Enzyme characterization of lactic acid bacteria isolated from duck excreta

Dini Dwi Ludfiani¹, Widya Asmara², and Forita Dyah Arianti¹

1. Research Center for Sustainable Production Systems and Life Cycle Assessment, National Research and Innovation Agency (BRIN), Tangerang Selatan, Indonesia; 2. Department of Microbiology, Faculty of Veterinary Medicine, Universitas Gadjah Mada, Yogyakarta, Indonesia.

Corresponding authors: Widya Asmara, e-mail: wied_as@ugm.ac.id; Dini Dwi Ludfiani, e-mail: dini.d.ludfiani@gmail.com Co-author: FDA: fori001@brin.go.id

Received: 07-09-2023, Accepted: 19-12-2023, Published online: 20-01-2024

doi: www.doi.org/10.14202/vetworld.2024.143-149 **How to cite this article:** Ludfiani DD, Asmara W, and Arianti FD (2024) Enzyme characterization of lactic acid bacteria isolated from duck excreta, *Veterinary World*, 17(1): 143–149.

Abstract

Background and Aim: The production of lignocellulosic biomass waste in the agricultural sector of Indonesia is quite high annually. Utilization of lignocellulosic biomass waste through fermentation technology can be used as feed and biofuel. Fermentation technology requires the involvement of micro-organisms such as bacteria (lactic acid bacteria or LAB). LABs can be isolated from various sources, such as duck excreta. However, there have not been many reports of LAB from duck excreta. The present study aimed to characterize LAB enzymes isolated from duck excreta and obtain LAB enzymes with superior fermentation properties.

Materials and Methods: A total of 11 LAB cultures obtained from duck excreta in Yogyakarta, Indonesia, were tested. Enzyme characterization of each LAB was performed using the API ZYM kit (BioMérieux, Marcy-I'Etoile, France). The bacterial cell suspension was dropped onto the API ZYMTM cupule using a pipette and incubated for 4 h at 37°C. After incubation, ZYM A and ZYM B were dripped onto the API ZYM cupule, and color changes were observed for approximately 10 s under a strong light source.

Results: Esterase activity was moderate for all LABs. The activity of α -chymotrypsin, β -glucuronidase, α -fucosidase, and α -mannosidase was not observed in a total of 10 LAB. The phosphohydrolase and amino peptidase enzyme activity of seven LABs was strong. Only six LAB samples showed protease activity. The glycosyl hydrolase (GH) activity was observed in a total of 8 LAB, while the activity of 2 LAB was strong (*Lactococcus lactis* subsp. *lactis* K5 and *Lactobacillus brevis* M4A).

Conclusion: A total of 2 LABs have superior properties. *L. lactis* subsp. *lactis* K5 and *L. brevis* M4A have a high potential to be used in fermentation. They have the potential for further research, such as their effectiveness in fermentation, lignocellulose hydrolysis, feed additives, molecular characterization to detect specific enzymes, and their specific activities.

Keywords: API ZYM, duck, enzyme, excreta, lactic acid bacteria.

Introduction

The annual production of lignocellulosic biomass waste in Indonesia's agricultural sector is quite high, but its utilization is not optimal. Only 10%–20% of lignocellulosic biomass waste is burned or dumped [1, 2]. Processing lignocellulosic biomass waste into several value-added products is a good solution for agriculture, livestock, industry, and the environment. Lignocellulosic biomass waste can be used as feed, fertilizer, and biofuel by fermentation technology. Fermentation technology requires micro-organisms, such as lactic acid bacteria (LAB), yeast, or fungi, to degrade complex compounds (polysaccharides) into simple compounds (monosaccharides) [3]. LAB is a heterogeneous group of bacteria with significant

Copyright: Ludfiani, *et al.* Open Access. This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (http://creativecommons.org/licenses/ by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons.org/publicDomain Dedication waiver (http:// creativecommons.org/publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated.

Veterinary World, EISSN: 2231-0916

fermentation capacities [4] and is generally recognized as safe to use [5]. Gram-positive, microaerophilic, non-spore-forming, cocci or rod-shaped LABs are the characteristics. LABs consist of homofermentative LAB (homo-LAB) and heterofermentative LAB (hetero-LAB) [6]. Homo-LAB produces lactic acid as the main metabolic product, whereas hetero-LAB produces lactic acid and carbon dioxide (CO₂), as well as acetic acid and ethanol [7]. Homo-LABs are widely used in industry due to their high lactic acid production. Hetero-LABs are used for biofuel production because they produce acetic acid and butanol/ ethanol. LABs are a potential sweetener, producing ethanol, synthesis of biodegradable plastic polymers, and exopolysaccharides [8]. LAB can be used as a bio-preservative, enzyme, medicine, bio-additive [9], and green biorefineries [10] and have many beneficial properties.

LAB can be found and isolated from feces [11–13] and excreta [14–16] from various sources [17], and different environments [18]. Microorganisms present in the feces reflect groups of micro-organisms present in the gastrointestinal tract (GIT) [19]. The previous studies have reported that LAB can be obtained from the GIT of duck. LABs were isolated from the small intestine [20, 21], cecum, and colon of Muscovy ducks [22] or from the crop until the cecum of Aceh ducks [23]. Ducks can survive in various agroclimatic conditions [24]. Therefore, ducks have the ability to digest fiber, and the caecum of ducks can absorb 20% of fiber [25]. Fiber increases the weight and length of the GIT [26] and modulates the gut microbiome [27]. The cecum of ducks is highly developed and plays a significant role in microbial digestion. Cecum micro-organisms play an important role in the physiological processes of growth, metabolism [28], and host health maintenance [29]. Microorganisms of the caecum have superior properties in fiber degradation, and the isolation of bacteria from duck excreta is expected to produce bacteria with superior properties similar to those found in the caecum. It can be used in lignocellulosic biomass bioprocessing technology (particularly fermentation).

