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Research Article 研究报告

餐厨垃圾处理园区微生物群落结构与潜在功能

徐正琪[1,2]，彭星[3]，谢松[1,3]，易志刚[3]，袁李云[3]，赵庆松[3]，尹常凯[3]，刘妍好[1,2]，李骞[1]，尹华群[1,2]，孟德龙[1,2*]

1 中南大学 资源加工与生物工程学院，湖南 长沙
2 生物冶金教育部重点实验室，湖南 长沙
3 湖南仁和环保科技有限公司，湖南 长沙

徐正琪, 彭星, 谢松, 易志刚, 袁李云, 赵庆松, 尹常凯, 刘妍好, 李骞, 尹华群, 孟德龙．餐厨垃圾处理园区微生物群落结构与潜在功能[J]．微生物学报, 2025, 65(10): 4444-4457．
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摘　要：【目的】微生物在餐厨垃圾处理过程中扮演重要角色，深入解析其群落结构与功能特征有助于优化工艺流程、提升处理效率。【方法】采用 16S rRNA 基因扩增子高通量测序技术研究餐厨垃圾处理园区厌氧发酵系统、污水处理系统及空气净化系统(生物滤床和除臭塔)的微生物群落特征及潜在功能。【结果】各处理系统微生物群落多样性与组成显著不同：厌氧发酵系统多样性及丰富度较低，主要受温度、pH、生化需氧量(biochemical oxygen demand, BOD)等环境因子共同影响；功能分析表明，园区微生物以有机降解为主，厌氧发酵系统富集废水孢菌属(*Defluviitoga*)、甲烷热杆菌属(*Methanothermobacter*)和慢生微菌属(*Lentimicrobium*)，参与水解发酵与产甲烷过程；污水处理系统以 *Candidatus*_Anammoximicrobium、硝酸盐矛状菌属(*Nitrolancea*)和楚帕氏菌属(*Truepera*)为主，驱动有机物降解与氮素转化(如厌氧氨氧化、硝化-反硝化)；空气净化系统富集金黄杆菌属(*Chryseobacterium*)和副球菌属(*Paracoccus*)等，参与生物膜形成及挥发性有机物、硫化物降解代谢。【结论】各系统微生物群落特征与工艺条件密切相关，功能菌群富集指向其生态功能定位：厌氧发酵系统中产甲烷菌与协同降解菌共驱有机质转化与甲烷生成；污水处理系统氮循环相关菌群保障污染物高效去除；空气净化系统通过富集异养有机物降解菌及代谢复杂硫化物菌属[如鞘氨醇菌属(*Sphingobium*)、黄杆菌属(*Flavobacterium*)]提升除臭效率。本研究为餐厨垃圾处理中微生物功能调控与工程优化提供了理论支撑。

关键词：餐厨垃圾；微生物群落；功能预测；16S rRNA 基因分析；厌氧消化

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*Corresponding author. E-mail: delong.meng@csu.edu.cn
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Microbial community structures and potential functions in a food waste treatment facility

XU Zhengqi[1,2], PENG Xing[3], XIE Song[1,3], YI Zhigang[3], YUAN Liyun[3], ZHAO Qingsong[3], YIN Changkai[3], LIU Yanyu[1,2], LI Qian[1], YIN Huaqun[1,2], MENG Delong[1,2*]

1 School of Minerals Processing and Bioengineering, Central South University, Changsha, Hunan, China

2 Key Laboratory of Biometallurgy, Ministry of Education, Changsha, Hunan, China

3 Hunan Renhe Environment Co., Ltd., Changsha, Hunan, China

Abstract: [Objective] Microorganisms play a critical role in the treatment of food waste. Elucidating their community structure and functional characteristics is essential for optimizing treatment processes and improving operational efficiency. **[Methods]** We employed high-throughput 16S rRNA gene amplicon sequencing to investigate the microbial community structures and potential functions in three systems: the anaerobic digestion system, the wastewater treatment system, and the air purification system (including biofilters and deodorization towers), in a food waste treatment facility. **[Results]** The microbial communities differed significantly in diversity and composition across systems. The anaerobic digestion system exhibited lower microbial diversity and richness, primarily influenced by environmental factors such as temperature, pH, and biochemical oxygen demand (BOD). Functional analysis indicated that organic matter degradation was the dominant microbial function across the facility. Specifically, the anaerobic system was enriched with genera such as *Defluviitoga*, *Methanothermobacter*, and *Lentimicrobium*, which were involved in hydrolysis, fermentation, and methanogenesis. The wastewater treatment system was dominated by *Candidatus* Anammoximicrobium, *Nitrolancea*, and *Truepera*, which drove organic matter degradation and nitrogen transformation processes, including anaerobic ammonium oxidation (anammox), nitrification, and denitrification. The air purification system was enriched with *Chryseobacterium* and *Paracoccus*, which were associated with biofilm formation and the degradation of volatile organic compounds and sulfur-containing compounds. **[Conclusion]** The microbial community characteristics in each treatment system was closely associated with system-specific operational conditions. The enrichment of functionally distinct microbial taxa reflected their ecological roles. In the anaerobic digestion system, methanogens and syntrophic bacteria cooperatively facilitated organic matter degradation and methane production. In the wastewater treatment system, nitrogen-cycling bacteria ensured efficient nitrogen removal. In the air purification system, the enrichment of heterotrophic degraders and sulfur compound-metabolizing genera (e.g., *Sphingobium* and *Flavobacterium*) enhanced deodorization performance. These findings provide a theoretical basis for microbial community regulation and process optimization in food waste treatment facilities.

