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大蒜素对刺参生长、消化、非特异性免疫及 肠道菌群的影响*

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摘要 为研究饲料中添加大蒜素(allicin)对刺参(*Apostichopus japonicus*)生长、消化、免疫性能以及肠道菌群结构的影响,采用初始体质量为(50.25±3.21) g的健康刺参为研究对象,投喂添加0%(对照)、0.2%、0.4%、0.6%大蒜素的饲料,养殖周期为45 d,测定不同实验组生长率、免疫和消化酶指标以及肠道菌群结构差异。结果显示,添加大蒜素实验组的增重率和特定生长率均显著高于对照组($P<0.05$),其中,添加0.4%大蒜素组的增重率和特定生长率分别为(29.49±2.07)%和(0.57±0.13)%/d,显著高于其他各组($P<0.05$)。随大蒜素添加量的增加,刺参胰蛋白酶、淀粉酶和脂肪酶等消化酶活性以及体腔液碱性磷酸酶、酸性磷酸酶、溶菌酶和超氧化物歧化酶等非特异性免疫酶活性均呈先升高后下降的趋势;除酸性磷酸酶外,0.4%实验组消化酶和非特异性免疫酶活性均显著高于其他各组($P<0.05$)。刺参肠道菌群 OTU 数量差异不显著,Chao1 指数随大蒜素添加量的增加呈先升高后降低的趋势,ACE 指数、香农指数和辛普森指数等多样性指数随大蒜素添加量的增加呈下降趋势,0.6%实验组多样性指数最小。大蒜素的添加影响了刺参肠道微生物结构,其中,红杆菌属(*Rhodobacter*)丰度有上升趋势,大肠杆菌属(*Escherichia*)有下降趋势,梭菌属(*Clostridium*)呈先增加后下降的趋势,在大蒜素添加量为0.6%时菌群结构显著改变($P<0.05$)。LEfSe 分析显示,噬几丁质菌(Chitinophagales)、瘤胃球菌(Ruminococcaceae)、加德纳菌(Gardnerella)和双歧杆菌(Bifidobacteriales)为对照组显著优势菌($P<0.05$),表明这些菌随大蒜素的添加受到了明显抑制。研究结果表明,饲料中添加适量大蒜素能够提高刺参生长性能,促进刺参消化酶和非特异性免疫酶活性,改变刺参肠道菌群结构,饲料中大蒜素的适宜添加量为0.4%。

关键词 刺参; 大蒜素; 肠道菌群; 酶活

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刺参(*Apostichopus japonicus*)具有较高的食用及药用价值,被列为“海产八珍”之一。2022 年全国海参养殖面积达 24 万多公顷,养殖产量 24.85 万 t(农业农村部渔业渔政管理局等, 2023),已成为我国单一品种产值最大的海水养殖种类。刺参的缓慢运动和触手摄食习性决定了其摄食效率较低,特别是在池塘养殖模式下,刺参对投喂饲料的利用率低,易导致残饵腐败、污染水质等问题。此外,随着养殖规模和养殖密度的增大,病害问题日益凸显,而大量使用抗生素药物存在生态和食品安全风险(Stentiford *et al.*, 2012),因此,亟需开发具有诱食、抗菌及免疫增强作用的饲料添加剂。药用植物因其价格低廉、产量大、可再生等优势,成为目前新型饲料添加剂的热点(Awad *et al.*, 2017)。许多药用植物对水产动物的生长、免疫调节和抗菌能力有明显提升作用(Citarasu, 2010; Abarike *et al.*, 2018; Wang *et al.*, 2018)。

大蒜素(allicin),学名二烯丙基二硫醚($C_6H_{10}OS_2$),是从大蒜鳞茎中提取的由多种含硫成分组成的硫代磺酸盐,是大蒜的主要成分,在免疫和代谢中发挥重要作用,具有抗菌消炎、抗肿瘤、降低血压、调节血脂代谢等效果,对多重耐药细菌具有抗菌能力(van Loi *et al.*, 2019; de Greef *et al.*, 2021)。目前,大蒜素作为促生长剂多用于畜禽类饲料中,其特有的气味能够刺激畜禽肠胃分泌消化液,从而促进动物进食、提高采食量。在肉鸭、蛋鸡、白兔中添加适量大蒜素明显降低了饲料系数,且在平衡肠道菌群、降低动物腹泻上有一定功效(尹典等, 2021; 张顺泉等, 2023)。在鱼类、虾蟹类等水产动物中,大蒜素具有诱食作用,同时能够增强机体非特异性免疫性能和抗病性,提高生长性能(Lee *et al.*, 2012; Inoue *et al.*, 2016; Adineh *et al.*, 2020; Tazikeh *et al.*, 2020)。此外,大蒜素可影响动物肠道菌群,从而有利于宿主健康(Etyemez Büyükdeveci *et al.*, 2018)。目前,关于大蒜素在刺参中的应用尚未见报道。

课题组前期通过预实验发现大蒜素对刺参具有一定的诱集和诱食效果,但其长期应用效果及适宜的添加量仍有待研究。本研究拟通过养殖实验分析饲料中添加不同比例大蒜素对刺参消化、免疫及生长性能的影响,明确刺参饲料中大蒜素的适宜添加范围,以期大蒜素在刺参配合饲料中的应用提供参考依据。

