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Food Safety, Health Risks, and Nutritional Interactions: Contaminants, Processing, and Gut Health

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Content

CHAPTER I

Evaluation of Health Risks Associated with Heavy Metals in Meat Samples

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1. Introduction

Heavy metal pollution has garnered significant global attention. These metals are harmful due to their non-biodegradable nature. Humans encounter these pollutants via water, air, soil, and contaminated food (Mance, 1987). The health of humans and other organisms is directly impacted by heavy metals in food. Even though lead (Pb), cadmium (Cd), and chromium (Cr) are necessary micronutrients for the proper growth of the human body, they are only needed in very small amounts, usually just a few milligrams daily (Trevors & Alloway, 2012). urban growth, industry, and

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agriculture development lead to human exposure to environmental pollutants. The body takes in these pollutants through breathing in polluted air and consuming contaminated water and food that is part of the food chain. Overconsumption of Food containing heavy metals can be harmful for the well-being of individuals (Saei-Dehkordi & Fallah, 2011).

Meat and meat products are significant for human dietary intake. Red meat, particularly red meat is an excellent protein source and also provides minerals like Iron (Fe), zinc (Zn), calcium (Ca), selenium (Se), and vitamins (Haytowitz & Pehrsson, 2018). Red meat is also favored by a lot of meat eaters because of its low intramuscular fat content and cholesterol levels (Al-Zuhairi et al., 2015). Even with many benefits, red meat has the potential to contain harmful toxins from the accumulation of Hazardous concentrations of heavy metals and trace elements, this may heighten the likelihood of certain illnesses (Demirezen & Uruç, 2006; Rudy, 2009). Heavy metals are hazardous and detrimental to human health even in very small amounts (for example, vital trace elements like Zn, Fe, and Se are categorized with macroelements like magnesium (Mg), sodium (Na), and calcium (Ca), as well as elements like arsenic (As), cadmium (Cd), lead (Pb), nickel (Ni), mercury (Hg) (Mikulewicz et al., 2013).

The increase in heavy metals is a result of both the development of human civilization and the extraction of natural resources (Aslam et al., 2011; Grodzińska et al., 2003). Meat and its products derived from beef polluted by harmful metals are a major supplier of exposure to poisonous elements in the food system, potentially leading to severe health issues (Badis, 2014; Obeid et al., 2016). Heavy metals cannot be decomposed or removed and may accumulate in organs such as the liver, kidneys, and muscles. However, these organs eliminate harmful substances from the body, making them important for analyzing heavy metals (Abou-Arab, 2001). International organizations like the World Health Organization (WHO), the Food and Agriculture Organization (FAO), and the US Environmental Protection Agency (US-EPA) have established allowable levels of heavy metals in food items (Joint et al., 2011).

The main objective of this review is to synthesize current research findings on the contamination of meat with heavy metals samples and also to evaluate associated health risks. By comparing the contamination levels and regulatory frameworks of these countries, we aim to provide recommendations for improving food safety standards and mitigating health risks.

2. Types of Heavy Metals Found in Red Meat

2.1 Lead

Livestock lead pollution originates from their surroundings, both the food and water they consume. Typically, lead accumulates in the food chain in animals and plants (Halliwell, 2000). The primary route of lead exposure is through the consumption of food, along with air (mainly from petrol lead dust) and drinking water. Lead can contaminate plant food through air and soil, which can then be consumed by animals. Lead exposure can happen in humans through ingesting plants or animals contaminated with lead. Other ways to ingest lead include using containers with lead or pottery glazes containing lead (Yu & Tsunoda, 2004).

Lead is a toxic substance that disrupts important enzymes and different cell components, acting as a neuropoison (Cunningham & Saigo, 1997). Lead demonstrates toxic effects on the neurological, gastrointestinal, renal, and hemopoietic systems (Baykov, Stoyanov & Gugova, 1996). Within people, about 20 to 50 percent of inhaled lead serves no essential purpose, while 5–15% of the inorganic lead is absorbed. Inhaled organic lead absorbs 80% of its amount, while oral organic lead is quickly taken in. Lead is primarily found in the skin and tissue, as well as soft tissue mineralization in the bloodstream (Yu & Tsunoda, 2004).