Keywords: food waste; microbial community; functional prediction; 16S rRNA gene analysis; anaerobic digestion

随着城市化加速和居民生活水平提升，餐厨垃圾产生量持续攀升，已成为城市固体废弃物管理的重要挑战之一[1-2]。餐厨垃圾富含碳水化合物、蛋白质、脂质等有机成分，含水率高、盐分高、易腐败，极易滋生恶臭与有害物质，并携带多种病原微生物[3]和抗生素残留[4]，对生态环境和公共卫生构成威胁[5]。

传统处理方式，如填埋和焚烧，占用大量土地、污染地下水并排放温室气体[6]，难以满足可持续发展需求。相比之下，微生物处理技术(厌氧消化、好氧堆肥)因其无害化、资源化和减量化优势受到关注。厌氧消化在无氧条件下将有机物转化为甲烷及可做肥料的沼渣[7-8]，适用于高氮、高有机负荷环境，但氨氮、挥发性脂肪酸和高盐可能抑制微生物活性，降低处理效率[9]。好氧堆肥则在有氧条件下分解有机物，效果受原料组成、温度、含水率、pH 等因素影响[10-11]。

微生物在餐厨垃圾降解中起关键作用。细菌、微藻和真菌协同降解纤维素、淀粉和油脂，降低化学需氧量(chemical oxygen demand, COD)、总氮(total nitrogen, TN)等指标，同时产甲烷并去除臭气、分解有害物质，维持系统稳定[12-14]。餐厨垃圾处理园区通常集成生物滤床、除臭塔、厌氧发酵罐和污水处理单元。生物滤床以生物炭、火山岩为载体，为微生物提供附着基质，代谢去除异味；除臭塔结构类似，也用于除味。厌氧发酵罐分解有机质产沼气(用于发电、供热)及沼渣、沼液(用作肥料)。污水处理单元包括射流曝气池和序批式活性污泥池(sequencing batch reactor activated sludge process, SBR)。射流曝气池通过曝气供氧，促进好氧微生物分解有机物；SBR 通过周期性曝气、沉淀、排水，利用活性污泥去除有机物和氨氮。不同单元环境条件差异显著，微生物群落组成与功能随之变化：高氮、高负荷有利于厌氧罐中厌氧菌群，好氧区则促进好氧菌增殖。因此，解析各单元微生物结构及其与环境因子的相互作用，对工艺优化、效率提升具有重要意义。

现有研究多聚焦单一处理技术，分析微生物群落的组成、多样性及其在有机物降解、污染物去除中功能。例如，追踪厌氧消化过程中群落随阶段的演替动态，或探讨垃圾组成差异对群落的影响[15]。环境因素(pH、温度、盐度等)对群落结构与功能的作用也受关注，Chen 等[16]发现，5 mg/kg 抗生素降低纤维素酶活性，却刺激脂肪酶和蛋白酶活性，且 pH 和温度显著影响群落演替。此外，研究者尝试筛选高效菌株、优化工艺以提高效率。例如，Zhou 等[17]向反应器投加新型微生物制剂，使挥发性固体去除率达 46.91%。Zhang 等[18]添加纳米零价铁促进种间电子转移，提高甲烷产率并缩短周期。然而这些工作多针对单一单元，缺乏对整个园区多系统的系统研究。

本研究以某餐厨垃圾处理园区为对象，选取空气净化系统、厌氧发酵系统和污水处理系统，采用 16S rRNA 基因高通量测序分析各单元微生物多样性与组成差异，结合生物信息学解析群落代谢潜力及其与环境因子的关系，揭示不同系统微生物的生态功能分化，阐明其在污染物降解、臭气控制和系统稳定性中的作用，以期为餐厨垃圾处理的微生物调控、工艺优化与资源化利用提供理论依据与数据支持。

1 材料与方法

1.1 样品采集与处理

研究取样地为湖南省某餐厨垃圾集中处理园区(图 1)，分别从北向生物滤床(BL)、污水二级生物滤床(M)、除臭塔 1 (CA)、除臭塔 2 (CB)、射流曝气池(HA)、SBR 池(HB)、厌氧发酵罐 A (YA)和厌氧发酵罐 C (YC)采集样品。各工艺单元取 4–6 份重复样品，包括 10 g 固体和 1 000 mL 水样。取样瓶经紫外灭菌 30 min，水样用无菌水样袋收集。部分样品用于理化性质测定，其余用于 16S rRNA 基因测序。

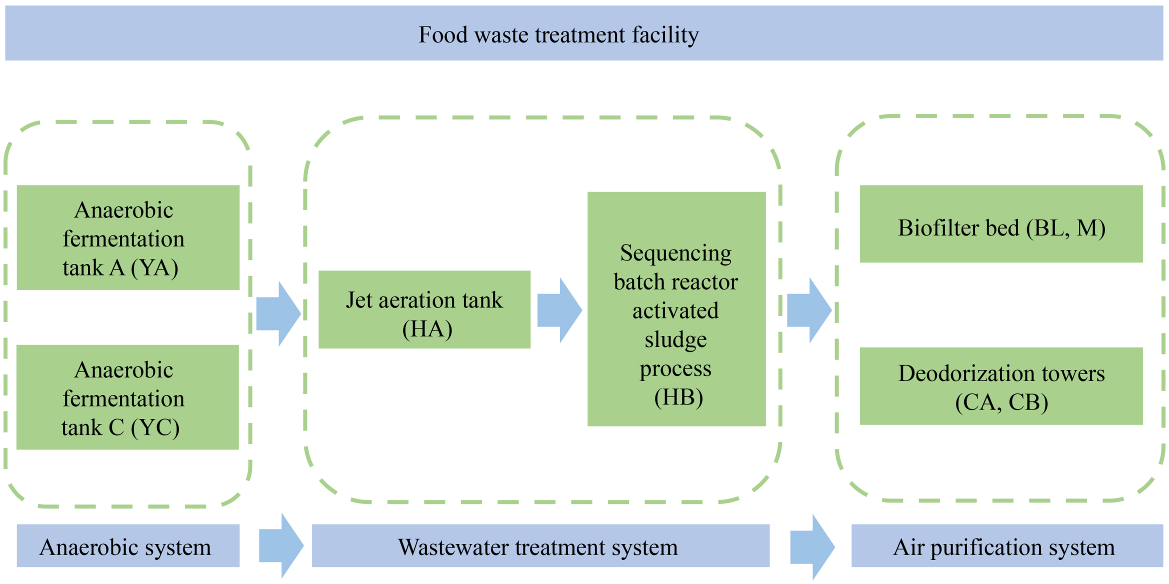


图1　餐厨垃圾处理流程图

Figure 1　Flow chart of food waste treatment.