1 材料与方法

1.1 实验材料

实验用刺参购自山东青岛瑞滋集团有限公司,挑

选活力良好、规格一致的刺参暂养于 2 m×3 m×1.6 m 室内水泥池中,幼参平均体质量为(50.25±3.21) g,暂养期间保持充气,每天投喂基础饲料以适应实验环境。

1.2 实验饲料

基础饲料由海带粉、马尾藻粉、发酵豆粕粉、多种维生素、多种矿物质、海泥等原料组成,饲料原料均粉碎至 200 目以上,按比例混匀,营养水平为 8.92% 粗蛋白、1.48% 粗脂肪、35.46% 粗灰分(以干基计算)。饲料级大蒜素呈白色粉末状,购于鹤壁兴旺生物科技有限公司,纯度为 99.9%。在基础饲料中分别添加 0.2%、0.4%、0.6% 的大蒜素制成 3 种实验饲料,以不含大蒜素的基础饲料为对照饲料,实验前按添加比例将大蒜素溶于适量海水后与基础饲料混合均匀,制成半固体饲料,−20 ℃ 保存待用。

1.3 实验设计与日常管理

刺参幼参暂养 1 周后随机分为 4 个实验组,分别投喂大蒜素添加量为 0%(对照组)、0.2%、0.4% 和 0.6% 的饲料(标记为 A0、A2、A4 和 A6),每组 3 个重复,每个重复 30 头刺参。实验时间为 2023 年 10 月 13 日至 11 月 25 日,养殖周期为 45 d,实验容器为 150 L 蓝色塑钢养殖桶,每个桶内放置海参专用聚乙烯附着基 2 框。实验期间连续充气,溶解氧>5 mg/L,盐度为 31~34,室内自然水温为 10.2~17.8 ℃。每日定时投喂饲料,先将半固体饲料添加适量海水搅拌呈悬浊液后均匀泼洒投喂,并依据刺参摄食情况适当调整。每天换水 1/3~2/3,虹吸清除水桶底部残饵及粪便,每 10 d 更换一次附着基和清底。

1.4 样品采集

实验开始和结束时称量刺参总重量并计数,称重前 48 h 停止投喂,称量时先将刺参在黑暗中沥水 5 min。每个重复随机抽取 10 头刺参,称量体重和体壁重,随机取 3 头刺参在冰盘上解剖后,用一次性吸管采集体腔液,取其肠道,用灭菌生理盐水冲洗后再用吸水纸去除表面水分,将肠道切割为小段分装于冻存管中,其中,肠道中段的一部分用于消化酶活性分析,肠道中段的另一部分用于菌群结构分析;体腔液在 4 ℃ 下 5 000 r/min 离心 10 min,取上清液于冻存管内,液氮冷冻后在−80 ℃ 下保存,用于消化酶和非特异性免疫酶活性的测定。

1.5 生长情况测定

增重率(WGR, %)= $100 \times (W_t - W_0) / W_0$;

特定生长率(SGR, %/d)= $(\ln W_t - \ln W_0) / t$;

出皮率(BWR, %)= $100 \times W_w / W_b$;

式中, W_0 为刺参的初始总重(g), W_t 为刺参的终末总重(g), t 为养殖实验天数(d), W_w 为体壁重(g), W_b 为体重(g)。

1.6 酶活性测定

采用南京建成生物工程研究所有限公司的试剂盒测定肠道胰蛋白酶(TRY)、脂肪酶(LPS)和淀粉酶(AMS)等消化酶活性, 体腔液溶菌酶(LZM)、碱性磷酸酶(AKP)、酸性磷酸酶(ACP)、超氧化物歧化酶(SOD)等非特异性免疫酶活性的测定参照试剂盒说明书。

1.7 肠道菌群结构分析

样品总 DNA 提取后应用细菌 16S rDNA V3~V4 区引物(338F: 5'-ACTCCTACGGGAGGCAGCA-3'和 806R: 5'-GGACTACHVGGGTWTCTAAT-3')进行 PCR 扩增, 产物经纯化、定量和均一化后应用 Illumina Novaseq 6000 测序平台进行序列测序。原始数据经拼接、过滤、去除嵌合体等处理后获得有效序列, 使用 Usearch 软件以 97.0%相似度水平为阈值对操作分类单元(operational taxonomic units, OTU)进行聚类。使用 QIIME2 软件对样品序列进行多样性分析。采用 STAMP 软件, 比较组间丰度差异, 构建物种分布图。

基于物种分类结果进行 LefSe (LDA effect size)分析, 构建差异菌群物种信息树状图, 筛选显著差异菌群 ($P < 0.05$, LDA > 3.0)。高通量测序分析由北京百迈客生物科技有限公司(青岛)完成, 数据分析利用百迈客云平台(<https://www.biocloud.net/>)完成。

1.8 数据处理与分析

采用 SPSS 16.0 软件对数据进行单因素方差分析(one-way ANOVA), 采用 Duncan 多重比较分析不同处理组间的差异显著性, 差异显著水平为 $P < 0.05$, 所有数值用平均值±标准差(Mean±SD)表示。

2 结果与分析

2.1 生长情况

各实验组刺参成活率均为 100%。由表 1 可知, 随着大蒜素含量的增加, 各实验组刺参的增重率及特定生长率出现先增长后降低的趋势, 最大值出现在 A4 组; 添加大蒜素后各组增重率、特定生长率均显著高于对照组 A0 ($P < 0.05$), A4 组的饲料增重率、特定生长率和出皮率最高, 分别为 $(29.49 \pm 2.07)\%$ 、 $(0.57 \pm 0.13)\%/d$ 和 $(56.09 \pm 1.07)\%$, 显著高于其他各组 ($P < 0.05$)。

