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Microbiota and Food Safety of *Acheta domesticus*: Perspectives and Challenges

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Abstract

This work highlights the food safety risks associated with *Acheta domesticus* as a food and/or food ingredient and provides recommendations to address these risks. The review presented an updated analysis of the microbiota content and its food safety risks in the edible house cricket, *Acheta domesticus*, the main insect produced industrially. It is promoted as a sustainable and nutritious alternative to support food security.

This review synthesises current quantitative evidence on the microbiota and associated food-safety risks of the house cricket (*Acheta domesticus*), the principal insect reared at industrial scale and promoted as a sustainable, protein-rich food ingredient. Studies reporting original microbial data from fresh insects and a range of processed products (dried, powdered, freeze-dried, cooked, boiled, and fermented) were compiled. Results indicate that fresh *A. domesticus* frequently harbours elevated microbial loads, often exceeding European safety criteria for total aerobic counts, Enterobacteriaceae, and spore-forming bacteria. Although standard post-harvest processing substantially reduces total microbial burdens in most cases, a persistent core microbiome remains, notably thermotolerant spore-forming bacteria (e.g., *Bacillus cereus* and *B. cytotoxicus*) and toxigenic fungi (e.g., *Aspergillus flavus*, *Mucor* spp.). Given these findings and the absence of specific regulatory frameworks in many jurisdictions, there is a critical need for mandatory implementation of Good Agricultural Practices (GAP) and Hazard Analysis and Critical Control Point (HACCP) systems across insect-rearing and processing chains. Effective food-safety management should include validated thermal treatments, strategies to target spore control, routine microbiological monitoring, and the development of clear, science-based regulatory standards to ensure the quality and safety of insect-derived food products.

Keywords: house cricket, microbiological risks, insect regulatory framework.

Introduction

The global population's rapid growth and climate change have increased the challenges to agri-food systems, alongside rising greenhouse gas emissions, soil degradation, water pollution, and land scarcity (Pilco-Romero *et al*., 2023; Zhang *et al*., 2024). These aspects negatively impact crop and livestock productivity, increasing the number of people at risk of food insecurity

(Kelemu *et al*., 2015; Nadeau *et al*., 2015; Pilco-Romero *et al*., 2023). Food agri-systems are changing toward revalorization of traditional ingredients while adopting new technologies to develop sustainable products and support the circular economy (Monroy-Torres *et al*., 2021; Ververis *et al*., 2022; Pilco-Romero *et al*., 2023; Zhang *et al*., 2024). This includes promoting non-conventional plants, ancestral grains, flowers, apiculture products, and edible insects (Ververis *et al*., 2022; Pilco-Romero *et al*., 2023; Zhang *et al*., 2024). The inclusion of edible insects raises questions about safety and microbiological risks that need to be addressed (Ververis *et al*., 2022; van Huis *et al*., 2013; Psarianos *et al*., 2023; Siddiqui *et al*., 2024; Pilco-Romero *et al*., 2023).

Orthoptera are among the most widely cultivated edible insects (Omuse *et al*., 2024), mainly *Acheta domesticus, Gryllus bimaculatus, Locusta migratoria, Oxya yezoensis, Gryllodes sigillatus, Gryllotalpidae, Sphenarium purpurascens, Melanoplus differentialis*, and *Brachystola* spp. (Milanovic *et al*., 2016; Garofalo *et al*., 2017, 2018; Grabowski and Klein, 2017; Osimani *et al*., 2017; Vandeweyer *et al*., 2017; Fasolato *et al*., 2018; Ibarra-Herrera *et al*., 2020; Carreto *et al*., 2023; Ma *et al*., 2023). In 2020, about 19 insect species were marketed for human consumption in the EU, particularly in Austria, the UK, the Netherlands, Denmark, Finland, and Belgium (Bermúdez-Serrano, 2020). The insect market is estimated at $3.3 billion in 2023 and projected to reach $17 billion by 2032 (Shahbandeh, 2022). *A. domesticus* is the major industrially produced insect (van Huis *et al*., 2013; Arcos-Estrada *et al*., 2020; Kim *et al*., 2020; Psarianos *et al*., 2023). Its protein, antioxidants, minerals, and dietary fibre content (Ververis *et al*., 2022; Pilco-Romero *et al*., 2023; Siddiqui *et al*., 2024; Zhang *et al*., 2024) make it suitable for a range of food products thanks to its techno-functional properties (Pilco-Romero *et al*., 2023; Lucas-González *et al*., 2019; Siddiqui *et al*., 2024). Although *A. domesticus* is among the most widely consumed and farmed insects globally, its microbial risks remain unclear. The number of studies has increased in recent years to address this gap. The European Regulatory Commission first established specific criteria for microbiological hygiene in insects used as food or in insect-based products sold for human consumption (EU 2015/2283; Turck *et al*., 2016). These criteria were initially insufficient and have since been improved; however, there is still a need for more information about specific species, rearing conditions, and process parameters to be followed.