采用 Devex 气体采样袋收集空气净化系统(BL、M、CA、CB)出气口气体，以气相色谱-质谱联用仪测定臭气成分及浓度。色谱条件：DB-5 柱 (60 m×0.32 mm×1.0 μm)，载气 He 1.5 mL/min；35 ℃保持 10 min，以 4 ℃/min 升至 140 ℃，再升至 250 ℃并保持 5 min；扫描范围 15–300 amu，EI 70 eV。

1.2　理化性质测定

pH 和温度由园区控制台实时记录；BOD_5、COD、TN、NH_3-N 分别按 HJ 505—2009[19]、HJ 924—2017[20]、HJ 636—2012[21]、HJ 535—2009[22]测定。

1.3　DNA 提取、PCR 扩增、建库与测序

水样经 0.22 μm 滤膜抽滤，滤膜与固体样本使用 HiPure Soil DNA Mini Kit (广州美基生物科技有限公司)提取 DNA。以引物 341F (5′-CCTAYGGGRBGCASCAG-3′) 和 806R (5′-GGACTACNNGGGTATCTAAT-3′)扩增 16S rRNA 基因 V3–V4 区。PCR 反应体系(50 μL)：2×*Es Taq* MasterMix 25 μL，正、反向引物(10 μmol/L)各 2 μL，模板 DNA 2 μL，补足无核酸酶水。PCR 反应条件：94 ℃ 2 min；94 ℃ 30 s，55 ℃ 30 s，72 ℃ 30 s，共 30 个循环；72 ℃ 2 min；4 ℃保存。PCR 产物纯化后建库，DNBSEQ 平台测序。原始数据已提交 NCBI sequence read archive (SRA) 数据库，编号为 PRJNA1232257。

采用 QIIME 2 (2020.6)[23]构建微生物群落特征表。Vsearch 合并双端序列，cutadapt[24]去除双端序列中的接头，quality-filter[25]对合并后的序列进行质控，dada2[26]对双端序列进行去噪(分别从正向和反向读取序列的 5′端去除 29 个和 18 个碱基)、去嵌合体处理和特征表构建，使用 feature-classifier[27]基于 Silva 138 数据库[28]对代表性序列进行物种注释。

1.4　微生物群落分析

基于 16S rRNA 基因的分类结果，用 R 语言对园区微生物群落的总体分布情况进行分析。利用 R 语言 microeco 包[29]绘制门、属水平相对丰度柱状图。计算 α 多样性指数(Shannon、Chao1 等)评估样品内丰富度和均匀度，并基于 β 多样性(Bray-Curtis 距离)进行主坐标分析

(principal co-ordinates analysis, PCoA)。对理化性质数据进行去趋势对应分析(detrended correspondence analysis, DCA)，根据第一轴 Axis lengths>4 的结果，选择典范对应分析(canonical correlation analysis, CCA)，计算 CCA 模型中方差膨胀因子，评估环境变量的多重共线性，删除共线性环境因子，明确主导微生物群落结构的关键环境因子。进一步通过线性判别分析(linear discriminant analysis effect size, LEfSe)，设置 LDA 效应值阈值为 4.0，显著性水平 P<0.05，筛选显著丰度变化的微生物属。使用 PICRUSt2[30]软件结合 KEGG (Kyoto encyclopedia of genes and genomes)数据库[31]预测微生物功能。

2 结果与分析

2.1 餐厨垃圾处理园区不同单元的理化特性

理化数据结果(表 1)表明，各处理系统运行环境差异明显。污水处理系统(HA、HB)呈酸性且温度较高(36 ℃)，利于有机污染物快速降解；厌氧发酵系统(YA、YC)在高温(55 ℃)偏碱性条件下运行，BOD_5、COD 及氨氮浓度显著高于其他单元，表明其有机物与氮负荷最高。空气净化系统中，生物滤床(BL、M)温度 20−25 ℃，BL 偏酸且 BOD_5、COD 高于 M (中性至偏碱)，二者挥发性有机物的吸附与降解能力可能不同；除臭塔(CA、CB)均偏酸、温度 23 ℃，其中 CB 的 BOD_5、COD 高于 CA，TN 与 NH_3-N 浓度相近。

臭气测定结果(表 2)显示，除臭塔对硫化氢、氨等常见恶臭物质的去除效果最佳，浓度显著低于其他单元；但对二甲基硫醚、二硫化碳等复杂硫化物去除率较低。BL 组臭气浓度高，尤以二硫化碳和三甲胺突出；M 组二甲基硫醚、二甲基二硫醚、三甲胺浓度分别为 3.40、3.00、4.30 mg/m^3，均处于较低水平。

表1 各处理单元理化性质

Table 1 Physical and chemical properties of each treatment unit

Group	pH	T/℃	$c(BOD_5)$/(mg/L)	c(COD)/(mg/L)	c(TN)/(mg/L)	$c(NH_3\text{-}N)$/(mg/L)
HA	5.70±0.24	36.00±1.50	732.28±5.30	2 478.46±271.97	2 264.32±17.43	807.11±3.73
HB	5.70±0.06	36.00±2.00	749.98±1.50	2 786.15±271.96	515.49±3.45	75.53±0.00
CA	6.30±0.10	23.00±0.50	32.12±1.58	145.23±43.52	50.24±6.03	7.08±0.18
CB	6.48±0.05	23.00±0.00	436.52±14.83	1 247.70±163.18	53.29±1.72	17.48±0.37
YA	8.00±0.15	55.00±0.00	13 070.02±114.57	20 853.85±3 535.53	5 082.32±215.58	2 912.90±1.86
YC	8.00±0.09	55.00±0.50	8 219.03±30.43	17 200.00±2 175.71	5 310.98±21.56	2 928.69±9.30
BL	6.90±0.11	21.00±1.50	430.92±7.23	2 776.93±271.96	34.39±12.94	7.35±1.68
M	7.96±0.19	25.00±0.00	18.92±2.95	283.70±65.27	98.41±0.00	22.74±0.37