表 1 饲料中大蒜素添加水平对刺参生长性能的影响

Tab.1 Effect of dietary allicin levels on the growth performance of sea cucumber *A. japonicus*

组别 Group	初始重量 Initial weight/g	终末重量 Final weight/g	增重率 WGR/%	特定生长率 SGR/(%/d)	出皮率 BWR/%
A0	1 389.52±8.21 ^a	1 690.08±8.31 ^d	21.68±1.27 ^d	0.44±0.25 ^d	51.80±0.78 ^b
A2	1 391.25±7.02 ^a	1 729.67±7.96 ^c	25.24±1.17 ^b	0.50±0.32 ^b	56.06±1.97 ^a
A4	1 419.17±6.89 ^a	1 853.30±9.53 ^a	29.49±2.07 ^a	0.57±0.13 ^a	56.09±1.07 ^a
A6	1 416.02±6.52 ^a	1 765.51±7.52 ^b	23.97±0.97 ^c	0.48±1.13 ^c	53.29±1.08 ^b

注: 不同上标字母表示组间差异显著($P < 0.05$), 下同。

Note: Different superscript letters indicate significant differences between groups at $P < 0.05$ level. The same below.

2.2 非特异性免疫酶活性

由表 2 可知, 随着饲料大蒜素添加量的增加, 各实验组刺参体腔液的 ACP、AKP、LZM 和 SOD 等酶活性呈先增加后降低的趋势, 其中, 对照组这 4 种酶的活性最低, 均显著低于 A2、A4 和 A6 组($P < 0.05$); A4 组 ACP、AKP、LZM 和 SOD 等免疫酶活性最高, 分别为 (19.93 ± 2.70) U/mL、 (12.32 ± 0.39) U/mL、 (2.84 ± 0.13) U/mL 和 (126.93 ± 5.13) U/mL, 其中, AKP、LZM 和 SOD 酶活性均显著高于其他实验组($P < 0.05$), ACP 酶活性与 A2 组差异不显著, 但显著高于其他实

验组($P < 0.05$)。

2.3 消化酶活性

由表 3 可知, 随饲料中大蒜素添加量增加, 各实验组刺参肠道 TRY、LPS 和 AMS 等消化酶活性呈先增加后降低的趋势, 最大值出现在 A4 组, 分别为 (48.23 ± 2.50) U/mg prot、 (5.15 ± 0.20) U/mg prot 和 (6.58 ± 0.15) U/mg prot, 均显著高于其他实验组 ($P < 0.05$); 对照组 A0 的 3 种消化酶活性最小, 显著低于 A2、A4 和 A6 组($P < 0.05$)。

表 2 饲料中大蒜素添加水平对刺参免疫酶活性的影响

Tab.2 Effect of dietary allicin levels on the immune enzyme activity of sea cucumber *A. japonicus*

组别 Group	酸性磷酸酶 ACP/(U/mL)	碱性磷酸酶 AKP/(U/mL)	溶菌酶 LZM/(U/mL)	超氧化物歧化酶 SOD/(U/mL)
A0	16.39±0.73 ^c	9.49±0.47 ^c	1.42±0.07 ^c	87.86±0.28 ^d
A2	19.06±0.38 ^a	11.43±0.63 ^b	2.10±0.20 ^b	103.48±3.57 ^b
A4	19.93±2.70 ^a	12.32±0.39 ^a	2.84±0.13 ^a	126.93±5.13 ^a
A6	18.08±0.31 ^b	10.72±0.58 ^b	1.90±0.98 ^b	95.68±2.29 ^c

表 3 饲料中不同大蒜素添加量对刺参消化酶活性的影响

Tab.3 Effect of dietary allicin levels on the digestive enzyme activity of sea cucumber *A. japonicus*

组别 Group	胰蛋白酶 TRY /(U/mg prot)	脂肪酶 LPS /(U/mg prot)	淀粉酶 AMS /(U/mg prot)
A0	33.11±3.95 ^c	3.06±0.09 ^c	4.81±0.25 ^d
A2	42.30±1.71 ^b	4.27±0.36 ^b	5.59±0.21 ^b
A4	48.23±2.50 ^a	5.15±0.20 ^a	6.58±0.15 ^a
A6	41.13±0.97 ^b	4.33±0.23 ^b	5.14±0.17 ^c

表 4 投喂不同大蒜素含量饲料后刺参
肠道菌群 Alpha 多样性分析

Tab.4 Alpha diversity analysis of intestinal microbiota in the sea cucumber *A. japonicus* after feeding diet of different allicin levels

组别 Group	ACE index	Chao1 index	Simpson index	Shannon index
A0	588.02 ^a	591.35 ^a	0.94 ^a	6.02 ^a
A2	580.61 ^a	592.99 ^a	0.94 ^a	5.98 ^a
A4	564.35 ^a	569.37 ^a	0.92 ^a	5.67 ^a
A6	448.03 ^a	452.97 ^a	0.90 ^a	5.19 ^a