Isolation and characterization of LAB from duck excreta have not been widely reported, and the novelty of this study was to characterize LAB from duck excreta based on enzyme profiles. Many previous studies have reported on the isolation and characterization of LAB from human feces [30, 31], animal feces [32–34], and chicken excreta using general probiotic criteria. Ludfiani et al. [35] tested LAB isolated from chicken and duck excreta for sensitivity to antibiotics. In this study, enzyme characterization of LAB was performed to obtain LAB with superior hydrolase activity that can be used in lignocellulosic biomass fermentation applications. Enzyme characterization was previously carried out on fecal samples from dogs suffering from acute non-hemorrhagic diarrhea treated with Enterococcus faecium DSM 32820 to determine the effectiveness of the treatment and changes in the microbial community [36]. We screened LAB from raw milk and dairy products to obtain LAB with high α -galactosidases production [37]. LAB obtained from artisanal cheese from Caucasus has the potential to produce bioamines (tyramine and putrescine) [38]. LAB from various dairy sources was screened for β -galactosidase activity for whey acid valorization [39]. According to Vieco-Saiz et al. [40], LAB exhibits specific enzymatic properties. Hydrolytic enzymes (hydrolases) are enzymes that catalyze the cleavage of substrates, consisting of glycoside hydrolases (glycosidases), esterases, lipases, nucleotidases, peptidases, and phosphatases. The potential hydrolase activity of LAB isolated from duck excreta has not been reported. Bacteria and actinomycetes isolated from the stump and soil of wilted banana plants can produce hydrolases [41]. Extremophile bacteria isolated from a hot spring in South Sulawesi demonstrated hydrolase activity [42]. Yeast isolated from the GIT of Gvmnopleurus sturmi and ruminant feces showed cellulase production [43].

This study aimed to characterize LAB enzymes isolated from duck excreta and obtain LAB with

superior fermentation properties. Bacteria with superior properties are expected to optimize the processing of lignocellulose biomass waste as feed, food, and biofuel (bioethanol) through fermentation technology.

Materials and Methods

Ethical approval

This study was approved by Research Ethics Committee, Faculty of Veterinary Medicine, Universitas Gadjah Mada, Indonesia (Ethical clearance number: 0028/EC-FKH/Int./2020).

Study period and location

This study was conducted in the Microbiology Laboratory of the Center for Food and Nutrition Studies, Universitas Gadjah Mada, Indonesia. LAB cultures were obtained from duck excreta at duck farms in Bantul, Yogyakarta.

Bacteria

LAB cultures were obtained from Dini Dwi Ludfiani and Widya Asmara, the bacteria isolated from duck excreta in Yogyakarta, Indonesia. A total of 11 LABs were tested, of which nine have been identified biochemically and molecularly (*Lactobacillus brevis* M4A, *Lactococcus raffinolactis* H12, *Lactobacillus brevis* H23, *Lactobacillus brevis* H54, *Lactobacillus pentosus* 3B, *Lactococcus lactis* subsp. *lactis* K5, *Lactobacillus plantarum* BJ3, *Lactococcus lactis* BJ11, and *Lactobacillus plantarum* K3.0).

Enzymatic profile characterization

Enzyme characterization of each LAB was performed using the API ZYM kit according to the manufacturer's protocol (BioMérieux, Marcy-I'Etoile, France). Bacterial cell suspension from culture media on deMan, Rogosa, Sharpe (MRS) agar (Merck, Darmstadt, Germany) overnight (turbidity McFarland tube No. 5) was dropped onto the API ZYM cupule using a pipette (65 μ L), then the plastic lid was placed on the tray and incubated for 4 h at 37°C. The tray was not illuminated in bright light. ZYM A (tension active agent) and ZYM B (diazonium salt) were then dripped onto the API ZYM cupule, and the tray was placed under a strong source of light for about 10 s. Color changes were observed and compared with the API ZYM color scale reference from 0 (no activity) to 5 (maximum activity) [44]. The enzyme profiles are shown in Table-1. All LAB enzyme profile descriptions were based on the color change in the cupule.

Results

The enzyme activity of LAB varied (Table-2). The esterase activity of all LAB was moderate. All LAB samples did not show α -chymotrypsin, β -glucuronidase, α -fucosidase, and α -mannosidase activity (except LAB BJ7.0). The phosphatase activity (Naphthol-AS-BI-phosphohydrolase) and amino peptidase activity (leucine arylamidase and valine arylamidase) of LAB were strong, except that of *L. plantarum* K3.0, *L. raffinolactis* H12, LAB BJ1, and LAB BJ7

S. No.	Enzyme assayed for	pН	Substrates						
1.	Control								
2.	Alkaline phosphatase	8.5	2-naphthyl phosphate						
3.	Esterase (C4)	6.5	2-naphthyl butyrate						
4.	Esterase lipase (C8)	7.5	2-naphthyl caprylate						
5.	Lipase (C14)	7.5	2-naphthyl myristate						
6.	Leucine arylamidase	7.5	L-leucyl-2-naphthylamide						
7.	Valine arylamidase	7.5	L-valyl-2-naphthylamide						
8.	Cystine arylamidase	7.5	L-cystyl-2-naphthylamide						
9.	Trypsin	8.5	N-benzoyl-DL-arginine-2-naphthylamide						
10.	α-chymotrypsin	7.5	N-glutaryl-phenylalanine-2-naphthylamide						
11.	Acid phosphatase	5.4	2-naphthyl phosphate						
12.	Naphthol-AS-BI-phosphohydrolase	5.4	Naphthol-AS-BI-phosphate						
13.	α-galactosidase	5.4	6-Br-2-naphthyl-αD-galactopyranoside						
14.	β-galactosidase	5.4	2-naphthyl-βD- galactopyranoside						
15.	β-glucuronidase	5.4	Naphthol-AS-BI- β D-glucuronide						
16.	α-glucosidase	5.4	2-naphthyl-αD-glucopyranoside						
17.	β-glucosidase	5.4	6-Br-2-naphthyl-βD-glucopyranoside						
18.	N-acetyl-β-glucosaminidase	5.4	1-naphthyl-N-acetyl-βD-glucosaminide						
19.	α-mannosidase	5.4	6-Br-2-naphthyl-αD-mannopyranoside						
20.	α -fucosidase	5.4	2-naphthyl-αL-fucopyranoside						

Table-1: Enzyme profile of API ZYM kit.

