT516462
L39	<i>Staphylococcus</i>	<i>Staphylococcus xylosus</i> CCM 2738 ^T	99.65%	MT516472
L40	<i>Oceanobacillus</i>	<i>Oceanobacillus aidingensis</i> AD7-25 ^T	100.00%	MT516463
L41	<i>Staphylococcus</i>	<i>Staphylococcus pseudoxylosus</i> S04009 ^T	99.23%	MT516473
L72	<i>Bacillus</i>	<i>Bacillus swezeyi</i> NRRL B-41294 ^T	99.72%	MT516446
L81	<i>Nocardiopsis</i>	<i>Nocardiopsis deserti</i> H13 ^T	99.22%	MT516478
L82	<i>Staphylococcus</i>	<i>Staphylococcus nepalensis</i> NCTC 13834 ^T	99.71%	MT516469
L93	<i>Salinicoccus</i>	<i>Salinicoccus amylolyticus</i> JC304 ^T	99.81%	MT516466
L111	<i>Bacillus</i>	<i>Bacillus siamensis</i> KCTC 13613 ^T	99.79%	MT516445
L152	<i>Staphylococcus</i>	<i>Staphylococcus ureilyticus</i> ATCC 49330 ^T	99.65%	MT516470

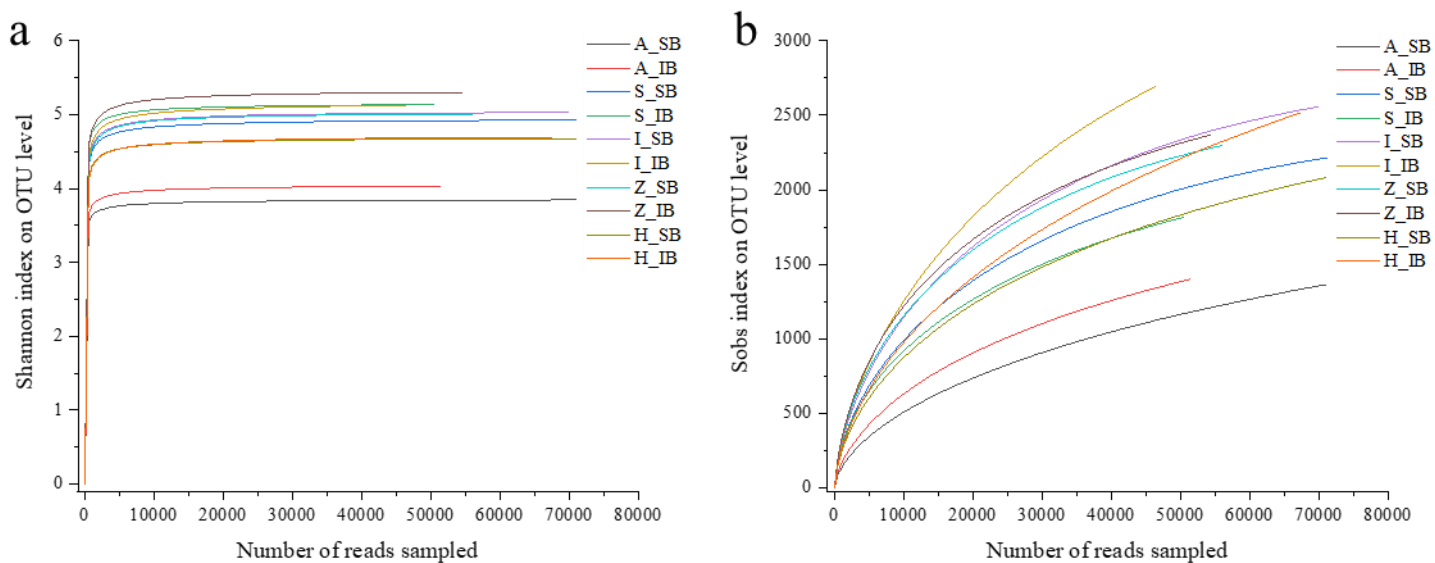


Fig. S1. Rarefaction curves of 16S rRNA gene sequencing of the wet-salted ovine skins from five areas. a: the rarefaction curve was assembled using Shannon index; b: the rarefaction curve was executed using Sobs algorithm. A, S, I, Z and H represent Australia, Spain, Inner Mongolia (China), Zhejiang Province (China) and Hebei Province (China), respectively. SB and IB indicate the surface and the inside of the wet-salted ovine skins, respectively.