Several studies have examined the microbiological profile and potential toxic compounds in various insects (Garofalo *et al*., 2017; Osimani *et al*., 2017; Fernandez-Cassi *et al*., 2019; Ververis *et al*., 2022). That is why standardized data collection will improve the implementation of this information for academia, industry, and policymakers (Ververis *et al*., 2022). Studies on *A. domesticus* focus on food safety due to its diverse bacterial communities, which can vary depending on diet, climate conditions, and farming practices (Aleknavičius *et al*., 2022; Ververis *et al*., 2022; Hance *et al*., 2025). The gut microbiome in insects plays a key role in metabolism, immune system function, and digestion (Engel and Moran, 2013; Jung *et al*., 2014; Beltrán-Soro *et al*., 2023). Understanding cricket microbiota may enhance farming efficiency and improve the nutritional quality of insect products. It may also help identify and control potential pathogens. This review primarily focuses on the food safety of *A. domesticus* for human consumption. Consequently, this review aims to describe the house cricket microbiota profile, assess the microbial risks associated with its use in food, and identify key data gaps. Based on documented hazards arising from poor hygiene, external contamination, and inadequate processing, recommendations are provided for the safe rearing, harvesting, and processing of both whole insects and derivative products.

This work aims to describe the house cricket microbiota profile, assess the risks in the food context, and identify key data gaps.

Search analysis

The research was conducted in the electronic bibliographic databases Science Direct, Dialnet, PubMed, and Springer using different combinations of search terms (*Acheta domesticus*, cricket, house cricket, crickets, microbiota, microbiological hazard, microbiome, microbiological hazards, microbiological risk, microbiological risks, microorganism, microorganisms, pathogen or pathogens). No restrictions were applied regarding the year of publication or language. Duplicates were removed after the search was completed. After that, a manual comparison was conducted using reference lists from selected articles and those generated by Google Scholar. Additionally, the Generative AI tools, Elicit and Research Rabbit, were utilized strictly as complementary search aids to identify and compare scientific articles; these tools were not primary data sources. The correlation of author, institution/country/topic features was also used to identify additional articles. The last collection of articles took place on May 14, 2025.

To ensure the integrity of the corpus, all final article selections and inclusions were validated manually through a screening process; studies without original quantitative data or those focusing on different genera were excluded. Publications providing original data in the fields of microbiology, toxicology, and microbial hazards of fresh and processed products on complete adults of *A. domesticus* and/or late instar nymphs. Additional criteria included reporting only from primary research and publications in English, French, and Spanish. Articles were excluded if they did not identify the insect species. The data on whole insects included fresh, frozen, freeze-dried, roasted, sterilized, fermented, blanched, fried, flour, or foods with a percentage of cricket.

Bibliometric analysis

From an initial pool of 1,596 records, the results of manual screening are presented in Table 1. More than one-third of these studies are published in Insects, Journal of Food Microbiology, Foods, Applied and Environmental Microbiology, and European Food Research and Technology. These journals frequently include studies that applied traditional microbiology techniques and metagenomic analysis of *A. domesticus* microbiota. Of the studies, 41% use dried crickets, 20% focus on whole, fresh insects, and 20% examine foods containing crickets. The remaining corpus consists of 12% frozen insect samples, 6% entire insect freeze-dried samples, 6% whole roasted samples, and individual mentions for whole sterilized, fermented, blanched, fried, and pulsed electric field-treated samples. Many studies mentioned multiple origins. Sixty-one different insect samples grouped by country of origin were analysed and displayed in Figure 1. These studies were conducted on insect species typically harvested from the wild, cultivated, reared on farms, and/or purchased from local markets.

Table 1.- Manual screening process

Process step	Identified studies	Excluded studies
Identification	1596 total registers	1488 excluded (duplicated studies and gut microbiota of other species)
Screening	108 studies to analyse	39 excluded (without original data, different cricket genus like *Gryllus, Teleogryllus,* or *Sphenarium*)

Eligibility (full text)	59 studies to evaluate	10 excluded (entomopathogen or cricket pathogens approach).
Inclusion	59 final records **set**	N/A

Most of these publications were open access, and almost 50% of the studies originated in Europe, where entomophagy has a limited tradition. Interestingly, only 32% of the studies are from countries with an entomophagy tradition, such as Mexico, Nigeria, Kenya, Thailand, Lao, and Jamaica. In these countries, other insects are consumed, and the house cricket is not the principal species, although its consumption is increasing. In these regions, edible insects are typically collected from the wild (corn fields and meadows) rather than raised on farms; however, there are limited food safety practices, minimal handling, packaging, and unclear regulations in Asia, Africa, Latin America, and Oceania that limit industrial growth and agricultural innovation (Lähteenmäki-Uutela *et al*., 2017).

Figure 1.- Geographical distribution of *A domesticus* studies and characteristics of the samples.

Insect regulatory framework

In Europe, *Alphitobius diaperinus, Acheta domesticus, Locusta migratoria* and *Tenebrio mollitor* are classified as novel food ingredients by the European Food Safety Authority and are sold because they have been proven safe for human health (EFSA 2017/893). In the United States, numerous farms, restaurants, and grocery stores currently offer insect-based products, despite the absence of comprehensive regulations. This regulatory uncertainty has hindered business and market expansion (Lähteenmäki-Uutela *et al*., 2021). Unlike the European Union, insects in the U.S. are considered conventional food under the Food, Drug, and Cosmetic Act. Therefore, insects or insect products must be clean, safe, and meet the declared safety standards for processing, rearing, harvesting, packaging, and marketing (United States Code Title 21; Brody, 2016).