Source: BioMérieux, Marcy-I'Etoile, France

Table-2: Enzyme profile of LAB.

Enzyme profile	M4A	H23	H54	3B	BJ3	КЗ.0	H12	К5	BJ11	BJ1.0	BJ7.0
Phosphatase											
Alkaline phosphatase	-	-	+	+	+	+	+	+	+	+	+
Acid phosphatase	+	+	+	+	+	+	+	+	+	+	+
Naphtol-AS-BI-phosphohydrolase	+	+	+	+	+	+	+	+	+	+	+
Esterase											
Esterase (C4)	-	-	+	+	+	+	+	+	+	+	+
Esterase lipase (C8)	+	+	+	+	+	+	+	+	+	+	+
Lipase (C14)	+	+	+	+	+	-	+	+	+	+	+
Amino peptidase											
Leucine arylamidase	+	+	+	+	+	+	+	+	+	+	+
Valine arylamidase	+	+	+	+	+	-	+	+	+	+	+
Cystine arylamidase	+	+	+	+	+	-	-	+	+	+	+
Protease											
Trypsin	+	+	+	+	+	-	-	+	-	-	-
α-chymotrypsin	-	-	-	_	-	-	-	_	-	-	-
Glycosyl hydrolase											
α -galactosidase	+	-	-	—	-	-	-	-	-	-	-
β-galactosidase	-	+	+	+	+	-	-	+	+	+	-
β-glucuronidase	-	-	-	—	-	-	-	-	-	-	-
α-glucosidase	-	+	-	-	+	-	-	+	+	+	-
β-glucosidase	+	+	+	+	+	-	-	+	+	+	-
N-acetyl-β-glucosaminidase	+	-	-	-	+	-	-	+	+	+	-
α -mannosidase	-	-	-	_	-	-	-	_	-	-	+
α-fucosidase	-	-	-	-	—	-	-	-	-	-	-

LAB=Lactic acid bacteria

showed moderate phosphohydrolase activity and low amino peptidase activity. Only six LAB showed protease activity, but they had low activity. The glycosyl hydrolase activity of LAB varied. Glycosyl hydrolase activity of *L. lactis* subsp. *lactis* K5 and *L. brevis* M4A was strong, whereas that of *L. plantarum* BJ3, *L. lactis* BJ11, and LAB BJ1 was moderate.

Discussion

Hydrolytic enzyme plays a central role in biochemistry (catalysis) [45]. Bacteria produce a number of enzymes that play specific roles. The use of the bacterial strains with beneficial potential. According to Muñoz-Quezada *et al.* [46], the API ZYM system enables strains to be characterized according to their enzymatic type and level of activity. API ZYM is a semi-quantitative micromethod used in systematic and rapid studies to evaluate enzyme profile [47]. API ZYM is a class of hydrolases consisting of phosphatases, esterases, amino peptidases, proteases, and glycosyl hydrolases. Hydrolases play a role in the cleavage of molecular bonds, such as ester, glycosidic, ether, peptide, and phosphatase bonds [48].

API ZYM in this study helps to quickly characterize

Enzymatic hydrolysis is required in the degradation of complex compounds such as lignocellulose. Hydrolytic enzymes are used for food, feed, biofuel, paper, and pulp in up to 75% of all industries [49].

In this study, the seven LABs showed strong catabolic activities (production of amino peptidases and phosphohydrolases) and low esterase lipase activity. Similar to Rondón et al. [50], the activity of amino peptidase, phosphatase, and phosphohydrolase from Lactobacillus salivarius is strong. All Lactobacillus spp. strains studied by Pisano et al. [51] showed high amino peptidase activity (leucine and valine arylamidase). LABs with high peptidase and low esterase/lipase activity may be useful in fermented dairy milk (cheese production) for improving the texture and reducing bitterness [52]. Amino peptidases are exopeptidases that cleave amino acid residues from the N-terminus [53]. This enzyme is widely used in the food industry for the hydrolysis of organophosphate compounds and biopeptide and amino acid synthesis [54].

Proteolytic activity plays an important role in fermentation through secondary catabolic reactions, especially for organoleptic properties, flavor development and texture improvement [55, 56]. Proteolytic activities of microbes produce different hydrolysis products, and lipases produce esters, aldehydes, ketones, lactones, and alcohols. These factors contribute to different sensory characteristics [57]. The proteolytic system of LAB consists of cell envelope proteinase, short peptide and amino acid transport systems, and a multitude of intracellular peptidases [58].