表2 各处理单元臭气浓度

Table 2 Odor concentration of odors in each group

Group	Hydrogen sulfide (mg/m^3)	Ammonia (mg/m^3)	Dimethyl sulfide (mg/m^3)	Dimethyl disulfide (mg/m^3)	Trimethylamine (mg/m^3)	Styrene (mg/m^3)	Carbon disulfide (mg/m^3)
CA	0.04±0.01	0.16±0.03	32.00±0.20	29.80±0.75	40.50±2.28	19.40±4.27	27.10±1.94
CB	0.04±0.00	0.16±0.01	32.00±1.36	29.80±0.90	40.50±1.95	19.40±2.31	27.10±1.22
BL	0.05±0.02	0.18±0.05	72.60±1.20	56.80±1.16	96.30±2.10	22.20±1.09	204.00±11.67
M	0.06±0.01	0.13±0.00	3.40±0.21	3.00±0.18	4.30±0.29	1.20±0.02	3.60±0.30

2.2 微生物群落结构与多样性

为揭示处理过程中的微生物特征，本研究对操作分类单元(operational taxonomic unit, OTU)进行了门、属水平分析。门水平上(图 2A)，厌氧发酵系统以热袍菌门(*Thermotogota*)和芽孢杆菌门(*Bacillota*)为优势；污水处理及空气净化系统则以假单胞菌门(*Proteobacteriota*)和拟杆菌门(*Bacteroidota*)为主，髌骨细菌门(*Patescibacteria*)和疣微菌门(*Verrucomicrobiota*)也占有一定丰度。属水平上(图 2B)，厌氧发酵系统优势为废水袍菌属(*Defluviitoga*)和 MBA03；污水处理系统富集 AKYH767、废水袍菌属、*Candidatus*_Anammoximicrobium 和楚帕氏菌属(*Truepera*)；空气净化系统则以金黄杆菌属(*Chryseobacterium*)、*Roseobacter_clade_CHAB-I-5_lineage* 和黄杆菌属(*Flavobacterium*)等为主。

α 多样性结果(图 2C、2D)表明，厌氧发酵系统群落多样性和丰富度最低；污水处理系统多样性略高于空气净化系统，两者物种丰富度相近。

2.3 微生物群落与环境因子相关性

典型分析显示，温度、pH、BOD_5 显著影响微生物群落结构，并与厌氧发酵系统呈正相关，与其他系统呈负相关，其中 pH 影响最显著(图 3A)。氨气浓度与生物滤床(BL)群落结构密切相关，而硫化氢则与除臭塔(CA、CB)样本关联更强，说明不同臭气组分选择性富集特定菌群(图 3B)。Bray-Curtis 距离箱线图表明，M 组微生物群落与其他单元差异显著；HA 组与生物滤床及厌氧发酵系统间也显著分化(图 3C)。PCoA 进一步显示，BL 组与厌氧发酵系统样本在主坐标轴上明显偏离其他组，凸显各处理系统群落结构独特性(图 3D)。

2.4 不同处理系统特征微生物分析

LEfSe 分析表明，污水处理系统、厌氧发酵系统及空气净化系统分别具有 6、6 和 16 个显著差异属(图 4)。污水处理系统特征属为遥远杆状菌属(*Abditibacterium*)、*Candidatus* Anammoximicrobium、硝酸盐矛状菌属(*Nitrolancea*)、OLB14、AKYH767 和楚帕氏菌属被鉴定为特征微生物。厌氧发酵系统特征属包括甲烷热杆菌属(*Methanothermobacter*)、慢生微菌属(*Lentimicrobium*)、甲烷袋状菌属(*Methanoculleus*)、醋微菌属(*Acetomicrobium*)、废水袍菌属和 MBA03。空气净化系统特征属为 *Candidatus*_Nomurabacteria、鞘氨醇菌属(*Sphingobium*)、脱硫弧菌属(*Desulfovibrio*)、*Chthoniobacter*、产甲烷细条菌属(*Methanoregula*)、*Gastranaerophilales*、金黄杆菌属、C39、黄杆菌属、不黏柄菌属(*Asticcacaulis*)、替斯崔纳菌属(*Tistrella*)、非适应螺菌属(*Insolitispirillum*)、*Roseobacter_clade_CHAB-I-5_lineage*、A4b、副球菌属(*Paracoccus*)和索氏菌属(*Thauera*)。

2.5 基于 PICRUSt2 的微生物功能预测

KEGG level 2 分析结果显示，各系统在代谢、外源生物降解与脂质代谢等通路富集，实现污染物高效去除(图 5A)。KEGG level 3 进一步揭示，细菌分泌、精氨酸-脯氨酸代谢、丙氨酸-天冬氨酸和谷氨酸代谢、氨基糖-核苷糖代谢、细菌趋化性、碱基切除修复、ABC 转运蛋白及细菌运动蛋白等功能在各系统不同丰度富集；β-内酰胺抗性、细菌毒素及丙氨酸代谢等功能也被富集，体现微生物降解有机质与去除病原的多样性与灵活性(图 5B)。

3 讨论

研究表明，各处理系统的微生物群落多样性与结构存在明显差异。厌氧发酵系统因缺氧、高温(55 °C)及微碱性等环境胁迫，群落丰富度与多样性最低。相较而言，其他系统在 20−36 °C、偏酸性以及低有机质(BOD_5<800 mg/L、COD<3 000 mg/L)的环境条件下形成了更丰富复杂的微生物群落。在主要驱动因子 pH、T 和 BOD_5 的影响下，空气净化系统和污水处理系统的群