2.4 肠道菌群结构

对各实验组刺参肠道菌群进行结构分析,共获得 696 个 OTU,从构建的韦恩图可以看出(图 1),A0、A2、A4、A6 组特有 OTU 数量分别为 1、0、1、5 个,共有 OTU 数量为 608 个,其中,A6 组特有 OTU 数量最多。根据 OTU 分类进行 Alpha 多样性分析,结果显示,随大蒜素添加量增加,ACE 指数、Simpson 指数和 Shannon 指数均呈下降趋势,最小值出现在 A6 组;Chao1 指数呈先增加后降低的趋势,A4 组最大,A6 组最小,分别为 592.99 和 452.97,但各组多样性指数差异均不显著($P>0.05$) (表 4)。

为进一步探究不同大蒜素含量饲料投喂下刺参肠道菌群微生物的群落差异性,基于 OTU 水平对 4 个实验组样品进行 PCA 分析,结果见图 2。PCA1 的贡献率为 95.63%,PCA2 的贡献率为 2.25%,总贡献率为 97.88%。各组内样品集聚在一起,表明生物学重复性较好,A4 组和 A6 组与其余组样品距离较远,说明这 2 组菌群结构差异较其余组大。

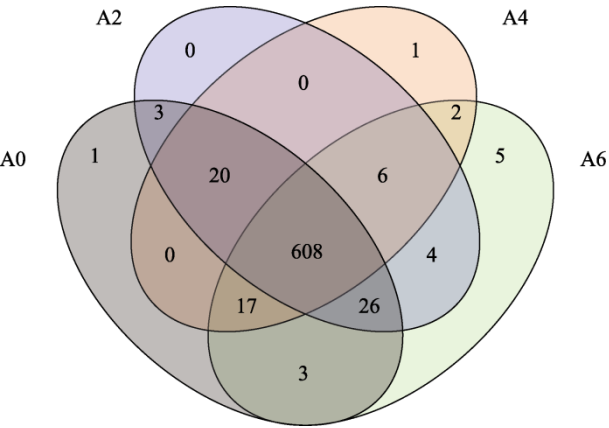


图 1 投喂不同大蒜素添加量饲料后刺参
肠道菌群 OTU 分析韦恩图

Fig.1 OTU analysis among intestinal microbiota of sea cucumber *A. japonicus* at different dietary allicin supplement levels

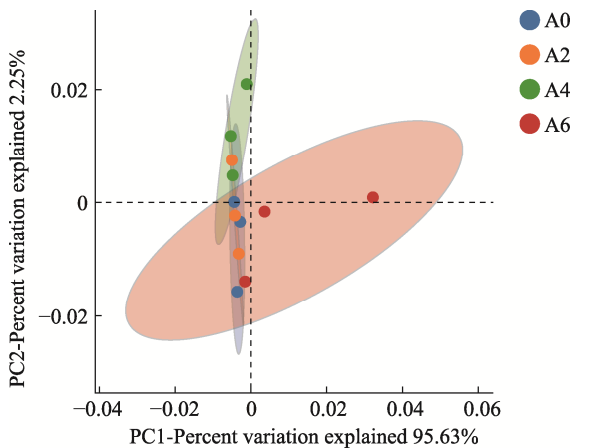


图 2 投喂不同大蒜素含量饲料后刺参
肠道菌群 PCA 分析图

Fig.2 PCA analysis of intestinal microbiota in sea cucumber *A. japonicus* after feeding diet of different allicin levels

基于门水平, 各组刺参肠道丰度前十的优势菌门见图 3a, 各组肠道菌群组成基本一致, 主要以厚壁菌门(Firmicutes)、变形菌门(Proteobacteria)、拟杆菌门(Bacteroidota)和螺旋菌门(Spirochaetota)组成, 前4优势菌门相对丰度总和随大蒜素浓度增加有增高趋势, 但差异较小, 分别为 90.30%、90.36%、91.17%、92.54%。随着大蒜素添加量的增加, 厚壁菌门相对丰度呈先增加后降低的趋势, 并在 A2 组达到最大, A2 组丰度与 A0 和 A4 差异不显著, 显著高于 A6 组 ($P<0.05$) (图 3c); 变形菌门则相反, 随着大蒜素浓度的增加呈先降低后上升的趋势, A4 组丰度最小, A6 组丰度最大, 且显著高于其他各组 ($P<0.05$) (图 3d); 拟杆菌门呈先增加后降低的趋势, 在 A6 组中显著降低

(图 3e)。

基于属水平, 各组优势菌群如图 3b 所示, 丰度较大的优势菌群主要为大肠杆菌属(*Escherichia*)、红杆菌属(*Rhodobacter*)、梭菌属(*Clostridium*)、链球菌属(*Streptococcus*)、密螺旋体属(*Treponema*)、球孢菌属(*Terrisporobacter*)等。大肠杆菌属在 A4 组丰度最大, 显著高于 A2 和 A6 组, 在 A6 组丰度最小, 显著低于其他各组 ($P<0.05$) (图 3f); 红杆菌属在 A0、A2 和 A4 组差异不显著, A6 组丰度最大且显著高于其余各组 ($P<0.05$) (图 3g); 梭菌属随大蒜素浓度增加呈先增后降的趋势, A2 组丰度最大, 与 A2 和 A4 组差异不显著, A6 组丰度最小且显著低于其他各组 ($P<0.05$) (图 3h)。