LAB can efficiently degrade polysaccharides using carbohydrate active enzyme (CAZyme). CAZyme acts synergistically to breakdown cell wall components (such as cellulose and hemicellulose) [59]. CAZyme plays a role in the biosynthesis, modification, binding, and catabolism of carbohydrates, which are divided on the basis of their catalytic activities [60]. CAZyme plays an important role in the synthesis and degradation of polysaccharides and their derivatives [61]. Based on the CAZymes database (http://www.cazy.org), CAZymes are divided into five categories: (1) glycoside hydrolases (GH), (2) glycosyl transferases (GT), (3) polysaccharide lyases (PL), (4) carbohydrate esterases (CE), and (5) auxiliary activities (AA). GH plays a role in the hydrolysis and/or rearrangement of glycosidic bonds, GT plays a role in the formation of glycosidic bonds, PL plays a role in breaking non-hydrolytic glycosidic bonds, CE plays a role in the hydrolysis of carbohydrate esters, and AA is a redox enzyme that works together with CAZymes. According to Madhavan et al. [62], carbohydrase enzymes have a fairly high potential for development because they are widely used in the food, feed, and pharmaceutical industries and are predicted to continue to increase their use in the industry. CAZyme in ruminants degrades lignocellulosic into short-chain fatty acids (acetic acid, propionic acid,

and butyric acid) through different metabolic pathways. Acetic acid, butyric acid, and propionic acid are produced through the wood–Ljungdahl pathway, the acetate CoA-transferase pathway, the butyrate kinase pathway, the acrylate pathway, the succinate pathway, and the propanediol pathway [63].

Enzymes that play a role in the degradation of lignocellulosic are lignases or ligninolytic enzymes (such as laccase, manganese peroxidase, lignin peroxidase, and versatile peroxidase), cellulases or cellulolytic enzymes (such as β -glucosidase, endoglucanase, and exoglucanase), and hemicellulases or hemicellulolytic enzymes (such as xylanase, β -glucosidase, acetyl esterase, α -galactosidase, endoglucanase, and mannanase) [64]. Based on the enzyme information in Braunschweig enzyme database, strain Lactobacillus spp. and Lactococcus spp. produce lignases, cellulases, and hemicellulases (such as lignin peroxidase, cellulase, α -glucosidase, β -glucosidase, β -galactosidase on L. brevis; cellulase, β -glucosidase, β -galactosidase on L. pentosus; laccase, cellulase, α -glucosidase, β -glucosidase, α -galactosidase, β -galactosidase, α -mannosidase, and N-acetyl- β -glucosaminidase on L. plantarum).

Some LAB in this study showed activity of β -galactosidase, α -glucosidase, β -glucosidase, and N-acetyl-β-glucosaminidase, and only L. brevis M4A showed α -galactosidase activity. The activity of α -galactosidase, β -galactosidase, α -glucosidase, β -glucosidase, and N-acetyl-B-glucosaminidase was similar to that of LAB isolated from silage, milk, and rumen in the study by Colombo et al. [52]. Rada [65] reported that some of the LABs were both α -galactosidase and α -glucosidase positive. Some of *Lactobacillus* spp. in study Pisano et al. [51] showed activity of α-galactosidase, β -galactosidase, α -glucosidase, β -glucosidase, and N-acetyl-β-glucosaminidase. L. plantarum, which was found in fermented food, also showed the highest hydrolase activity, such as β -glucosidase, and it has potency as a biotransformation agent for cellulosic biomass [66].

 α -galactosidase plays an important role in the hydrolysis of glycolipids and glycoproteins [67]. Moreover, Lactobacillus strains have α -galactosidase that hydrolyzes non-digestible carbohydrates into digestible carbohydrates during fermentation [68]. The β -galactosidase enzyme is generally extracted from Lactobacillus [69] and Pediococcus probiotic strains and is commonly used in food technology for the hydrolysis of lactose [70]. The β -galactosidase or lactase plays an important role in the hydrolysis of the β -1,4 glycosidic bond between galactose and glucose [71]. β -galactosidase is one of the characteristics of probiotics for increasing lactose tolerance [72]. β-glucosidase acts to cleave cellobiose into glucose, and β -glucosidase belongs to cellulose, which is used for the hydrolysis of biomass [73]. β-glucosidase releases glucose from cellobiose glycosidic bonds in the final step of cellulolysis or during the hydrolysis of lignocellulosic biomass [74–76]. α -glucosidase hydrolyzes the terminal non-reducing end of the α -1,4 linkages of starch and maltose with glucose release [77].

Four LAB in this study were homo-LAB (*L. bre*vis H23, *L. brevis* H54, *L. lactis* BJ11, and LAB BJ7.0) and seven LAB were hetero-LAB (*L. brevis* M4A, *L.* raffinolactis H12, *L. pentosus* 3B, *L. lactis* subsp. lactis K5, *L. plantarum* BJ3, *L. plantarum* K3.0, and LAB BJ1.0). Homo-LAB produces lactate acid through the Embden–Meyerhof–Parnas and pentose phosphate/ glycolic pathways, whereas hetero-LAB produces lactate acid, CO₂, acetic acid, and ethanol through the phosphoketolase pathway [78].

Conclusion

A total of 2 LABs had superior properties. *L. lactis* subsp. *lactis* K5 and *L. brevis* M4A have a high potential to be used in fermentation. They have the potential for further research, such as their effectiveness in fermentation, lignocellulose hydrolysis, feed additives, molecular characterization to detect specific enzymes, and their specific activities.

Authors' Contributions

DDL: Formal analysis and methodology. WA and FDA: Conception of the study. DDL, WA, and FDA: Drafted, reviewed, and revised the manuscript. All authors have read, reviewed, and approved the final manuscript.

Acknowledgments

This study was supported by Ministry of Education, Culture, Research, and Technology Indonesia (PMDSU scheme) under grant number 6/E1/KP.PTNBH/2020 and supported by the Postdoctoral Program at National Research and Innovation Agency (BRIN) Indonesia.

Competing Interests

The authors declare that they have no competing interests.

Publisher's Note

Veterinary World remains neutral with regard to jurisdictional claims in published institutional affiliation.