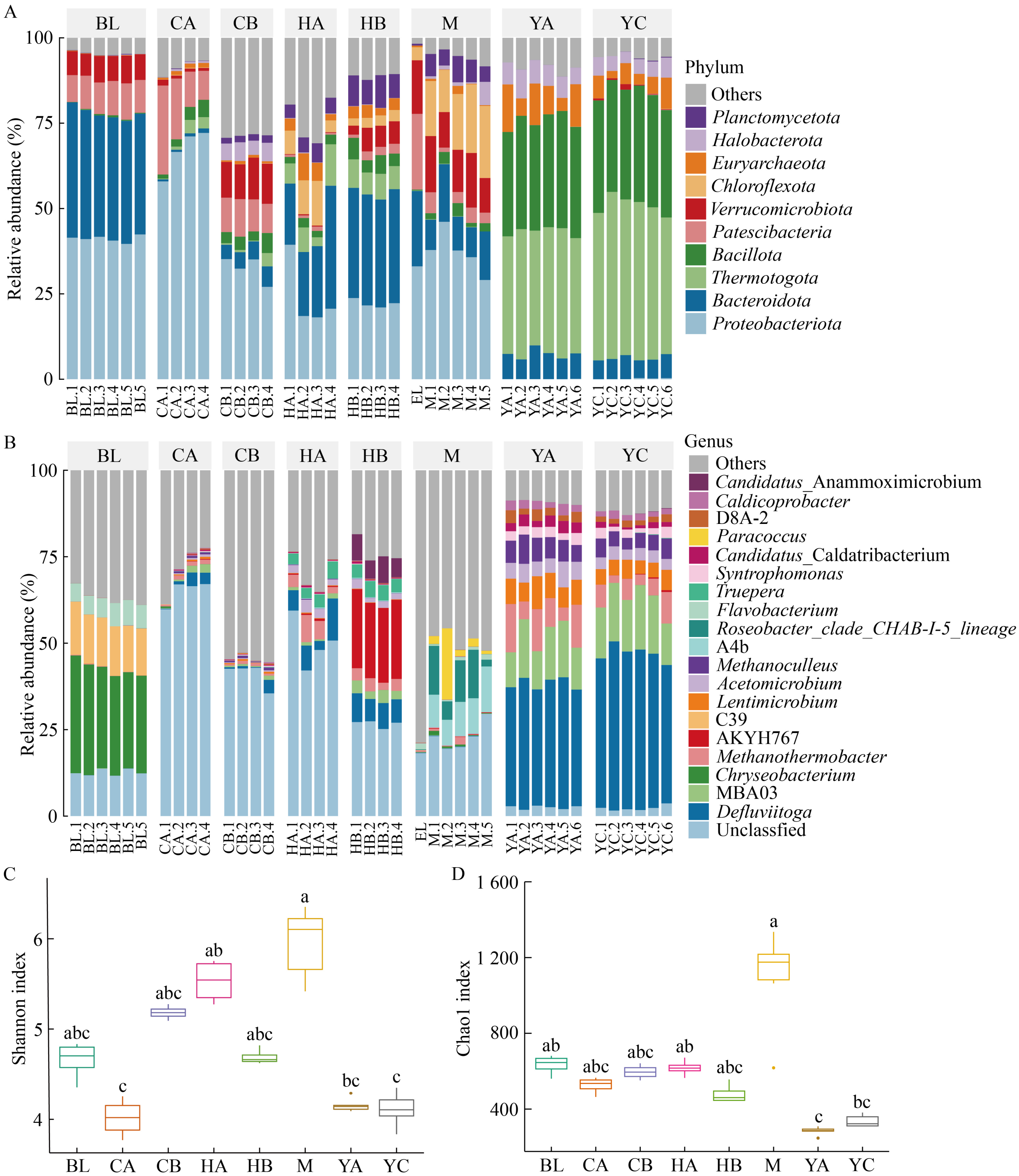


图2 各组物种分类图及多样性分布。A：门水平组成；B：属水平组成；C：Shannon指数；D：Chao1指数。

Figure 2 Taxonomic composition and diversity distribution of species in each group. A: Phylum level taxonomic; B: Genus level taxonomic; C: Shannon index; D: Chao1 index.