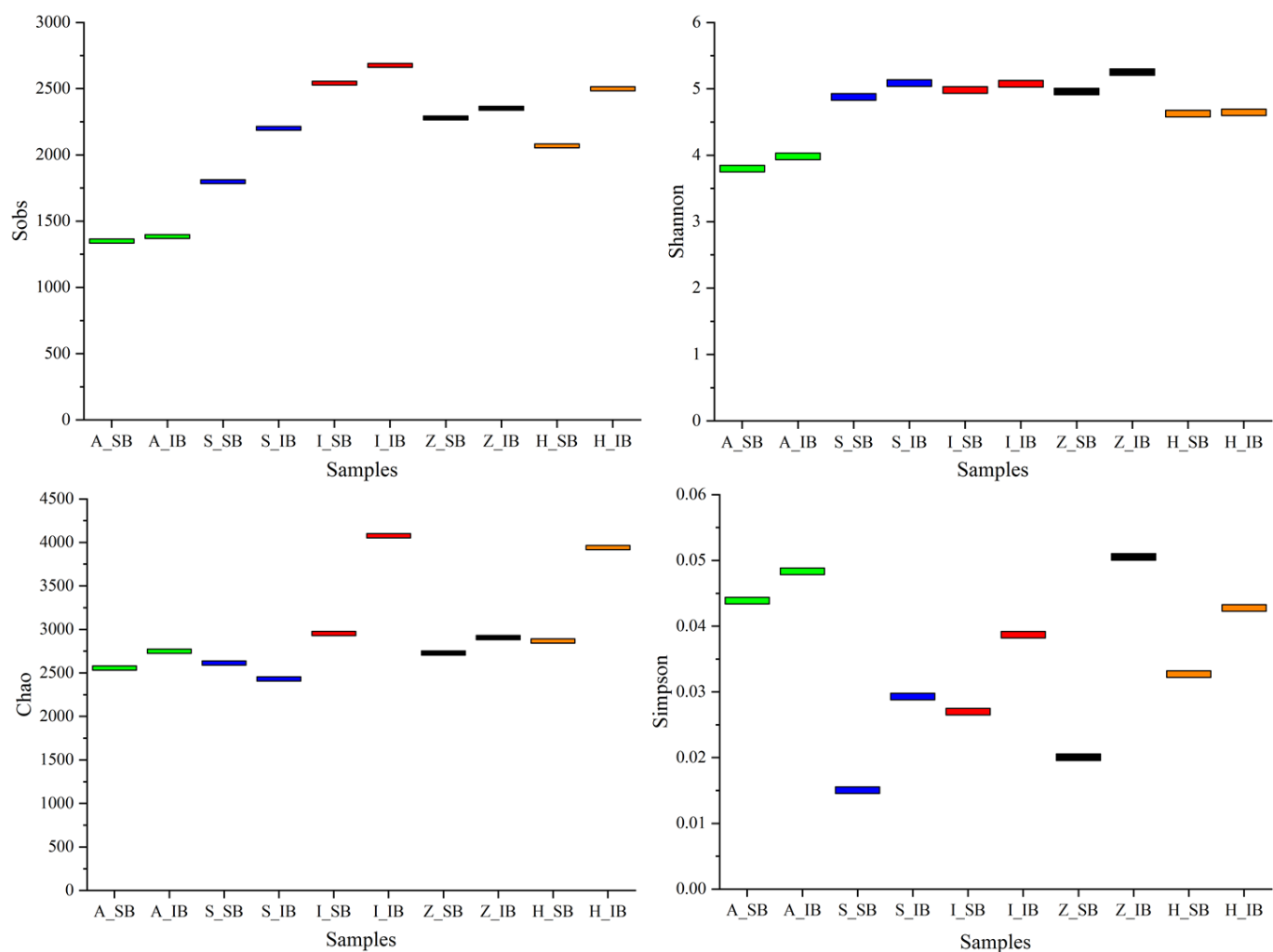


Fig. S2. Alpha diversity analysis of microorganisms present in the interior and exterior of wet-salted ovine skins from five different areas at indices Sobs, Shannon, Chao and Simpson. A, S, I, Z and H represent Australia, Spain, Inner Mongolia (China), Zhejiang Province (China) and Hebei Province (China), respectively. SB and IB indicate the surface and the inside of the wet-salted ovine skins, respectively.