Regarding Asian countries, in China, insects are categorised as novel foods; however, the China National Food and Drug Administration has not yet implemented comprehensive national legislation or safety standards, despite its millenary tradition of entomophagy (Xie *et al*., 2024). In the absence of federal regulation, certain regions have established local food safety standards for edible fresh and frozen silkworm pupae (*Bombyx mori*). These rules included rearing conditions, harvesting, testing, use as additives, packaging, and marketing standards, in accordance with the National Food Safety Standards GD778 and GB14881 (DBS45 030-2016 Local Food Safety Standard, Guangxi). In Japan, the Ministry of Agriculture, Forestry, and Fisheries considers insects a new protein source as part of the Green Food System Strategy (Tokunaga *et al*., 2025) to support the industrial and scientific development of entomophagy. Currently, whole insects and insect-based foods only need to meet safety standards, but when considered as novel additives, they require pre-market authorization and safety declarations from the Ministry of Health, Safety, and Welfare (Lähteenmäki-Uutela *et al*., 2021; Caparros *et al*., 2024). Thailand is the major cricket producer, the first Asian country with established laws and standards for cricket production (Tiwasing *et al*., 2025), and the first to implement Good Agricultural Practices since 2017. They focus on farm production, agricultural practices, hygiene, and pesticide levels in food (Hanboonsong and Durst, 2020). As a pioneer, Thailand ensures the safe and high-quality production of insects to meet export requirements for the EU and global markets (Caparros *et al*., 2024).

Oceania countries also consume insects, according to the Australia and New Zealand Food Standard Code, only four insect species (*A. domesticus, O. smaragdina, T. mollitor*, and *Z. morio*) are approved for human consumption (Caparros *et al*., 2024); other species are habitually eaten but cannot be sold publicly (Lähteenmäki-Uutela *et al*., 2021). Although farmers can work with pest insects with written approval, there are no specific commerce regulations for marketing these products (Lähteenmäki-Uutela *et al*., 2021). Australia also regulates the importation of insects for food or feed.

In indigenous regions of Africa and Latin America, insects have been traditionally consumed. In Mexico, insects are not considered novel food or new ingredients. Currently, there are no specific laws governing insect-based products; however, initiatives within organic agriculture guidelines, such as Article 144 of the Organic Law, aim to establish parameters for insect production. On the other hand, insect farms are limited, often focusing on non-traditional insects (*A. domesticus*), primarily because insects are typically harvested in wild environments (Lähteenmäki-Uutela *et al*., 2021). Additionally, countries such as Brazil and Argentina lack clear laws regarding the use of insects as food products (Caparros *et al*., 2024). These countries, like many in Latin America, follow the CODEX Alimentarius (Lähteenmäki-Uutela *et al*., 2017), but they have no specific regulations on the use of insects as food. Numerous initiatives in Africa (South Africa and Nigeria) aim to promote insect production; however, there is a lack of regulations governing farming and processing practices (Usman and Yusuf, 2020; Tanga *et al*., 2025).

A comparative analysis of global frameworks reveals three distinct approaches: the EU employs a precautionary 'Novel Food' model requiring pre-market safety authorization; the USA treats insects as conventional food under existing safety standards without specific comprehensive rules; and Latin America, Africa, China, and Japan often operate with partial, local, or non-existent legislation. While the EU leads in specific microbiological criteria, pioneers like Thailand demonstrate that emerging markets can successfully implement Good Agricultural Practices (GAP) to meet international export standards.

Microbiota of fresh *A. domesticus*

Scientific research has broadly analyzed cricket microbiota, allowing for a clear distinction between the intrinsic microbiota, primarily determined by host habits and metabolism, and extrinsic microorganisms introduced through diet or environmental contamination during rearing. In this section, the dominant trends in *A. domesticus* microbiota research, including a strong focus on bacterial community dynamics, are discussed to propose recommendations for ensuring the food safety of whole fresh crickets. Colony forming unit (CFU) is used to evaluate the microbial load of whole fresh *A. domesticus*, Table 2. Their microbial load did not meet the European Food Safety Authority (EFSA) standards for human consumption (EFSA 2023/5). The total aerobic count (TAC) ranged from 7.0 to 9.2 Log_{10} CFU/g, values considerably higher than 5 Log_{10} CFU/g, which is established as a safety parameter (EFSA 2023/5).

Noteworthy Enterobacteria load varies between 5.9 and 8.0 Log_{10} CFU/g (Klunder *et al*., 2012; Vandeweyer *et al*., 2018; Fernandez-Cassi *et al*., 2020); these values are higher than the value established by the EFSA (EU 2015/2283). Also, the CFU reported values for yeasts and moulds are higher than the regulatory limits for yeasts and moulds (2 Log_{10} CFU/g), as well as those of *Bacillus cereus* <2 Log_{10} CFU/g, *E. coli* <2 Log_{10} CFU/g, and *Staphylococcus aureus* <2 Log_{10} CFU/g. The presence of *B. cereus* and *S. aureus* indicates a potential risk of foodborne illness.

Indeed, the only parameter that met the regulations was the absence of *Salmonella*. Notably, the presence of lactic acid bacteria (LAB) suggests that *A. domesticus* could have probiotic properties.

Table 2.- Reported range of microbial load of fresh *A. domesticus*.