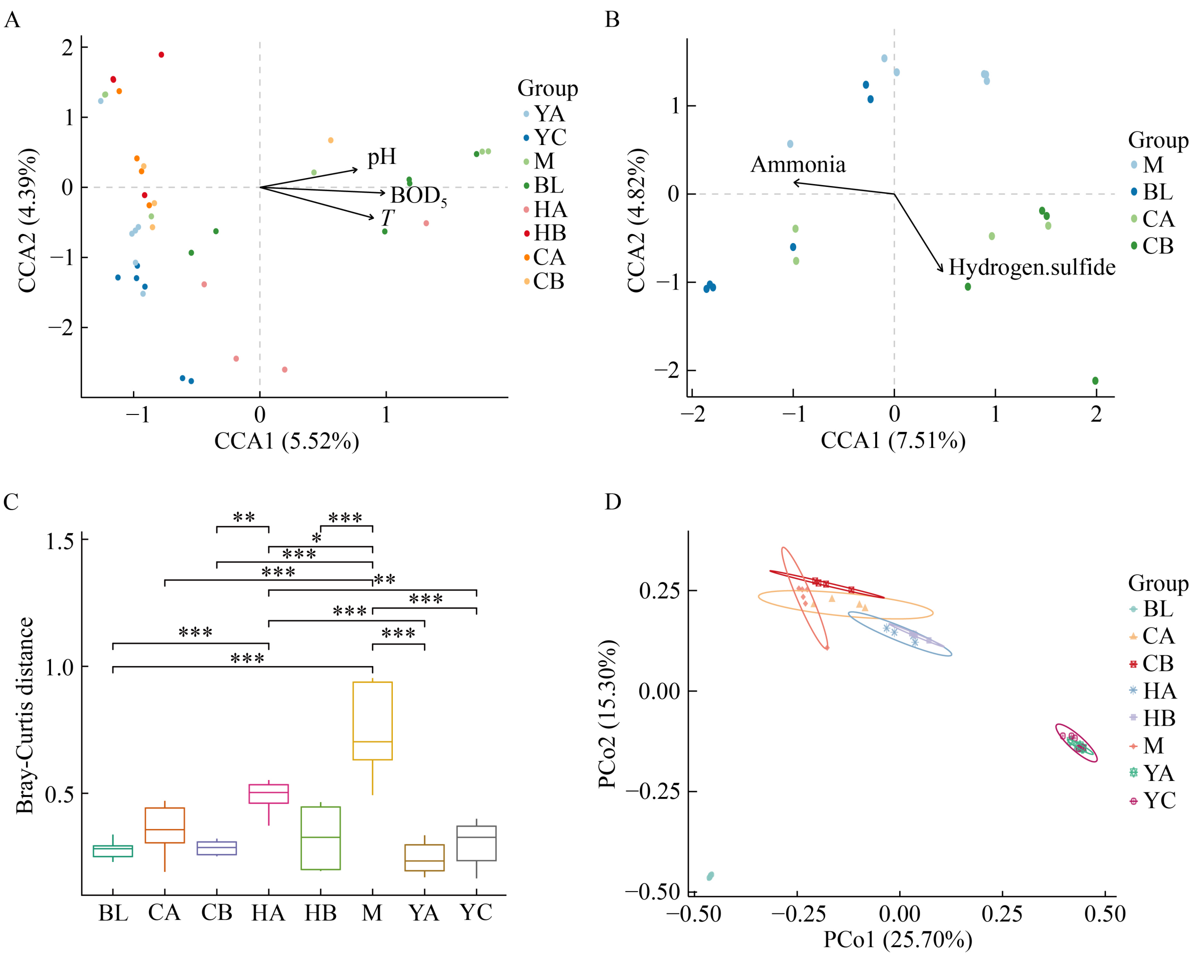


图3　微生物与环境因子的关系。A：基于理化性质的CCA；B：基于臭气因子的CCA；C：Bray-Curtis距离箱线图；D：PCoA。

Figure 3　Relationships between microorganisms and environmental factors. A: CCA based on physicochemical properties; B: CCA based on odor factors; C: Bray-Curtis distance box line plot; D: PCoA analysis.

落结构整体相似，厌氧发酵系统与二者显著不同。中性至微碱性条件可增强产甲烷菌活性，低 pH 易引起挥发性脂肪酸累积并抑制产甲烷菌，从而干扰厌氧消化过程。同时，控制 pH 有助于减少硫化氢生成[32]。BOD_5 反映不同阶段液体异质性，影响微生物群落组成及其代谢响应[33]。温度则调控微生物生长速率和生态竞争关系，塑造群落结构[34]。群落结构的差异不仅反映微生物对环境的适应性，也对应着各系统在有机物降解与污染物去除方面的功能分工。

餐厨垃圾含有大量有机物，各系统微生物以其为代谢底物，展现出强有机代谢功能，协同完成污染物降解，但功能结构仍存在差异。厌氧发酵系统中废水袍菌属和醋微菌属等微生物代谢复杂碳水化合物生成乙酸、氢气和二氧化碳，为甲烷热杆菌属等产甲烷菌提供底物[35-36]，醋微菌属和共养单胞菌属(*Syntrophomonas*)可促进非电活性菌协同代谢，提升产甲烷效率[37]。污水处理系统中，楚帕氏菌属和醋微菌属降解有机物减轻系统负荷[38-39]，遥远杆状菌属、硝酸盐矛状菌属与 *Candidatus* Anammoximicrobium 等菌群共同驱动硝化、反