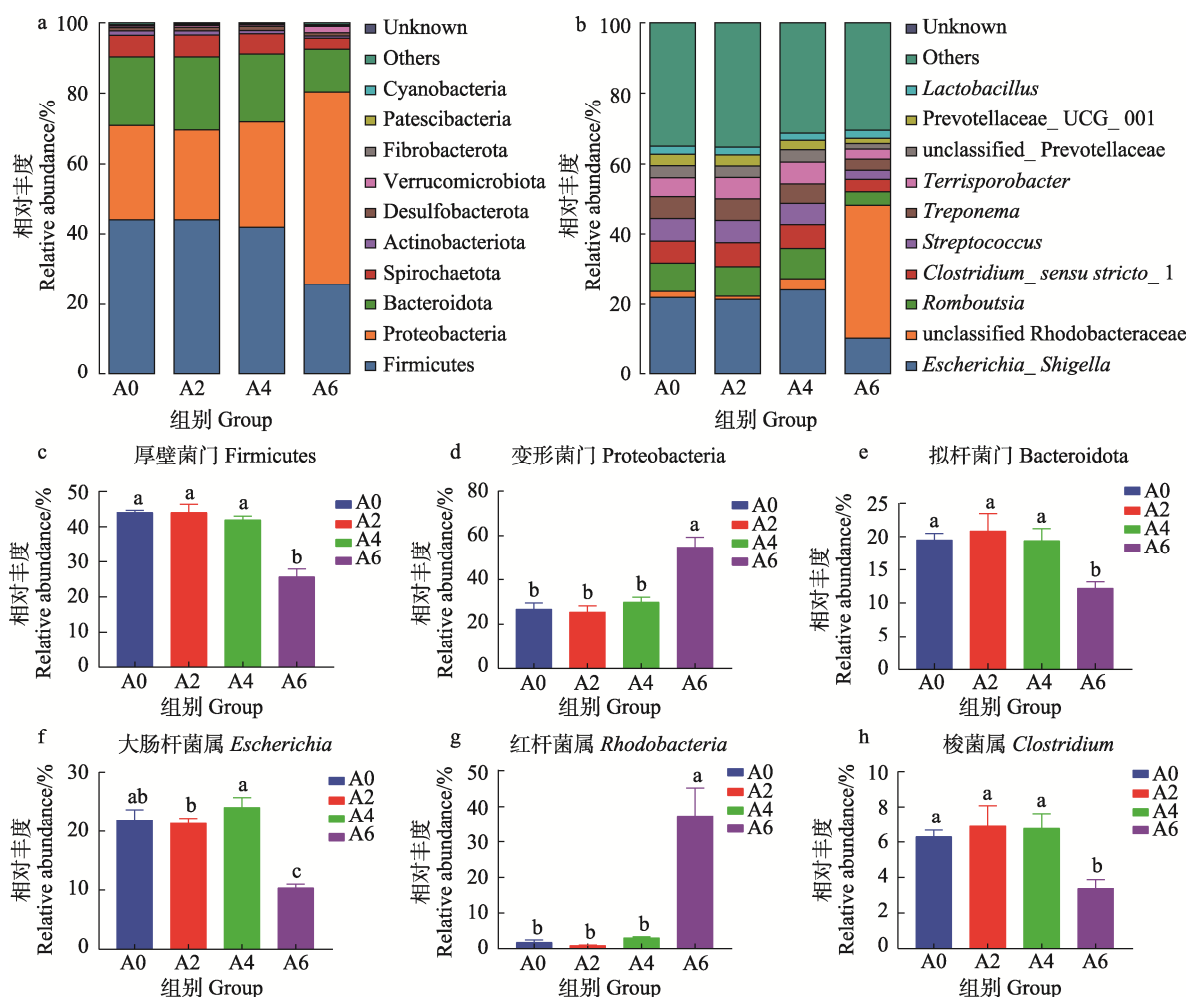


图 3 投喂不同大蒜素含量饲料后刺参肠道菌群组成

Fig.3 Intestinal microbiota composition in the sea cucumber *A. japonicus* after feeding diet of different allicin levels

a: 门水平相对丰度堆积图; b: 属水平相对丰度堆积图; c~h: 主要差异菌相对丰度条形图。

a: Histogram of relative abundance at phylum level; b: Histogram of relative abundance at genus level;

c~h: Histogram showing relative abundance of the main different bacteria.

根据 LEfSe 分析不同分组间存在显著性差异的细菌类群(图 4a)。其中, A0 组肠道的显著性差异菌群为噬几丁质菌(Chitinophagales)、瘤胃球菌科

(Ruminococcaceae)、加德纳菌(*Gardnerella*)和双歧杆菌目(Bifidobacteriales); A2 组显著性差异菌群主要是梭菌属、球孢菌属和 Prevotellaceae; A4 组显著性