Parameter	Colony counts (Log_{10} CFU/g)	EFSA 2023/5 (Log_{10} CFU/g)	Reference
Total aerobic colonies	7.0-9.2	5.0	Vandeweyer *et al*., 2018; Fröhling *et al*., 2020.
Enterobacteria	5.9-8.0	1.69	Klunder *et al*., 2012; Vandeweyer *et al*., 2018.
Lactic acid bacteria	6.7-7.8	-	Klunder *et al*., 2012; Vandeweyer *et al*., 2018.
Yeasts and Fungi	5.2-8.2	2.0	Klunder *et al*., 2012; Nyangena *et al*., 2020.
Aerobic spore-forming	2.2-5.0	<2.0	Vandeweyer *et al*., 2018; Nyangena *et al*., 2020.
Anaerobic spore-forming	2.2-4.0	<2.0	Vandeweyer *et al*., 2018; Nyangena *et al*., 2020.
Bacillus cereus	2.7-9.3	<2.0	Fernández-Cassi *et al*., 2020; Fröhling *et al*., 2020.
Staphylococcus aereus	7.7-9.1	<2.0	Fernández-Cassi *et al*., 2020; Fröhling *et al*., 2020.
Faecal coliforms	6.1-6.7	<1.0	Nyangena *et al*., 2020; Fernandez-Cassi *et al*., 2020
Salmonella spp.	Absence in 25 g.	Absence in 25 g.	Fernandez-Cassi *et al*., 2020; Mitchaothai *et al*., 2024.

Note: ***EFSA***, *European Food Safety Authority*.

Remarkably, fresh samples (30) do not comply with at least one of the EFSA's microbiological safety parameters for TAC, enterobacteria, moulds, yeasts, spore-forming bacteria, and faecal coliforms. These parameters were exceeded by all raw samples, including spore-forming bacteria and coliforms. Continuous monitoring, control of microbial contamination, and obligatory further processing are essential to guarantee the safety of *A. domesticus* as a food source. In addition to the development of guidelines by regulatory agencies in each country to ensure safety in rearing units intended for human consumption.

Regarding the intrinsic profile, studies by Aleknavičius *et al*. (2022) and Vandeweyer *et al*. **(2017)** identify *Bacteroides* and *Parabacteroides* as dominant and typical members of the endogenous intestinal community in *A. domesticus*. However, Aleknavičius *et al*. (2022) noted *A. domesticus* is intrinsically characterized by *Pseudomonadaceae* and *Akkermansia*. Metagenomic studies have identified the predominant species in the microbiota of fresh-whole *A. domesticus*. The results are shown in Table 3.

Table 3.- Microbial composition of *A. domesticus* fresh samples analysed by metagenomics.

Source	Analytical Method	Family / Genera	Reference
Reared/ commercial	Amplicon-based, 16S rRNA gene V3-V4 region (466 bp)	*Wolbachia* *Faecalibacterium* *Parabacteroides* *Bacillus* *Streptococcus* *Klebsiella* *Escehrichia* *Shigella* *A flavus* *Muccor*	Fernandez-Cassi *et al*., 2020.
Reared/ Laboratory	Amplicon-based, 16S ribosomal RNA gene region (V3–V4). 341F/785R primers	*Parabacteroides* 31.97% *Bacteroides* 14.65 % *Enterococcus* 1.16% *Akkermansia* 1.03% *Acinetobacter* 0.49%	Aleknavičius *et al*., 2022
Reared/ Laboratory	Amplicon-based, 16S ribosomal RNA gene region (V2, V4 and V8)	Class level: *Gammaproteobacteria* 44% *Clostridia* 12.25% *Bacilli* 15.0% *Erysipelotrichia* 3.0% *Bacteroidia* 22.75% *Flavobacteria* 1.5%	Beltran *et a*l., 2023.
Reared/ Laboratory	Nanopore sequencing MinION	*Citrobacter* *Enterobacter* *Acinetobacter* *Klebsiella*	Lim *et al*., 2024.

		Fusobacterium *A. domesticus densovirus AdDV* *Invertebrate Iridovirus 6 II6*	
Reared/ commercial	Target-Free Screening (for exploratory purposes): DNA sequencing (PacBio) and RNA sequencing (Ion Proton S5XL)	Species level: *Iflavirus AdIV* *Tombusviridae* Virgaviridae *Slow bee paralysis virus* *Invertebrate Iridovirus 6 II6*	De Miranda *et al*., 2021
Reared/ Laboratory	Whole Genome Sequencing (Illumina MiSeq platform)	*Klebsiella pneumoniae* *Staphylococcus warneri* *Staphylococcus gallinarum* *Staphylococcus arlettae* *Mammaliicoccus sciuri* *Enterococcus faecalis* *Bacillus cereus*	Bello *et al*., 2023
Reared/ commercial	Amplicon-based, V4 region of the 16S rRNA gene	*Lactococcus sp.* *Erwinia oleae* *Enterococcus sp.* *Photorhabdus sp.* *Enterobacteriaceae sp.* *Parabacteroides sp.* *Clostridiales sp.* *Bacteroides sp.* *Pseudomonadaceae sp.* *Buttiaxella agrestis*	Vandeweyer *et al*., 2017.

The dominant phyla in the microbiota of *A. domesticus* (Table 3) are Pseudomonadota (Proteobacteria), Bacillota (Firmicutes), Bacteroidota (Bacteroidetes), and Verrucomicrobiota (Verrucomicrobia) (Fernandez-Cassi *et al*., 2020; Aleknavičius *et al*., 2022; Beltrán *et al*., 2023). Actinobacteria are present in lower amounts at higher rearing temperatures (Beltrán *et al*., 2023). In fresh crickets, the predominant class is Gammaproteobacteria (Beltrán *et al*., 2023), followed by Clostridia, Bacilli, Erysipelotrichia, and Bacteroidia. While orders comprise Bacillales at 54%, Bacteroidales at 21.2%, and Lactobacillales at 8.9% (Garofalo *et al*., 2017). On the other hand, Enterobacteriaceae, Clostridiaceae, Lachnospiraceae, Bacillaceae, Staphylococcaceae, Rikenellaceae, and Porphyromonadaceae (Fernandez-Cassi *et al*., 2019) emerge as the most reported families among those orders. Notably, Parabacteroidetes is more common under controlled rearing conditions, and Bacteroidota is prevalent in wild crickets (Osimani *et al*., 2018; Aleknavičius *et al*., 2022). Interestingly, many of the genera found are essential to human gut health (Engel and Moran, 2013).