References

- 1. Hanafi, E.M., El Khadrawy, H.H., Ahmed, W.M. and Zaabal, M.M. (2012) Some observations on rice straw with emphasis on updates of its management. *World Appl. Sci. J.*, 16(3): 354–361.
- Vasić, K., Knez, Z. and Leitgeb, M. (2021) Bioethanol production by enzymatic hydrolysis from different. *Molecules*, 26(753): 1–23.
- Min, K.H., Yin, F.H., Amin, Z., Mansa, R.F., Wong, C.M., Ling, V., Fran, R., Clemente, M. and Wong, M. (2022) An overview of the role of lactic acid bacteria in fermented foods and their potential probiotic properties. *Borneo Int. J. Biotechnol.*, 2: 65–83.
- Abedi, E. and Hashemi, S.M.B. (2020) Lactic acid production - producing microorganisms and substrates

sources-state of art. Heliyon, 6(10): e04974.

- Raman, J., Kim, J.S., Choi, K.R., Éun, H., Yang, D., Ko, Y.J. and Kim, S.J. (2022) Application of lactic acid bacteria (LAB) in sustainable agriculture: Advantages and limitations. *Int. J. Mol. Sci.*, 23(14): 7784.
- Oliveira, A.S., Weinberg, Z.G., Ogunade, I.M., Cervantes, A.A.P., Arriola, K.G., Jiang, Y., Kim, D., Li, X., Gonçalves, M.C.M., Vyas, D. and Adesogan, A.T. (2017) Meta-analysis of effects of inoculation with homofermentative and facultative heterofermentative lactic acid bacteria on silage fermentation, aerobic stability, and the performance of dairy cows. J. Dairy Sci., 100(6): 4587–4603.
- Blajman, J.E., Vinderola, G., Paez, R.B. and Signorini, M.L. (2020) The role of homofermentative and heterofermentative lactic acid bacteria for alfalfa silage: A meta-analysis. *J. Agric. Sci.*, 158(1–2): 107–118.
- 8. Tarraran, L. and Mazzoli, R. (2018) Alternative strategies for lignocellulose fermentation through lactic acid bacteria: The state of the art and perspectives. *FEMS Microbiol. Lett.*, 365(15):1–14.
- Kim, D., Lee, K.D. and Choi, C. (2021) Role of LAB in silage fermentation: Effect on nutritional quality and organic acid production - An overview. *AIMS Agric. Food*, 6(1): 216–234.
- Lübeck, M. and Lübeck, P.S. (2019) Application of lactic acid bacteria in green biorefineries. *FEMS Microbiol. Lett.*, 366(3): fnz024.
- Adetoye, A., Pinloche, E., Adeniyi, B.A. and Ayeni, F.A. (2018) Characterization and anti-salmonella activities of lactic acid bacteria isolated from cattle faeces. *BMC Microbiol.*, 18(1): 96.
- Kook, S.Y., Chung, E.C., Lee, Y., Lee, D.W. and Kim, S. (2019) Isolation and characterization of five novel probiotic strains from Korean infant and children's faeces. *PLoS One*, 14(10): e0223913.
- Jomehzadeh, N., Javaherizadeh, H., Amin, M., Saki, M., Al-Ouqaili, M.T.S., Hamidi, H., Seyedmahmoudi, M. and Gorjian, Z. (2020) Isolation and identification of potential probiotic *Lactobacillus* species from feces of infants in southwest Iran. *Int. J. Infect. Dis.*, 96: 524–530.
- Robledo-Cardona, S., Ramírez-Hincapié, S. and Correa-Álvarez, J. (2018) Implementation of a non-invasive bioprospecting protocol for isolation of *Lactobacillus* from feces of hens under foraging conditions. *Ing. Cienc.*, 14(28): 93–111.
- 15. Wang, J., Ishfaq, M., Guo, Y., Chen, C. and Li, J. (2020) Assessment of probiotic properties of *Lactobacillus salivarius* isolated from chickens as feed additives. *Front. Vet. Sci.*, 7: 415.
- Ludfiani, D.D., Asmara, W., Hastuti Wahyuni, A.E.T. and Astuti, P. (2021) Identification of *Lactobacillus* spp. on basis morphological, physiological, and biochemical characteristic from Jawa super chicken excreta. *BIO Web. Conf.*, 33: 06012.
- 17. Arshad, F.A., Mehmood, R., Hussain, S., Annus Khan, M. and Khan, M.S. (2018) Lactobacilli as probiotics and their isolation from different sources. *Br. J. Res.*, 5(3): 43.
- Bazireh, H., Shariati, P., Azimzadeh Jamalkandi, S., Ahmadi, A. and Boroumand, M.A. (2020) Isolation of novel probiotic *Lactobacillus* and *Enterococcus* strains from human salivary and fecal sources. *Front. Microbiol.*, 11: 597946.
- Naumova, N.B., Alikina, T.Y., Zolotova, N.S., Konev, A.V., Pleshakova, V.I. and Lescheva, N.A. (2021) Bacillus-based probiotic treatment modified bacteriobiome diversity in duck feces. *Agriculture*, 11(5): 406.
- Nurcahyo, H., Suyanta, Dale, A. and Furqon, F.Y.A. (2019) Isolation and characterization of lactic acid bacteria (LAB) from small intestine content of duck (*Anas* spp.) as a probiotic candidate. *J. Phys. Conf. Ser.*, 1397(1): 012043.
- 21. Xie, Z.L., Bai, D.P., Xie, L.N., Zhang, W.N., Huang, X.H. and Huang, Y.F. (2015) Intestinal lactic acid bacteria from

Muscovy duck as potential probiotics that alter adhesion factor gene expression. *Genet. Mol. Res.*, 14(4): 12262–12275.