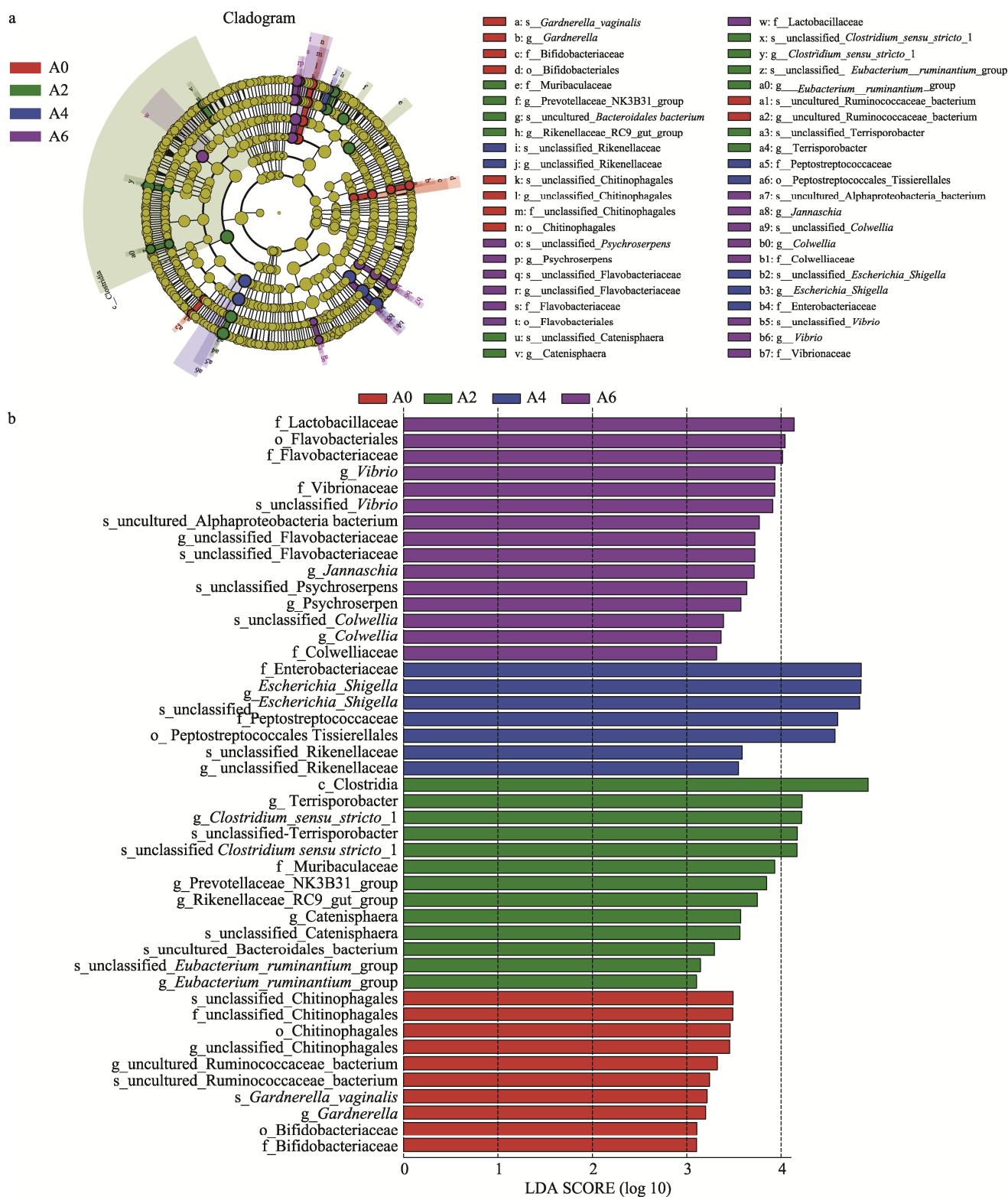


图 4 投喂不同大蒜素含量饲料后刺参肠道菌群 LEfSe 分析环形树状图(a)和柱状图(b)
Fig.4 LEfSe analysis ring dendrograms (a) and histogram (b) of intestinal microbiota in sea cucumber *A. japonicus* after feeding diet of different allicin levels

差异菌群为肠杆菌科(Enterobacteriaceae)、大肠杆菌属和理研菌科(Rikenellaceae); A6组显著性差异菌群主要为乳杆菌科(Lactobacillaceae)、黄杆菌科(Flavobacteriaceae)、弧菌科(Vibrionaceae)和Psychroserpens(图4b)。

3 讨论

本研究结果表明,饲料中添加0.2%~0.6%大蒜素均提高了刺参生长性能,其中,添加0.4%大蒜素时,刺参增重率以及特定生长率显著提高。根据已有研究,大蒜素在水产动物饲料中的添加量不尽相同,其适宜添加量范围为0.04~40 g/kg (Valenzuela- Gutiérrez *et al.*, 2021)。本研究刺参饲料适宜的大蒜素添加量为0.4%,处于中下水平,低于罗非鱼(*Oreochromis niloticus*)饲料中1.5%的添加量(Aly *et al.*, 2008)及鲶鱼(*Clarias gariepinus*)鱼苗饲料中1.0%的添加量(Thanikachalam *et al.*, 2010),但明显高于鲟鱼日粮中40 mg/kg (0.004%)的大蒜素添加量(吴春昊, 2021)。这可能与不同物种对于大蒜素的喜食程度和耐受性差异有关。与本研究结果相似,先前研究也表明适量的大蒜素对凡纳对虾(*Penaeus vannamei*)、淡水鲳(*Colossoma macropomum*)、虹鳟(*Oncorhynchus mykiss*)、鲢点石斑鱼(*Epinephelus coioides*)等水产动物的生长有促进作用(Inoue *et al.*, 2016; Adineh *et al.*, 2020; Tazikeh *et al.*, 2020),这可能与大蒜素中的生物活性物质能够对体细胞生长产生积极影响有关(Vaseeharan *et al.*, 2011)。此外,大蒜素属于有机硫化物,其刺激性气味是大多数水生动物化学感受器的兴奋剂,能够刺激食欲,进而增加水产动物的摄食量。如大蒜素能够提高大黄鱼(*Larimichthys crocea*)食欲基因神经肽Y(NPY)的基因表达量,增强大黄鱼食欲(Huang *et al.*, 2020);通过引诱实验发现大蒜素显著提高了鲈鱼(*Lateolabrax japonicus*)的摄食活动,提高了其采食量(Shang *et al.*, 2019)。