Other components of the microbiota, such as viruses, Archaea, and Eukarya, are scarcely reported. Fernández-Cassi *et al*. (2020) observed the presence of *Aspergillus flavus* and *Mucor circinelloides* in whole crickets fed with different substrates in laboratory conditions. Diet acts as a critical vector for introducing bacteria and fungi into the cricket's digestive system. For instance, Vandeweyer *et al*. (2018) found a striking similarity among the feed, box substrate, and the insects, where the plant-associated genus *Erwinia* became dominant within the crickets. Similarly, Fernandez-Cassi *et al*. (2020) identified direct transmission of *Mucor circinelloides* from contaminated feed to reared insects. Since some strains of this fungus produce toxins and others are pathogens, rearing practices must be designed to prevent contamination of crickets with these strains. De Miranda *et al*. (2021) reported that only 1% of faecal genetic material consisted of viruses; these viruses are essential for regulating microbiota structure. The principal families found were Iflavirus, Caudavirales, and Levivirales (de Miranda *et al*., 2021). Hepatitis A virus, hepatitis E virus, and norovirus genogroups have not yet been identified, indicating a low risk to human food safety (Vandeweyer *et al*., 2020). However, most studies have focused on their pathogenic capacity, overlooking their ecological roles.

The primary concern for food safety is the presence of pathogenic and opportunistic bacteria. The sporulated bacillus is a risk group that includes *B. cereus* and *B. cytotoxicus* (Fasolato *et al*., 2018; Fernández-Cassi *et al*., 2020; Frigerio *et al*., 2020; Bello *et al*., 2025). Furthermore, *Enterobacter* and *Acinetobacter* spp. (Aleknavičius *et al*., 2022; Mitchaothai *et al*., 2024), *Klebsiella pneumoniae* and *Enterococcus faecalis* (Bello *et al*., 2025) represent a risk. It also harbours beneficial genera with probiotic properties, such as *Lactobacillus, Lactococcus*, and *Micrococcus* (*M. luteus*) (Vandeweyer *et al*., 2017; Fernandez-Cassi *et al*., 2020). Despite there are reports of *E. coli* and *Salmonella spp*. (Nyangena *et al*., 2020), most sequencing studies do not detect them (Grabowski and Klein, 2017; Fuentes-Gardiola *et al*., 2024), suggesting that strict hygiene in rearing is essential to limit pathogens and ensure compliance with regulatory criteria (EU, 2015/2283; EFSA, 2024).

Facility hygiene and post-harvest handling introduce additional microbiological risks. Regarding drinking water and pipes, Mitchaothai *et al*. (2024) found that water sources and PVC pipes are the primary sources for *Klebsiella* spp. and *Enterobacter* spp. contamination; these pathogens proliferate due to humidity and the accumulation of frass near water delivery systems. Additionally, the oviposition substrate (e.g., soil or peat) is identified as the primary source of soil-derived bacterial endospores. This environmental pressure is constant, as Grispoldi *et al*. (2021) demonstrated that the load of *Enterobacteriaceae* and aerobic bacteria on rearing box surfaces increases significantly throughout the production cycle, acting as a continuous source of recontamination. Continuous monitoring, control of microbial external contamination, and further processing are crucial to ensure the safety of *A. domesticus*. Regulatory agencies should establish guidelines to maintain safety in rearing units for human consumption. Alongside traditional microbial techniques, metagenomics and other omics complement the food safety assessments. The referenced studies provide a comprehensive understanding of the microbiota of the fresh house cricket, highlighting the ongoing need to monitor and prevent contamination during rearing and processing.

Microbiota of Processed *A. domesticus*

Processing treatments significantly alter the microbial profile of *A. domesticus*. While most methods successfully reduce contaminant microorganisms associated with fresh crickets, thermotolerant spore-forming bacteria often remain. The composition of the cultivated microbiota in processed house cricket products, including whole dried crickets, flour, pastes, freeze-dried products, breads, bars, and supplements, has been reported by several authors. The identified microorganisms were summarized in Table 4.

Table 4.- Total colony counts of the cultivable microbiota of processed *A. domesticus*.

References
Fuentes-Gardiola *et al*., 2024; Bellegia *et al*.,
Klunder *et al*., 2012.
Klunder *et al*., 2012.
Nyangena *et al*., 2020.
Aleknavičius *et al*., 2022.
Fröhling *et al*., 2020.
Caparros *et al*., 2017.
Caparros *et al*., 2017.
Psarianos *et al*., 2020.
Bartkiene *et al*., 2023.
Psarianos *et al*., 2020; Sweers *et al*., 2025.