- 22. Herdian, H., Istiqomah, L., Damayanti, E., Suryani, A.E., Anggraeni, A.S., Rosyada, N. and Susilowati, A. (2018) Isolation of cellulolytic lactic-acid bacteria from Mentok (*Anas moschata*) gastro-intestinal tract. *Trop. Anim. Sci. J.*, 41(3): 200–206.
- 23. Risna, Y.K., Harimurti, S., Wihandoyo. and Widodo (2020) Screening for probiotic of lactic acid bacteria isolated from the digestive tract of a native Aceh duck (*Anas platyrhynchos*). *Biodiversitas*, 21(7): 3001–3007.
- 24. Maharani, D., Hariyono, D.N.H., Putra, D.D.I., Lee, J.H. and Sidadolog, J.H.P. (2019) Phenotypic characterization of local female duck populations in Indonesia. *J. Asia Pac. Biodivers.*, 12(4): 508–514.
- Samur, S.I.N., Suwignyo, B. and Suryanto, E. (2020) The effect of Alfalfa (*Medicago sativa* L.) on different basal feeds for hybrid duck performance. *E3S Web. Conf.*, 200: 03013.
- Han, H.Y., Zhang, K.Y., Ding, X.M., Bai, S.P., Luo, Y.H., Wang, J.P. and Zeng, Q.F. (2017) Effect of dietary fiber levels on performance, gizzard development, intestinal morphology, and nutrient utilization in meat ducks from 1 to 21 days of age. *Poult. Sci.*, 96(12): 4333–4341.
- Hao, Y., Ji, Z., Shen, Z., Wu, Y., Zhang, B., Tang, J., Hou, S. and Xie, M. (2021) Effects of total dietary fiber on cecal microbial community and intestinal morphology of growing White Pekin duck. *Front. Microbiol.*, 12: 727200.
- Lyu, W., Liu, X., Lu, L., Dai, B., Wang, W., Yang, H. and Xiao, Y. (2021) Cecal microbiota modulates fat deposition in Muscovy ducks. *Front. Vet. Sci.*, 8: 609348.
- 29. Saleh, T.F. and Altaey, O.Y. (2023) Histomorphometrical and histochemical study of caecum in adult Muscovy ducks (*Cairina moschata*). Adv. Anim. Vet. Sci., 11(6): 1021–1029.
- Adedeji, O.E., Chae, S.A., Ban, O.H., Bang, W.Y., Kim, H., Jeon, H.J., Chinma, C.E., Yang, J. and Jung, Y.H. (2022) Safety evaluation and anti-inflammatory activity of *Lactobacillus johnsonii* IDCC 9203 isolated from feces of breast-fed infants. *Arch. Microbiol.*, 204(8): 470.
- 31. Li, B., Pan, L.L. and Sun, J. (2022) Novel probiotic lactic acid bacteria were identified from healthy infant feces and exhibited anti-inflammatory capacities. *Antioxidants* (*Basel*), 11(7): 1246.
- Lee, H.J., Lee, J.B., Park, S.Y., Choi, I.S. and Lee, S.W. (2022) Antimicrobial activity of dominant *LigiLactobacillus animalis* strains in healthy canine feces and their probiotic potential. *FEMS Microbiol. Lett.*, 369(1): fnac115.
- Zhang, Q., Wang, M., Ma, X., Li, Z., Jiang, C., Pan, Y. and Zeng, Q. (2022) *In vitro* investigation on lactic acid bacteria isolated from yak faeces for potential probiotics. *Front. Cell. Infect. Microbiol.*, 12: 984537.
- Pinillos-Miñano, R.M., Rodriguez-Portilla, L.M.I., Hatta-Sakoda, B.A. and Estela-Escalante, W.D. (2022) Isolation of lactic acid bacteria from the feces of ring-tailed coati (*Nasua nasua*), biochemical and fermentative aspects related to coffee fermentation. *Appl. Biochem. Microbiol.*, 58(1): S102–S112.
- 35. Ludfiani, D.D., Asmara, W., Wahyuni, A.E.T.H. and Astuti, P. (2020) Antibiotic susceptibility of lactic acid bacteria isolated from duck and Jawa super chicken excreta intended for use as probiotic. *Vet. Pract.*, 21(2): 165–167.
- Kubašová, I., Štempelová, L., Maďari, A., Bujňáková, D., Micenková, L. and Strompfová, V. (2022) Application of canine-derived *Enterococcus faecium* DSM 32820 in dogs with acute idiopathic diarrhoea. *Acta Vet. Brno.*, 72(2): 167–183.
- Prasad, B., Narang, A. and Mishra, M. (2020) Recovery and screening of α-galactosidase producing lactic acid bacteria from fermented dairy products. *J. Basic Appl. Res. Biomed.*, 6(1): 32–37.
- 38. Kochetkova, T.V., Grabarnik, I.P., Klyukina, A.A., Zayulina, K.S., Gavirova, L.A., Shcherbakova, P.A.,

Kachmazov, G.S., Shestakov, A.I., Kublanov, I.V. and Elcheninov, A.G. (2023) The bacterial microbiota of artisanal cheeses from the Northern Caucasus. *Fermentation*, 9(8): 719.