2.2 Cadmium

Cadmium is a highly significant metallic element within humans' diet and nutrition surroundings. The primary contact is confined factories related to dye, plating with metal, batteries, and specific plastics. Contamination with cadmium, such as from smelters or industries, as well as the use of Cd in waste groundwater, fertilizers, and sludge. may lead to minimal contamination for humans by consuming polluted foods like leafy greens, grains, and cereals (Baykov, Stoyanov & Gugova, 1996).

It remains uncertain whether cadmium has any beneficial effects. However, it does cause a range of toxicology and biochemistry disorders (Reesal & et al., 1987). Cd is a harmful substance that builds up in the ecological cycle on land, primarily concentrating within the kidney and liver tissues (Zasadowski & et al., 1999). The renal toxicity of cd can be reduced or eliminated through the intake of zinc, copper, and selenium. Improved development of metallothionein in the liver and renal cortex is suggested as the preventive effects of zinc and copper pre-treatment (Pizent & et al., 2001).

2.3 Mercury

Increased quantities are also seen in seafood dishes. Organic mercury compounds readily pass through biological membranes and have an affinity for fats. The two primary fish species with elevated mercury levels are those with lean liver and fatty fish. As fish age and move up the food chain, methyl mercury tends to increase. In older large predatory sea creatures such as swordfish, sharks, redfish, halibut, and tuna, this results in elevated levels of mercury (Oehlenschläger, 2002).

The consumption of mercury vapors produced through thermal volatilization can result in increased amounts of mercury toxicity, resulting in severe damage to the lungs and neurological system, which can be life-threatening. Reduced erythrism may result from high frequent exposure; it is distinguished by trembling hands, being easily excited, having difficulty remembering, sleeping, feeling apprehensive, and sometimes experiencing delirium. This is evident in employees in the felt-hat sector who come into contact with mercury (Hu, 2002).

2.4 Arsenic

Arsenic is frequently present in natural water sources and is often linked to geological sources, although examples of human behavior, such as using arsenic insecticides and fossil fuels, can have a notable impact in some regions. In oxidation, states III and V, arsenic may be found in natural waters as arsenic acid (H_3AsO_3) and its salts and as arsenic acid (H_3AsO_5) and its salts (Sawyer et al., 2003). Arsenic is a frequent pollutant found in wells in certain regions across the globe. In regions of Taiwan and Chile, deep-water wells are recognized for being contaminated with arsenic, which may result in long-lasting toxicity (Tsai et al., 1999).

The harmful consequences of arsenic vary according to its oxidation state and are also influenced by various chemical compounds. Inorganic arsenic is considered to cause cancer and is mainly associated with diseases of the skin, bladder, liver, and lungs (ATSDR, 2007). For many years, arsenic has been regarded as harmful in its inorganic form, specifically in terms of toxicity that is sub-chronic, hereditary toxicity, progressive toxicity, acute toxicity, and generative toxicity (Chakraborti & et al., 2004). Prolonged exposure to arsenic greatly raises the risk of developing several types of cancer, including liver, skin, lung, bladder cancers, and potentially colon and kidney cancers (Hu, 2002).

2.5 Other Heavy Metals

In addition to cadmium, arsenic, lead, and mercury, other heavy metals like zinc, copper, nickel, and chromium also pose significant health risks through various exposure routes, including food contamination. Chromium and nickel, for instance, can be toxic at relatively low concentrations, impacting renal and hepatic function. Copper and zinc, while essential at trace levels, can become hazardous when accumulated in excessive amounts (Abd Elnabi et al., 2023; Jacob et al., 2018).