Process	Total aerobic counts	Enterobacteria	Lactic acid bacteria	Yeasts and moulds	Spore forming bacteria
Dried/powder	1.98-4.8	1.0-2.1	2.0-4.87	1.0-3.1	1.0-4.0
Boiled 1 min & dried	3.1-3.8	1.3-3.2	-	-	2.0-2.8
Boiled 5 min & dried	5.4-5.6	1-1.3	-	-	1.7-2.0
Boiled & oven dried	1.0-1.8	-	-	-	-
Blanching	2.3-4.39	<1.0	-	-	-
Steamed	2.83	<2.1	-	<2.0	2.6-3.5
Microwave	4.0	-	-	1.5	1.4
Autoclaved	1.5-3.7	-	-	<1.0	
Freeze dried	4.0	6.0	-	<1.0-4.0	2.0
Fermented	5.0	-	5.66	-	-
Pulsed electric fields	6.0-6.5	5.5-7.0	-	3.5-5.0	<3.0

Note: Colony counts are shown in Log_{10} CFU/g.

TAC indicates that most processing treatments successfully meet EFSA regulatory parameters, except for dried, freeze-dried, and pulsed electric fields processes (Bellegia *et al*., 2023; Fuentes-Guardiola *et al*., 2024). *Cutibacterium variabile*, *Lactococcus garviae*, *Enterococcus haemoperoxidus*, and *Enterococcu*s spp. have been isolated from whole dried cricket powder (Garofalo *et al*., 2017). The genus *Corynebacterium* has also been isolated (Garofalo *et al*., 2017; Fernandez-Cassi *et al*., 2019). *C. variabile, E. haemoperoxidus*, and *Corynebacterium* are commensal bacteria and could be opportunistic in immunocompromised humans. *L. garviae* is a zoonotic pathogen, rarely an opportunistic human pathogen (Rossi *et al*., 2023).

Pathogens such as *Salmonella spp*. and *Listeria monocytogenes* are generally not detected in processed crickets (Fernández-Cassi *et al*., 2020); however, rare cases of *Salmonella* have been reported (Nyangena *et al*., 2020; Frentzel *et al*., 2022). Boiling and toasting decreased pathogen bacterial populations, lowered *Staphylococcus aureus* levels, and eliminated yeasts and moulds, Lac+ enteric bacteria, *Listeria,* and *Salmonella* (Nyangena *et al*., 2020). Noteworthy, LAB counts are consistently high, which limits the growth of enterobacteria and spore-forming bacteria (Belleggia *et al.,* 2023; Kittibunchakul *et al*., 2023). Again, the major concern is spore-forming bacteria like *B. cereus*, which are found at 1.0-4.0 Log_{10} CFU/g (EFSA, 2015; Frigerio *et al*., 2020; Frentzel *et al*., 2022), due to poor environmental hygiene and deficient processing and storage practices. Cross-contamination during processing also remains a significant challenge. Vandeweyer *et al*. (2018) reported an unexpected increase in total microbial load following drying and smoking. This rise was attributed to human handling or inadequately disinfected processing equipment.

Based on data synthesis from the corpus, an evaluation of processing efficacy for microbial load reduction was conducted, analysing results from all processed samples (30) reported in each reference (Table 4). After cricket processing, only 10 had an accepted microbial load according to EFSA (2015). Although some samples of aerobic bacterial endospores, which ranged from 1.7 to 5.0 Log_{10} CFU/g in raw insects, showed a significant reduction after blanching, others (with higher initial counts) showed no significant decrease. Final processed products, such as flour, biscuits, or breads, comply with EFSA regulatory limits.

The use of traditional microbiological analysis in processed *A. domesticus* samples provides a direct assessment of the total microbial load and the viability of these organisms, while sequencing techniques can detect microorganisms that might not be detected by traditional colony counts, even if they are not viable, as long as DNA is present.

The results of the metagenomic analysis are shown in Table 5. Processing treatments significantly alter the microbial profile; Frigerio *et al*. (2020) demonstrated that a stable core microbiota—including *Parabacteroides, Bacteroides*, and the Lachnospiraceae families—persists even in highly processed products such as protein bars and biscuits. This persistence is supported by findings from Ng *et al*. (2018), who determined that the microbial community remains stable at higher taxonomic levels (Phylum to Family) regardless of diet or environment.

Table 5. Metagenomic analysis of cricket products.

Product	Analytical Method	Taxa	Reference
Whole dried / powder	16s rRNA amplicon sequencing (V1-V3 region)	*Lactococcus garviae* *Enterococcus* spp. *Enterococcus haemopevoxidus* *Corynebacterium variable* *Parabacteroides* spp.	Garofalo *et al.,* 2017; Garofalo *et al*., 2018.
Whole dried/ powder	PCR DGGE	*Bacillus cereus* *Clostridium thermopalmarium* *Naxibacter intermedius* *Rufibacter* sp. *Pediococcus lolii* *Erwinia* sp. *Citrobacter* sp. *Tannerella forysthia* *Bacillus weihenstephanensis* *Streptomyces glaucosporus* *Bacillus subtillis* *Acinetobacter* sp. *Planomicrobium chinese* *Arthrobacter tecti*	Osimani *et al*., 2016
Roasted/ powder	Amplicon 16s rRNA Ilumina/pyrosequencing	*Bacillus amyloliquefaciens* *Bacillus glycinifermentans* *Bacillus licheniformis* *Bacillus safensis* *Bacillus sonorensis* *Bacillus subtillis* *Bacillus cereus* *Pseudobacillus badius* *Enterococcus faecium* *Enterococcus lactis* *Exigobacterium* sp. *Klebsiella pneumoniae* *Enterobacter hormaechei* *Acinetobacter baumamii* *Acinetobacter radioresistens* *Curtobacterium* sp.	Pal *et al*., 2024.
Flour	16 sRNA (V3-V4 region)	*Bacteroides* *Clostridiaceae* *Clostridiales*	Messina *et al*., 2019.