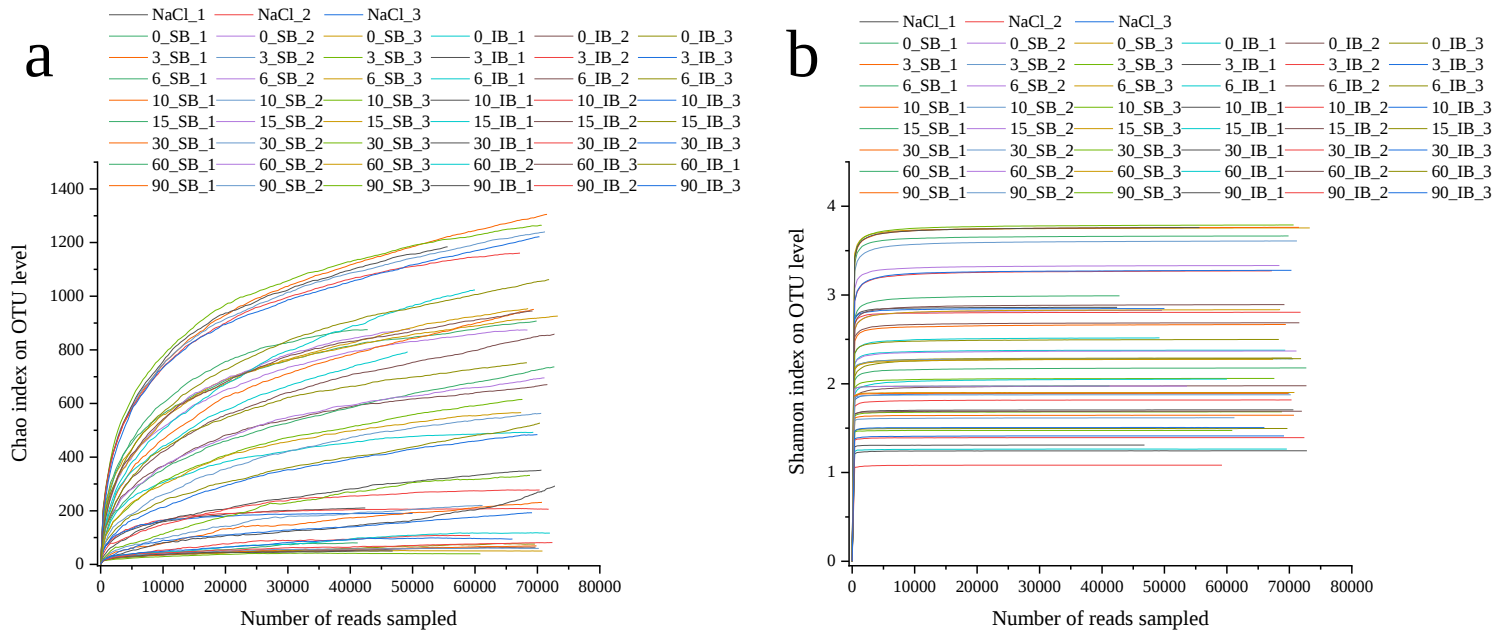


Fig. S3. Dilution curves of Chao (a) and Shannon (b) indices for microbial communities in homemade salt-preserved goatskin.

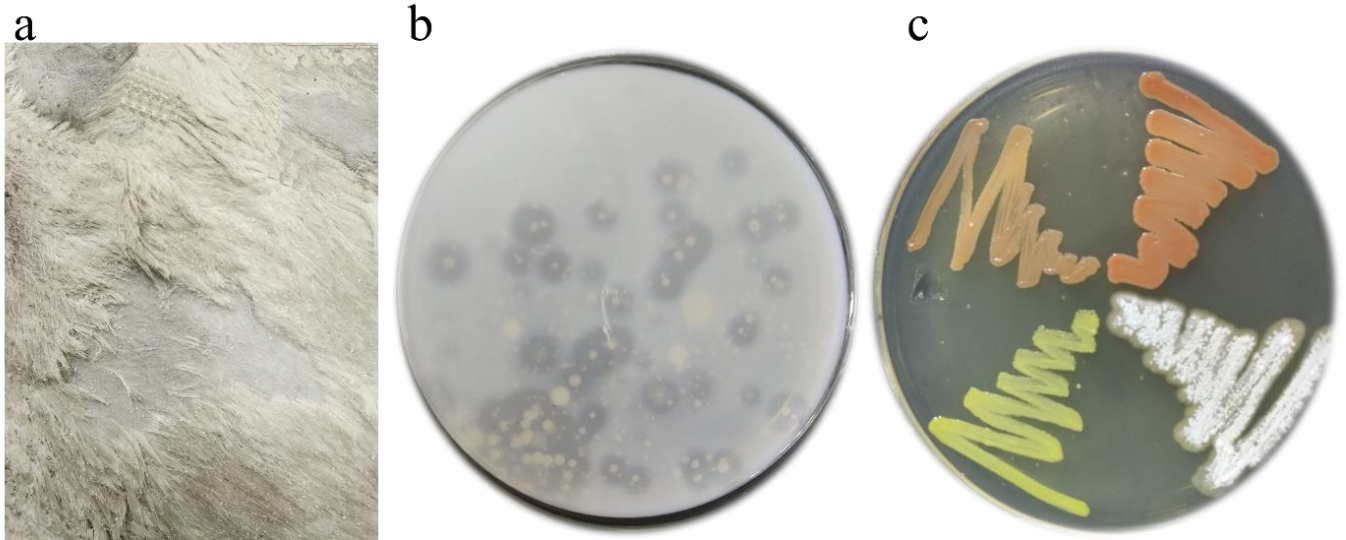


Fig. S4. Screening and characterization of protease-producing bacteria: a, localized dehairing of wet-salted goatskin; b, milk plate hydrolysis circle screening bacteria; c, characterization of protease-producing bacteria on the modified LB plates.