3. Health Risks Associated with Heavy Metal Consumption

3.1 General Effects of Heavy Metal Toxicity

Exposure to heavy metals can result in several detrimental health impacts, such as disorders of the nervous system, gastrointestinal tract, heart, and kidneys. Common symptoms include headaches, nausea, abdominal pain, and fatigue. Chronic exposure can result in more severe conditions like cognitive impairments and organ damage (Järup, 2003; Tchounwou & et al., 2012). For instance, mercury and lead are neurotoxins that can cause developmental issues in children, while cadmium and arsenic are linked to cancers and kidney damage (Genchi & et al., 2020; Heindel, Newbold & Schug, 2015).

3.2 Specific Health Risks for Each Heavy Metal

Each heavy metal poses unique health risks. Cadmium exposure primarily affects the kidneys, leading to renal dysfunction and osteoporosis (Tinkov & et al., 2018). Skin lesions, heart diseases, and various cancers are linked to arsenic exposure (Naujokas & et al., 2013). Lead exposure can cause neurodevelopmental issues in children and hypertension in adults (Needleman, 2004). Mercury is known for its neurotoxic effects, particularly impacting cognitive function and motor skills (Rice & et al., 2014). These specific risks underline the importance of minimizing exposure to these metals.

3.3 Bioaccumulation and Long-Term Effects

Bioaccumulation of heavy metals accumulation in the body happens gradually, as these metals are not easily excreted. This accumulation can lead to chronic health conditions even at low exposure levels. Long-term effects include persistent neurological deficits, chronic kidney disease, and an increased risk of cancers (Jaishankar & et al., 2014). The persistent nature of toxic metals in the environment and their ability to accumulate in biological systems make them particularly hazardous, requiring stringent regulations and monitoring to protect public health (Hanna-Attisha & et al., 2016).

4. Regulations and Heavy Metal Monitoring in Red Meat

The regulation of heavy metals in red meat is primarily overseen by governmental bodies like the European Food Safety Authority (EFSA) in Europe and the Food and Drug Administration (FDA) in the United States. Those organizations establish maximum allowable limitations on the amount of heavy metals in dietary items, including red meat, to ensure consumer safety. Additionally, international organizations like the Codex Alimentarius Commission establish global standards for food safety, including guidelines on permissible amounts of metals that are heavy in meat products (EFSA, 2022). The liver, kidney, and meat provide vital microelements, particularly iron, copper, zinc, and selenium) found in the human diet. But they can also contain harmful metal residues. Establishing guidelines for heavy metal levels in these organs has become crucial in numerous countries. An example is the set Permissible levels of lead (Pb) and cadmium (Cd) in wet weight measured in milligrams per gram in different parts of bovine: Meat contains 0.1 and 0.05, the liver contains 0.5 and 0.5, and the kidney contains 0.5 and 1, as established by the European Commission (Table 1)(Commission of the European communities, 2006). Codex Alimentarius Commission (CAC) has set a cap on the amount of Pb allowed in beef flesh and edible organs that matches the levels set by the Commission of the European Communities (CAC, 1996).

Table 1: FAO Recommended Allowable limits of heavy metals in meat products

Metals	Maximum Permissible Level (MPL) in mg/kg
Iron (Fe)	0.01
Copper (Cu)	0.05-0.5
Cadmium (Cd)	0.5
Lead (Pb)	0.1
Zinc (Zn)	0.3-1.0
Mercury (Hg)	0.1
Chromium (Cr)	0.05

Source: Amfo-Otu, Agyenim & Adzraku (2014)

5. Literature Research of Heavy Metals in Meat

The following (Table 2) summarizes various studies conducted to measure heavy metal contamination in red meat and meat products from different regions worldwide. It details the type of sample analysis, the methods used for measurement, the toxic elements found, and the key findings of each study. This literature review highlights the geographical variation in heavy metal contamination levels, the specific metals of concern, and the health risks associated with these contaminants. These studies highlight the importance of rigorous monitoring and regulation to safeguard consumer health and reduce the risks of heavy metal contamination in red meat.