- Kolev, P., Rocha-Mendoza, D., Ruiz-Ramírez, S., Ortega-Anaya, J., Jiménez-Flores, R. and García-Cano, I. (2022) Screening and characterization of β-galactosidase activity in lactic acid bacteria for the valorization of acid whey. JDS Commun., 3(1): 1–6.
- 40. Vieco-Saiz, N., Belguesmia, Y., Raspoet, R., Auclair, E., Gancel, F., Kempf, I. and Drider, D. (2019) Benefits and inputs from lactic acid bacteria and their bacteriocins as alternatives to antibiotic growth promoters during food-animal production. *Front. Microbiol.*, 10: 57.
- 41. Ardhi, A., Ahmad, K.C., Novrianti, H., Husna, E.Y., Yulis, M., Pratiwi, N.W. and Saryono, S. (2019) Hydrolytic enzymes-producing ability of species of actinomycetes and bacteria associated with wilted banana plants (*Musa* spp.). *Biodiversitas*, 20(4): 1147–1153.
- Indrayani, I., Putra, R.P., Hambali, A. and Ardiansyah (2022) Isolation and characterization of extremophile bacteria for hydrolytic enzyme production from Waepella Hot Spring, Sinjai, Indonesia. *Biodiversitas*, 23(12): 6345–6351.
- 43. Hanane, T., Najoua, B., Salsabil, H., Abdellatif, J.I., Dalila, B., Ahmad, I., BukharI, S.A.R., Irfan, M., Chen, L. and Hicham, B. (2022) Qualitative screening of yeast biodiversity for hydrolytic enzymes isolated from the gastrointestinal tract of a coprophage "*Gymnopleurus sturmi*" and dung of ruminants. *Fermentation*, 8(12): 692.
- 44. Karakas-Sen, A. and Karakas, E. (2018) Isolation, identification and technological properties of lactic acid bacteria from raw cow milk. *Biosci. J.*, 34(2): 985–999.
- Robinson, P.K. (2015) Enzymes: Principles and biotechnological applications. *Essays Biochem.*, 59: 1–41.
- 46. Muñoz-Quezada, S., Chenoll, E., Vieites, J.M., Genovés, S., Maldonado, J., Bermúdez-Brito, M., Gomez-Llorente, C., Matencio, E., Bernal, M.J., Romero, F., Suárez, A., Ramón, D. and Gil, A. (2013) Isolation, identification and characterisation of three novel probiotic strains (*Lactobacillus paracasei* CNCM I-4034, Bifidobacterium breve CNCM I-4035 and *Lactobacillus rhamnosus* CNCM I-4036) from the faeces of exclusively breast-fed infants. *Br. J. Nutr.*, 109(52): S51–S62.
- 47. Al-Abedi, H.F.H., Al-Attraqchi, A.A.F. and Khudaie, B.Y. (2020) Investigation of the hydrolytic enzyme activities of *Candida parapsilosis* isolated from milk samples of bovine mastitis by API ZYM and molecular method. *Indian J. Forensic Med. Toxicol.*, 14(3): 2443–2449.
- Gagler, D.C., Karas, B., Kempes, C.P., Malloy, J., Mierzejewski, V., Goldman, A.D., Kim, H. and Walker, S.I. (2022) Scaling laws in enzyme function reveal a new kind of biochemical universality. *Proc. Natl. Acad. Sci.*, 119(9): e2106655119.
- Shukla, E., Bendre, A.D. and Gaikwad, S.M. (2022) Hydrolases: The Most Diverse Class of Enzymes. IntechOpen, London, p1–16.
- Rondón, A.J., González, J., Rodríguez, M., Milián, G., Martínez, M.M., Beruvides, A., Valdivia, A. and Vera, R. (2020) *In vitro* metabolic activity of *Lactobacillus salivarius* and its effect on productive and health indicators of lactating calves. *Cuba. J. Agric. Sci.*, 54(2): 169–181.
- Pisano, M.B., Viale, S., Conti, S., Fadda, M.E., Deplano, M., Melis, M.P., Deiana, M. and Cosentino, S. (2014) Preliminary evaluation of probiotic properties of *Lactobacillus* strains isolated from Sardinian dairy products. *Biomed Res. Int.*, 2014: 286390.
- 52. Colombo, M., Castilho, N.P.A., Todorov, S.D. and Nero, L.A. (2018) Beneficial properties of lactic acid bacteria naturally occurring in dairy production systems. *BMC Microbiol.*, 18: 219.
- 53. Kieliszek, M., Pobiega, K., Piwowarek, K. and Kot, A.M. (2021) Characteristics of the proteolytic enzymes produced

by lactic acid bacteria. Molecules, 26(7): 1858.

- Nandan, A. and Nampoothiri, K.M. (2020) Therapeutic and biotechnological applications of substrate-specific microbial aminopeptidases. *Appl. Microbiol. Biotechnol.*, 104(12): 5243–5257.
- Li, S., Tang, S., He, Q., Hu, J. and Zheng, J. (2019) Changes in proteolysis in fermented milk produced by *Streptococcus thermophilus* in co-culture with *Lactobacillus plantarum* or *Bifidobacterium animalis* subsp. *lactis* during refrigerated storage. *Molecules*, 24(20): 3699.
- Rahmati, F. (2017) Characterization of *Lactobacillus*, *Bacillus* and *Saccharomyces* isolated from Iranian traditional dairy products for potential sources of starter cultures. *AIMS Microbiol.*, 3(4): 815–825.
- 57. Li, L.Q., Chen, X., Zhu, J., Zhang, S., Chen, S.Q., Liu, X., Li, L. and Yan, J.K. (2023) Advances and challenges in interaction between heteroglycans and *Bifidobacterium*: Utilization strategies, intestinal health and future perspectives. *Trends Food Sci. Technol.*, 134: 112–122.
- Tagliazucchi, D., Martini, S. and Solieri, L. (2019) Bioprospecting for bioactive peptide production by lactic acid bacteria isolated from fermented dairy food. *Fermentation*, 5(4): 96.
- 59. Munir, R. (2015) Cellulose Hydrolysis and Metabolism in the Mesophilic, Cellulolytic Bacterium, *Clostridium termitidis* CT1112. Department of Biosystems Engineering University, Manitoba, Canada.
- Tarrah, A., Pakroo, S., Lemos Junior, W.J.F., Guerra, A.F., Corich, V. and Giacomini, A. (2020) Complete genome sequence and carbohydrates-active enzymes (CAZymes) analysis of *Lactobacillus paracasei* DTA72, a potential probiotic strain with strong capability to use inulin. *Curr. Microbiol.*, 77(10): 2867–2875.
- 61. D'Rose, V. and Bhat, S.G. (2023) Whole genome sequence analysis enabled affirmation of the probiotic potential of marine sporulater *Bacillus amyloliquefaciens* BTSS3 isolated from *Centroscyllium fabricii*. *Gene*, 864: 147305.
- 62. Madhavan, A., Arun, K.B., Binod, P., Sirohi, R., Tarafdar, A., Reshmy, R., Kumar Awasthi, M. and Sindhu, R. (2021) Design of novel enzyme biocatalysts for industrial bioprocess: Harnessing the power of protein engineering, high throughput screening and synthetic biology. *Bioresour*. *Technol.*, 325: 124617.
- Zhang, H., Jiang, F., Zhang, J., Wang, W., Li, L. and Yan, J. (2022) Modulatory effects of polysaccharides from plants, marine algae and edible mushrooms on gut microbiota and related health benefits: A review. *Int. J. Biol. Macromol.*, 204: 169–192.
- Usmani, Z., Sharma, M., Awasthi, A.K., Sivakumar, N., Lukk, T., Pecoraro, L., Thakur, V.K., Roberts, D., Newbold, J. and Gupta, V.K. (2021) Bioprocessing of waste biomass for sustainable product development and minimizing environmental impact. *Bioresour. Technol.*, 322: 124548.
- 65. Rada, V. (1997) Detection of Bifidobacterium species by enzymatic methods and antimicrobial susceptibility testing. *Biotechnol. Tech.*, 11(12): 909–912.
- Lee, F.H., Wan, S.Y., Foo, H.L., Loh, T.C., Mohamad, R., Rahim, R.A. and Idrus, Z. (2019) Comparative study of extracellular proteolytic, cellulolytic, and hemicellulolytic