生物的生长性能与消化酶活性密切相关,本研究结果显示,添加大蒜素的各实验组消化酶活性与对照组相比均有提高,在添加0.4%大蒜素时最高,这与生长情况相一致。先前在鲈鱼、梭鱼(*Oreochromis niloticus*)等水产动物中也得出相似结果,适量大蒜素能显著提高养殖生物脂肪酶、淀粉酶以及胰蛋白酶活性(Xu *et al.*, 2020)。也有研究显示,大蒜可以促进小鼠(*Mus musculus*)胆汁酸的分泌来调节消化(Elkayam *et al.*, 2013); Hasssan 等(2019)研究表明,通过诱导鱼类肠道分泌消化酶可增加饲料营养物质的消化吸收。鉴于上述报道,推测大蒜素中生物活性物质可能通过

刺激消化酶的分泌增强刺参食欲、提高刺参消化吸收能力,进而提高了刺参生长性能,其具体的作用机制尚需进一步验证。

非特异性免疫酶是评价刺参免疫能力的重要指标。本研究发现,大蒜素的添加使刺参SOD、LZM、AKP和ACP活性均有所提升,表明大蒜素可通过调节非特异性免疫酶活性提高机体免疫性能。与本研究结果相似,投喂大蒜饲料3个月后的罗非鱼SOD、过氧化氢酶(CAT)活性均有所增强(Metwally, 2009);投喂大蒜提取物80 d后孔雀鱼(*Poecilia reticulata*)的AKP和ACP活性较对照组均有明显提高(Ahmadniaye Motlagh *et al.*, 2020)。有研究显示,大蒜素所含的酚类和皂苷具有抗氧化活性,这些化合物能够清除自由基和/或增强抗氧化内源性酶,增加细胞抗氧化酶的活性(Shang *et al.*, 2019)。此外,大蒜素对由病原导致的肠道炎症有抑制作用,能促进巨噬细胞的吞噬作用,提升机体免疫性能(Hamza *et al.*, 2021)。本研究中免疫酶活性随着大蒜素含量的增加呈先上升后下降的趋势,在大蒜素添加量为0.4%时,免疫酶活性呈最大值。在之前的研究也有长期或高剂量使用大蒜素会导致免疫活性下降的报道,如Irkin等(2014)发现,用含5 g/kg大蒜粉饲料投喂鲈鱼40 d时LZM活性达到峰值,而超过40 d, LZM活性呈下降趋势; Jahanbakhshi等(2022)研究发现,随着投喂饲料中大蒜素提取物浓度的增加,罗氏沼虾(*Macrobrachium rosenbergii*)抗氧化活性呈先增加后降低的趋势,当大蒜素浓度由10 g/kg上升为20 g/kg时,相关免疫基因的表达量开始下降。这些结果提示,大蒜素在养殖应用中需要合理控制用量及使用时间。

肠道菌群结构与机体生长、发育及免疫相关(Foysal *et al.*, 2018)。本研究发现,刺参肠道菌群多样性指数随大蒜素添加量增加基本呈下降的趋势,这与大蒜素在鱼、虾等水产动物应用中的相关研究具有一定相似性(Etyemez Büyükdeveci *et al.*, 2018), Foysal等(2018)也发现过量大蒜素会降低罗非鱼肠道菌群丰度。本研究结果显示,对照组显著优势菌有噬几丁质菌目、瘤胃球菌科、加德纳菌和双歧杆菌目,而在大蒜素添加组中显著减少,推测大蒜素可能对这些菌有显著抑制作用, Rabelo-Ruiz等(2022)也证实了大蒜素对双歧杆菌、弧菌和假单胞菌(*Pseudomonas*)具有抑制作用。菌群多样性降低及菌群结构的改变可能与大蒜素的抗菌性能有关。研究发现,大蒜素对革兰氏阴性菌如拟杆菌、大肠杆菌、假单胞菌以及革兰氏阳性菌如芽孢杆菌(*Bacillus*)、链球菌和葡萄球菌(*Staphylococcus*)