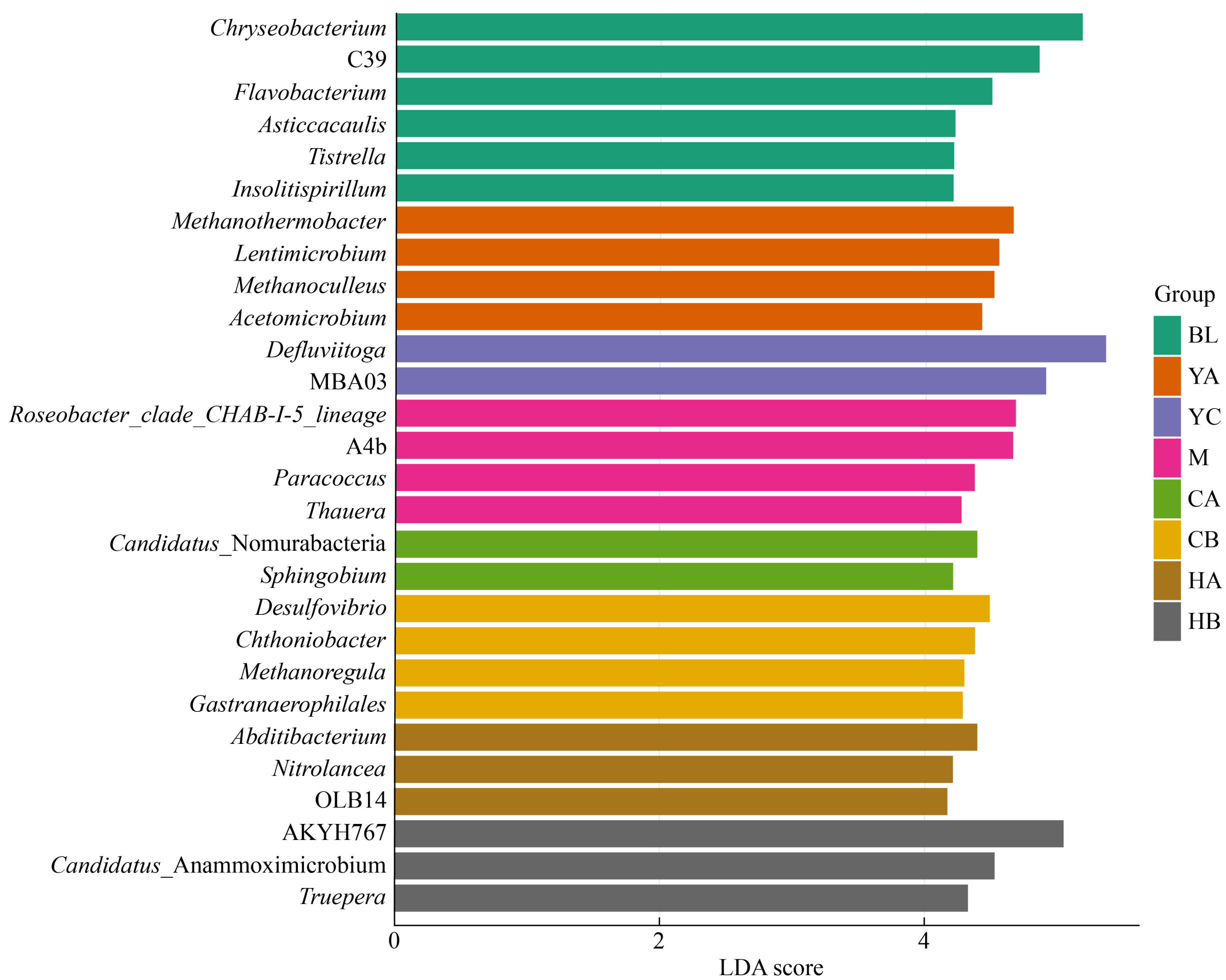


图4 线性判别分析

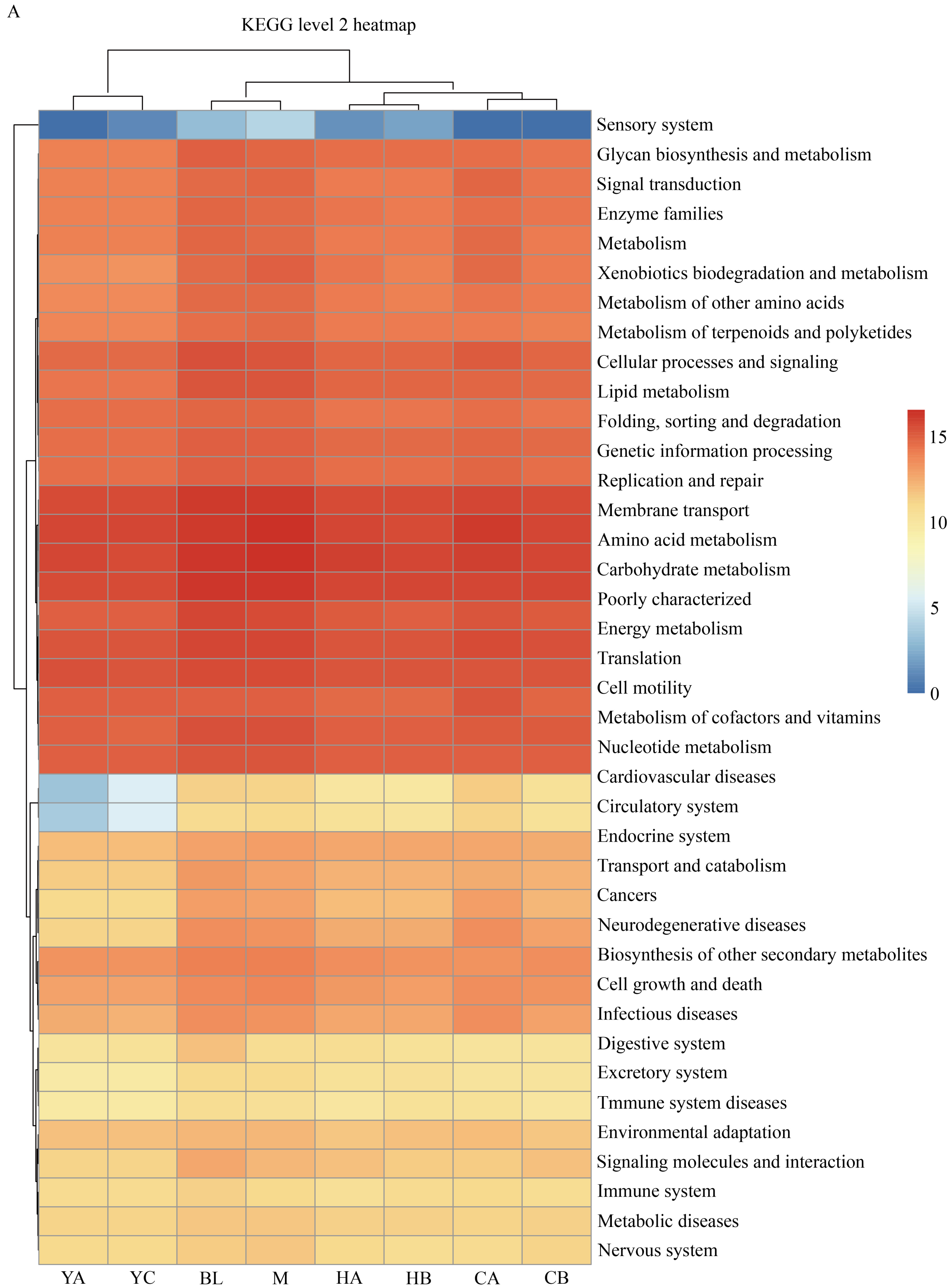
Figure 4 Linear discriminant analysis.

硝化与厌氧氨氧化过程，构建高效氮循环[40]。空气净化系统中副球菌属、金黄杆菌属和 *Chthoniobacter* 等异养菌通过碳水化合物、氨基酸和脂质代谢减少挥发性有机物积累，抑制臭气排放[38]。索氏菌属可在固体表面构建生物膜，吸附并降解硫化氢和氨气[41]，而鞘氨醇菌属与黄杆菌属则通过代谢复杂硫化物和芳香族化合物增强系统除臭功能[42]。

功能预测显示，不同系统微生物展现多样的生态适应策略。细菌分泌系统、鞭毛组装和趋化性通路的富集有助于微生物向污染物富集区域迁移并提升降解效率[43]。精氨酸-脯氨酸代谢与谷氨酸代谢通路的增强有助于抵御污染胁迫并维持菌群稳定[44]。β-内酰胺抗性与细菌毒素合成通路的富集表明环境污染可能诱导微生物群体形成抗逆性与潜在毒性，呈现污染环境中耐药性与毒力因子共富集的生态特征[43]。

4 结论

餐厨垃圾处理园区各工艺段的微生物群落特征差异显著，主要受 pH、温度和 BOD_5 等环境因子驱动，导致不同处理系统间群落多样性与组成出现明显差异。园区微生物以有机代谢为主，但不同系统微生物群落及功能与其工艺特征密切相关。厌氧发酵系统中以水解、产酸