		Coprococcus *Dysgonomonas* *Enterobacteriaceae* *Enterococcus* *Trabulsiella* *Gammaproteobacteria* *Lachnospiraceae* *Lactobacillus* *Luteimonas* *Porphyromonadaceae* *Ruminococcaceae* *Ruminococcus*	
Boiled/ Dried	16s rRNA PCR-DGGE	*Hespellia porcina* *Staphylococcus* spp. *Staphylococcus capitis* *Lysobacter* sp. *Pseudomonas* sp. *Hydrogenophilus hirschii* *Ruminococcus gauvreavii* *Clostridium* sp.	Milanovič *et al*., 2016; Milanovič *et al*., 2020.
Freeze-dried Flour	16s-23s rRNA internal transcripted spacer region PCR.	*Cronobacter sakazaki* (99% prob.)	Greenhalgh and Amund, 2019.
Freeze dried/ roasted/ cooked / dehydrated	16s rRNA gene sequencing	*Kokuria rhizophila* *Macrococcuss* spp. *Enterococcus faecium* *Pediococcus acidilactici* *Bacillus cereus* (sensu stricto group) *Bacillus thuringensis* *Bacillus cytotoxicus* *Lysinobacilluss* spp.	Fasolato *et al*., 2018.
Cracker and protein bar	High-throughput DNA Sequencing 16S rRNA genes (V3 and V4 hypervariable regions)	*Parabacteroides* *Enterobacter* *Bacteroides* *Enterococcus* *Lactococcus* *Alistipes* *Pseudomonas* *Dysgonomonas* *Ruminococcaceae* *Citrobacter* *Aeromonas* spp. *Neisseria* spp.	Frigerio *et al*., 2020.
Roasted/ dried/ boiled/ powder	Whole genome sequencing NextSeq500	*Bacillus cereus* *Bacillus cytotoxicus* *Clostridium perfringens* *Salmonella* spp.	Frentzel *et al*., 2022.

Commonly known as a human pathogen, *Staphylococcus* spp. was detected at low abundance in some processed samples, such as powdered crickets, along with*, Enterococcus haemoperoxidus*, and *Enterococcus* spp. (Garofalo *et al*., 2017*). Aeromonas* spp. and *Neisseri*a spp., were identified via High-Throughput Sequencing (Frigerio *et al*., 2020). Opportunistic pathogens, such as *Fusobacteria* and *Mycoplasma*, were detected at low frequencies in processed crackers and protein bars (Frigerio *et al*., 2020). However, as mentioned above, these species may not be viable, yet some toxins may remain.

In summary, combined processes are the most effective for reducing microbial load (, such as combining boiling or roasting followed by sun or oven drying (Nyangena *et al*., 2020). Since heat treatment destroys active cells, and drying reduces water activity (Klunder *et al*., 2012; Nyangena *et al*., 2020). For pathogenic endospores, a combination strategy is recommended, which may include steaming, heat-and-pressure, fermentation, and drying (Vandeweyer *et al*., 2017). We suggest investigating the synergistic effects of processes to achieve effective microbial inactivation while preserving the nutritive properties of the house cricket (Sweers *et al*., 2025).

The intrinsic microbiota of house crickets constitutes a dominant and stable "core"—composed mainly of genera such as *Bacteroides*, *Parabacteroides*, *Fusobacterium*, and the family Lachnospiraceae— (Vandeweyer *et al*., 2017; Frigerio *et al*., 2020; Aleknavičius *et al*., 2022). This core persists even after industrial processing and is primarily attributed to endogenous factors such as host metabolism and internal insect physiology (Ng *et al*., 2018). In contrast, the external microbiota is highly variable and is attributed to extrinsic factors (Vandeweyer *et al*., 2018; Fernandez-Cassi *et al*., 2020), such as diet composition, the quality of drinking water, contact with rearing surfaces like soil (Klunder *et al*., 2012; Fasolato *et al*., 2018), and hygiene conditions during handling, processing, and transport (Vandeweyer *et al*., 2018; Grispoldi *et al*., 2021; Mitchaothai *et al*., 2024). Indeed, these external microorganisms came from contamination. Nevertheless, when the metagenomic taxa data for raw cricket and its processed products were analyzed, a core of 19 genera was identified in Supplementary Table S_1. These genera were: *Cronobacter, Bacteroides, Clostridium, Enterococcus, Lactobacillus, Ruminococcus, Hespellia, Staphylococcus, Lysobacter, Pseudomonas, Hydrogenophilus, Parabacteroides, Enterobacter, Lactococcus, Citrobacter, Bacillus, Acinetobacter, Erwinia,* and *Klebsiella.*

Challenges and Perspectives

The main challenges for insects as food include consumer cultural resistance and food safety concerns. The safety of rearing and processing crickets for food relies on a wide diversity of factors, including correct sample collection, microbial analysis, strict hygiene and management practices, careful control of feedstocks and environmental conditions, and effective post-harvest treatments to reduce the microbial load.

Conventional colony-count methods can fail to recover many anaerobic microorganisms; therefore, culture-based approaches tailored to strict anaerobes should be employed (Wyants, 2019). High-throughput sequencing has made sequencing a rapid and effective strategy for microbial surveillance. Since sequencing and conventional microbiology methods are complementary, we recommend the development of extraction methods tailored to intestinal and whole-insect matrices, optimising of nucleic-acid purification protocols, and broad adoption of whole-genome sequencing approaches.