enzyme activities and biotransformation of palm kernel cake biomass by lactic acid bacteria isolated from Malaysian foods. *Int. J. Mol. Sci.*, 20(20): 4979.

- Fabris, E., Bulfoni, M., Nencioni, A. and Nencioni, E. (2021) Intra-laboratory validation of alpha-galactosidase activity measurement in dietary supplements. *Molecules*, 26(6): 1566.
- Wang, J., Hui, W., Cao, C., Jin, R., Ren, C., Zhang, H. and Zhang, W. (2016) Proteomic analysis of an engineered isolate of *Lactobacillus plantarum* with enhanced raffinose metabolic capacity. *Sci. Rep.*, 6: 31403.
- Vasudha, M., Prashantkumar, C.S., Bellurkar, M., Kaveeshwar, V. and Gayathri, D. (2023) Probiotic potential of β-galactosidase-producing lactic acid bacteria from fermented milk and their molecular characterization. *Biomed. Rep.*, 18(3): 23.
- Chanalia, P., Gandhi, D., Attri, P. and Dhanda, S. (2018) Purification and characterization of β-galactosidase from probiotic *Pediococcus acidilactici* and its use in milk lactose hydrolysis and galactooligosaccharide synthesis. *Bioorg. Chem.*, 77: 176–189.
- Yan, Y., Guan, W., Li, X., Gao, K., Xu, X., Liu, B., Zhang, W. and Zhang, Y. (2021) β-galactosidase GALA from *Bacillus circulans* with high transgalactosylation activity. *Bioengineered*, 12(1): 8908–8919.
- 72. De Albuquerque, T.L., de Sousa, M., Gomes e Silva, N.C., Girão Neto, C.A.C., Gonçalves, L.R.B., Fernandez-Lafuente, R. and Rocha, M.V.P. (2021) β-Galactosidase from *Kluyveromyces lactis*: Characterization, production, immobilization and applications - A review. *Int. J. Biol. Macromol.*, 191: 881–898.
- 73. Purwadari, T., Ketaren, P.P., Sinurat, A.P. and Sutikno, I. (2016) Identification and evaluation of fiber hydrolytic enzymes in the extract of termites (*Glyptotermes montanus*) for poultry feed application. *Indones. J. Agric. Sci.*, 4(2): 40–47.
- Suwan, E., Arthornthurasuk, S. and Kongsaeree, P.T. (2017) A metagenomic approach to discover a novel β-glucosidase from bovine rumens. *Pure Appl. Chem.*, 89(7): 941–950.
- Chen, A., Wang, D., Ji, R., Li, J., Gu, S., Tang, R. and Ji, C. (2021) Structural and catalytic characterization of TsBGL, a β-glucosidase from *Thermofilum* spp. ex4484_79. *Front. Microbiol.*, 12: 723678.
- 76. Konar, S., Sinha, S.K., Datta, S. and Ghorai, P.K. (2019) Probing the effect of glucose on the activity and stability of β -glucosidase: An all-atom molecular dynamics simulation investigation. *ACS Omega*, 4(6): 11189–11196.
- 77. Silano, V., Barat Baviera, J.M., Bolognesi, C., Cocconcelli, P.S., Crebelli, R., Gott, D.M., Grob, K., Lambré, C., Lampi, E., Mengelers, M., Mortensen, A., Rivière, G., Steffensen, I.L., Tlustos, C., Van Loveren, H., Vernis, L., Zorn, H., Herman, L., Aguilera, J., Andryszkiewicz, M., Arcella, D., Liu, Y., Nielsen, E., Norby, K. and Chesson, A. (2022) Safety evaluation of the food enzyme α-glucosidase from the *Aspergillus niger* strain AE-TGU. *EFSA J.*, 20(3): e07171.
- Wang, Y., Tashiro, Y. and Sonomoto, K. (2015) Fermentative production of lactic acid from renewable materials: Recent achievements, prospects, and limits. *J. Biosci. Bioeng.* 119(1): 10–18.