A
KEGG level 2 heatmap
Sensory system
Glycan biosynthesis and metabolism
Signal transduction
Enzyme families
Metabolism
Xenobiotics biodegradation and metabolism
Metabolism of other amino acids
Metabolism of terpenoids and polyketides
Cellular processes and signaling
Lipid metabolism
Folding, sorting and degradation
Genetic information processing
Replication and repair
Membrane transport
Amino acid metabolism
Carbohydrate metabolism
Poorly characterized
Energy metabolism
Translation
Cell motility
Metabolism of cofactors and vitamins
Nucleotide metabolism
Cardiovascular diseases
Circulatory system
Endocrine system
Transport and catabolism
Cancers
Neurodegenerative diseases
Biosynthesis of other secondary metabolites
Cell growth and death
Infectious diseases
Digestive system
Excretory system
Tmmune system diseases
Environmental adaptation
Signaling molecules and interaction
Immune system
Metabolic diseases
Nervous system
YA
YC
BL
M
HA
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15
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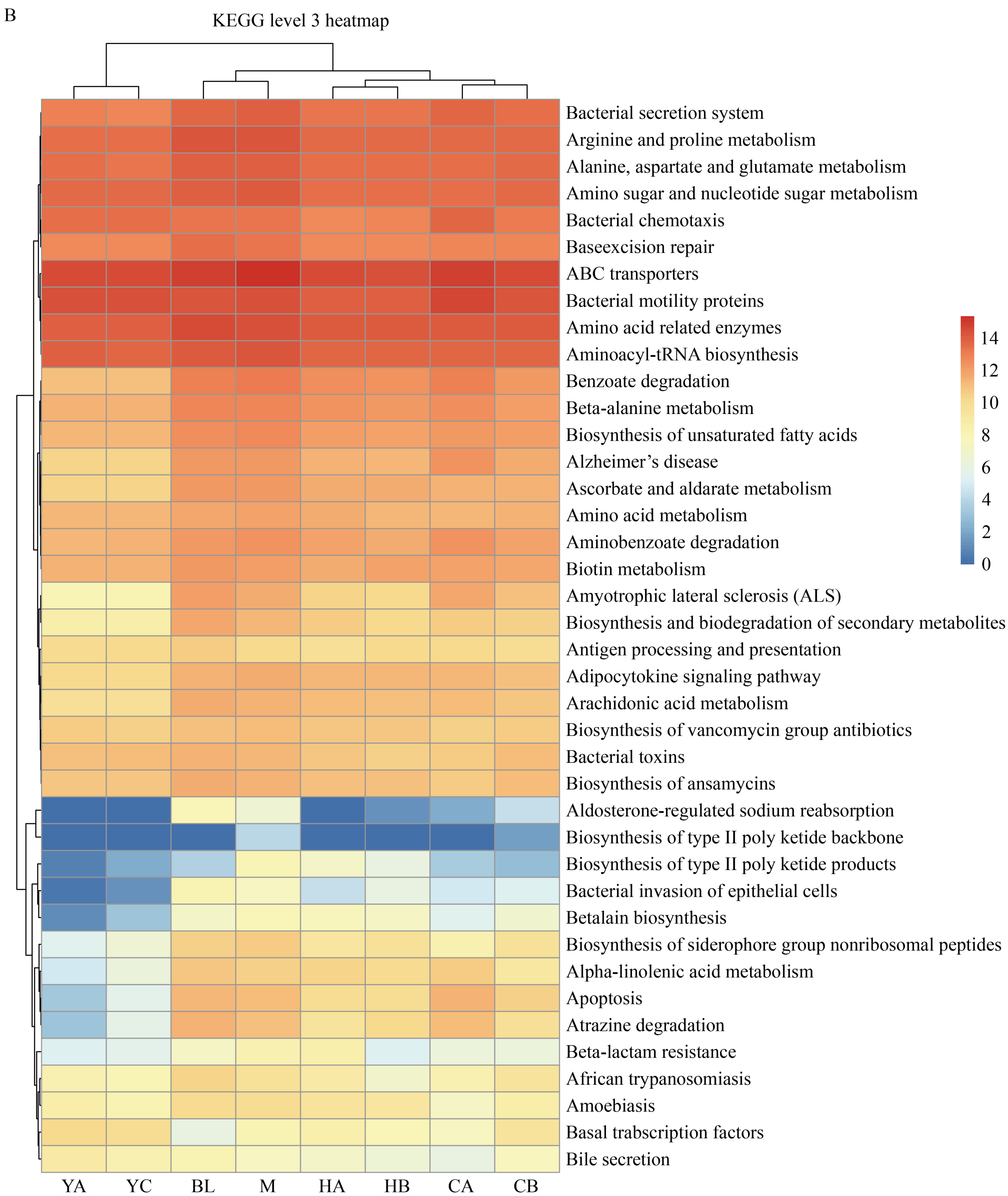

图5　功能预测分析

Figure 5　Functional prediction analysis. A: KEGG level 2 functional prediction; B: KEGG level 3 functional prediction.

及产甲烷功能为主，由产甲烷菌与发酵菌形成协同代谢网络；污水处理系统依托硝化-反硝化和厌氧氨氧化过程实现氮素循环与污泥浓缩脱氮，关键菌属包括硝酸盐矛状菌属、楚帕氏菌属和 *Candidatus* Anammoximicrobium；空气净化系统通过有机物降解和生物膜吸附机制减少臭气排放，副球菌属、黄杆菌属等菌属在此过程中作用显著。园区微生物群落表现出良好的环境适应性与污染胁迫响应能力，整个园区微生物显著富集有机物降解、氨基酸代谢、物质转运及抗性表达等功能通路。ABC 转运蛋白、碱基切除修复与 β-内酰胺抗性等通路的增强反映其在污染胁迫下具备主动响应与稳态调节机制。

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徐正琪：取样分析、论文撰写和修改；彭星：研究设计和构思；谢松：提供实验材料；易志刚：执行调研；袁李云：样品采集；赵庆松：协助实验操作；尹常凯：框架指导；刘妍妤：数据分析；李骞：论文审阅修改；尹华群：项目指导；孟德龙：实验设计、论文修改。

作者利益冲突公开声明

作者声明不存在任何可能会影响本文所报告工作的已知经济利益或个人关系。

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