Rearing conditions and overall hygiene directly affect microbial contamination (Grispoldi *et al*., 2021; Beltrán *et al*., 2023; Mitchaothai *et al*., 2024); thus, applying Good Agricultural Practices (GAP) and Hazard Analysis and Critical Control Points (HACCP) is a must for identifying, evaluating, and controlling potential hazards to ensure the final product's safety. Therefore, an "all-in, all-out" approach, which includes thorough cleaning and disinfection of structures at the end of each production cycle, is recommended as a strict control of environmental humidity is essential (Klunder *et al*., 2012; Grabowski and Klein, 2017). Second, daily removal of faeces and dead insects is necessary, involving cleaning the rearing boxes and collecting the crickets' waste while minimizing contact with the substrate (Vandeweyer *et al*., 2018; Frigerio *et al*., 2020; Mitchaothai *et al*., 2024). Additionally, workers must wear personal protective suits and wash their hands before, during, and after work to reduce the risk of contamination, particularly from human-derived bacteria such as *Escherichia coli* (Mitchaothai *et al*., 2024). In addition to regular cleaning and maintenance of drinkers and delivery systems, combined with appropriate disinfection procedures (e.g., chlorination or ozonation) and frequent replenishment of water, it is recommended to minimize the risk of contamination.

Therefore, it is essential to use substrates free of pathogenic species. A thorough assessment of the risk of Antimicrobial Resistance (AMR) is necessary, as feed can disseminate AMR genes, which impact the primary bacterial populations in the gut (Bello *et al*., 2025). In fact, the use of antibiotics in insect farms should be prohibited. Disinfectants must be applied judiciously to avoid the development of resistant bacteria and reduce the prevalence of antimicrobial resistance (AMR) genes (Donaghy *et al*., 2019). Biological alternatives—such as targeted dietary supplements (probiotics and prebiotics)—can beneficially modulate the cricket microbiota, by improving colony health and reducing disease incidence (Savio *et al*., 2022).

Post-harvest practices are ineffective: starvation does not appreciably reduce the total microbial load and should therefore be avoided (Inácio *et al*., 2021); simple water washing typically fails to achieve meaningful reductions in microbial load (Wynants *et al*., 2019; Fernández-Cassi *et al*., 2020). Thermal processing, by contrast, is an effective control for vegetative cells; for example, boiling for approximately five minutes substantially reduces counts of Enterobacteriaceae, yeasts, and moulds, while autoclaving or steaming for ≥15 minutes achieves more robust inactivation (Klunder *et al*., 2012; Caparros *et al*., 2017). Steam pasteurisation is often preferred in industrial settings for operational reasons (Frentzel *et al*., 2022). A persistent challenge is control of bacterial and fungal spores. To mitigate this risk, integrated (hurdle) approaches are recommended: combine thermal treatments with complementary technologies such as high-pressure processing, fermentation, dehydration, and irradiation to enhance decontamination efficacy (Sweers *et al*., 2025). In the finished product, preventing spore germination and outgrowth requires reducing water activity and maintaining strict temperature control during storage (Fasolato *et al*., 2018; Vandeweyer *et al*., 2018; Kittibunchakul *et al*., 2023). Additionally, the fermentation of cricket flour with LAB is a valuable tool for reducing pH and inhibiting the growth of undesirable pathogens (Bartkiene *et al*., 2023). Finally, minimize freeze–thaw cycles, as these can promote spore germination and compromise product safety (Fasolato *et al*., 2018). Collectively, these measures—combined with Good Hygiene Practices (GHP), validated HACCP plans, and routine microbiological monitoring—form the basis of an effective sanitary management strategy for insect production and processing. In summary, rearing and processing crickets for human consumption pose multiple food-safety challenges comparable to those of other animal-derived foods.

Perspectives on the consumption of crickets and cricket products vary across countries, with entomophagy being traditional in rural and indigenous regions and encountering prevalent cultural resistance in most Western nations. Akandwanaho *et al*. (2024) concluded that increasing insect consumption in rural Uganda requires awareness of the importance of using insects as a food source and of integrating insect rearing into household farming. This approach could be applied to other developing countries, but the products must be safe and sensorially and nutritionally attractive to consumers for consumer acceptance (Melgar-Lalane *et al*., 2019). However, entomophagy remains poorly accepted in many developed Western societies, where a substantial proportion of consumers report insect neophobia. McDade and Collins (2019) advocate applying concepts from innovation-diffusion theory and argue that the successful introduction of insect-based products requires building consumer trust, and remark that adoption barriers are reduced when established, trusted brands lead market entry. Furthermore, clear legislation establishing guidance and standards for hygienic insect handling, processing, and storage is indispensable to protect public health and to foster consumer confidence.

Conclusion

Despite its sustainability and economic potential as a protein source, *A. domesticus* represents a substantial microbiological risk in the fresh form, rendering appropriate post-harvest processing mandatory for human consumption. While conventional thermal processing treatments are generally effective, thermotolerant spore-forming bacteria and certain toxigenic fungi can persist after processing. Therefore, to ensure food safety and support responsible market expansion, the rigorous implementation of rearing and production management practices (GAP/HACCP) is essential. However, the feasibility of these measures should be evaluated through cost-benefit analyses, since validated controls may increase unit production costs. Finally, the paucity of specific regulatory frameworks in many jurisdictions, notably in parts of Latin America and Africa, where insect farming is growing annually, and in Western markets seeking authorization for novel insect-based foods, underscores the need for clear, science-based legislation and standards to govern insect production and protect public health.

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