均具有广泛的抑菌活性(Jakobsen *et al*, 2012), 此外, 大蒜素含生物碱单宁等化合物可能对某些菌群的增殖存在影响(Saha *et al*, 2017)。本研究中, 大蒜素添加比例达到 0.6%时, 菌群多样性指数最小, 菌群组成发生明显改变, 变形菌门、红杆菌属丰度显著增加, 厚壁菌门、拟杆菌门、梭菌属和大肠杆菌属丰度显著降低, 弧菌成为其显著优势菌之一。Shin 等(2015)研究指出, 变形菌门中大部分菌种被认为是水产动物的有害菌, 其丰度的增加可能导致动物炎症; 红杆菌能够促进水产动物的生长(Jia *et al*, 2020); 大肠杆菌属是肠道中的正常菌群, 具有条件致病性, 在机体免疫力低下时可能会引发肠道感染; 梭菌属可以发酵碳水化合物和糖类, 为机体供能, 进而促进生长, 增强免疫功能(周丽颖等, 2024); 弧菌类大部分属于水产致病菌, 如霍乱弧菌(*Vibrio cholerae*)、创伤弧菌(*Vibrio vulnificus*)等, 其丰度增加易引发水产动物的炎症与感染(Zhou *et al*, 2021)。据此分析, 本研究在添加 0.6% 大蒜素时刺参肠道有益菌和有害菌丰度均发生显著改变, 可能破坏了肠道微生物平衡, 导致肠道菌群失调, 从而造成该组刺参消化酶活性降低、生长速率下降, 但肠道微生态环境对机体的影响是多种菌群共同作用的结果, 其具体机制有待深入研究。综上所述, 饲料中添加适量大蒜素能够改善刺参肠道微生物结构, 但投喂过量大蒜素可能会导致肠道微生物结构失调, 不利于刺参生长。

4 结论

本研究首次分析了不同添加量的大蒜素对刺参生长、消化、免疫性能和肠道微生物的影响。结果表明, 饲料中添加适量大蒜素能够促进刺参的生长、提高消化酶活性、增强非特异性免疫功能以及改变肠道菌群结构, 刺参饲料中大蒜素适宜添加量为 0.4%。

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Effects of Dietary Allicin on the Growth, Digestion, Non-Specific Immunity, and Gut Microbiota of Sea Cucumber (*Apostichopus japonicus*)

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Abstract Sea cucumber (*Apostichopus japonicus*) is an important marine aquaculture species in China. In 2022, the total area of sea cucumber aquaculture in China reached >3.7 million acres, with a breeding yield of 24.85 tons. Sea cucumber aquaculture is the largest single variety of marine aquaculture species in China. With the increase of sea cucumber aquaculture scale and density, its feeding efficiency is low, which leads to low utilization rate of feed. It is easy to cause residual bait to mold and decay, polluting water quality and leading to frequent sea cucumber diseases. Therefore, antibiotic abuse has become abundant. However, the extensive use of antibiotic drugs poses ecological and food safety risks. Therefore, developing environmentally friendly and healthy feed additives that have feeding, antibacterial, and immune enhancing effects is urgently required. Our research group screened various sea cucumber attractants in the early stage and selected allicin for further feeding experiments based on the initial experimental results. To investigate the effects of adding allicin to feed on the growth, digestion, immune performance, and gut microbiota structure of sea cucumber (*Apostichopus japonicus*), healthy sea cucumber with an initial body weight of (50.25±3.21) g was used as the research object. Feed supplemented with 0% (control), 0.2%, 0.4%, and 0.6% allicin was used as feed for 45 days. The growth rate, immune and digestive enzyme indicators, as well as differences in gut microbiota structure of different experimental groups were determined. Weight gain and specific growth rates of the experimental group with added allicin were significantly higher than those of the control group ($P<0.05$), with the weight gain rate and specific growth rate of the group with added 0.4% allicin being (29.49±2.07)% and (0.57±0.13)%/d, respectively, significantly higher than the other groups ($P<0.05$). As the amount of allicin added increases, the activities of digestive enzymes such as trypsin, amylase, and lipase, as well as non-specific immune enzyme activities such as alkaline phosphatase, acid phosphatase, lysozyme, and superoxide dismutase in body fluid, all showed a trend of first increasing and then decreasing. Except for the ACP index, the digestion enzyme and non-specific immune enzyme activities of the 0.4% experimental group were significantly higher than those of the other groups ($P<0.05$). There was no

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significant difference in the number of OTUs in the gut microbiota of sea cucumber. The Chao1 index showed a trend of first increasing and then decreasing with the increase of allicin addition, while diversity indices such as ACE, Shannon, and Simpson indices showed a decreasing trend with the increase of allicin addition. The diversity index of the 0.6% experimental group was the smallest. The addition of allicin affected the gut microbiota structure of sea cucumber, with an increasing trend in the abundance of *Rhodobacter*, a decreasing trend in the abundance of *Escherichia coli*, and an initial increase followed by a decrease in the abundance of *Clostridium*. When the allicin addition was 0.6%, the microbial community structure changed significantly ($P<0.05$). LEfSe analysis showed that Chitinophagales, Ruminococcaceae, Gardnerella, and Bifidobacteriales were significantly dominant bacteria in the control group ($P<0.05$), indicating that these bacteria were significantly inhibited with the addition of allicin. The research results indicate that adding an appropriate amount of allicin to feed can improve the growth performance of sea cucumber, promote digestive and non-specific immune enzyme activity, increase the abundance of beneficial bacteria while inhibiting the proliferation of harmful bacteria, and change the structure of sea cucumber gut microbiota. The appropriate amount of allicin added to feed was 0.4%. To our knowledge, this is the first report to demonstrate the effect of different garlic concentrations on the growth performance and intestinal microbiota of sea cucumber. Dietary garlic supplementation was intestinal microbiota for sea cucumber when administered as feed additive in terms of promoting growth and inducing changes in the intestinal microbiota. Finally, our research findings suggest that dietary garlic supplementation may represent an antibiotic as growth promoter in aquaculture.

Key words Sea cucumber; Allicin; Gut microbial structure; Enzyme activity