Table 2: Studies examining heavy metal accumulation in processed and fresh meat

Year	Country/Region	Animal/Sample Number	Measuring Method	Toxic Elements	Result	Authors
2006	Jordan	mutton, liver and kidney sheep (Jordanian, imported Australian, Chinese) n=240	Atomic Absorption Spectrometry (AAS)	Pb	Australian mutton and liver had significantly higher lead levels than local and Chinese samples. Most mutton samples exceeded the international safe lead limit, posing health risks to animals and humans.	Massadeh & et al. (2006)
2018	Jordan (Irbid city)	Canned beef (Bos taurus Africanus), (n = 44)	Atomic Absorption Spectroscopy (AAS)	Pb, As, Cd, Ni, Cr	The samples' As, Cd, Cr, Ni, and Pb levels were above the guidelines established by international health organizations.	Massadeh & et al. (2018)
2017	Türkiye, Izmir	sheep, cow and chicken liver (n = 30)	Cold vapor atomic fluorescence spectrometry (CVAFS) for Hg, Graphite Furnace Atomic	Pb, Hg, Cu	Pb and Cd concentrations in all samples fell below the FAAS detection	Yayayürük & Erdem Yayayürük (2017)

			Absorption Spectrophotometry (GFAAS) for Cu, Cd, Fe, Mn, and Flame atomic absorption spectrometry (FAAS) for Pb		limit. The animal livers analyzed showed that the levels of copper were highest in sheep and cow.	
2017	Türkiye, Sivas	muscle, liver and kidney of cattle (n = 15)	Inductively coupled plasma-mass spectrometry (ICP-MS)	Cr, Cu, As	Cr levels were below the FAO/WHO limit, while Cu values exceeded.	Oymak & et al. (2017)
2011	Saudi Arabian markets	fish, meat, and meat products (n=120)	Atomic absorption spectrophotometer (AAS)	Fe, Mn, Cu, Zn, Pb, Cd and Hg	The highest levels of metals were detected in meat products, sausage > luncheon. Meanwhile, camel meat maintained the lowest values of most studied metals.	Alturiqi & Albedair (2012)
2024	Noakhali, Bangladesh	meat, poultry (Muscle, brain, and liver) (n=63)	Atomic absorption spectrophotometer (AAS)	Cd, Cr, Pb, Ni, Fe, and Cu	Specific edible tissues (muscle, brain, liver) surpassed certain heavy metals' maximum permissible	Chowdhury & Alam (2024)

					levels (MPL). This indicates potential health risks associated with consuming these tissues.	
2020	Kuwait	Sheep (muscle, liver, and kidney) (n=600)	Atomic absorption spectrophotometer (AAS)	Hg, As, Pb, Cd, and Cr	All samples tested had concentrations of heavy metals (excluding Cr) that went over the allowed limits	Abd-Elghany & et al. (2020)
2015	Riyadh City, Saudi Arabia	canned meats (n=13)	Flame atomic absorption spectrometry (FAAS), and inductively coupled plasma-optical emission spectrometry (ICP-AES)	Ni, Pb, Cd, Cu, Zn, Fe	Elevated concentrations of toxic metals like lead and Cd were discovered in canned meat products in Saudi Arabia. May present a risk to consumers.	Nasser (2015)
2020	The eastern and northern parts of Algeria	Ovine (n = 100)/ bovine (n = 80), (liver)	Graphite Furnace Atomic Absorption Spectrometry (GFAAS)	Cd, Pb	Levels of Pb and Cd in liver and kidney samples from cows (>4 years	Zenad & et al. (2020)

					old) and sheep (>1 year old) were discovered to surpass the EC's 2006 maximum limit. Consuming excessive amounts could lead to a possible risk to health.	
2013	Tanta City, Egypt	Buffaloes (Muscle and liver) (n = 36)	electrothermal atomic absorption spectrometry (EAAS)	Cd, Cr, Cu, Pb and Zn	The concentration of copper and zinc within the liver was greater and lesser compared to muscles, respectively.	Lotfy, Ezz & Hassan (2013)
2019	Egypt	Cows meat, and some chicken organs	flame atomic absorption spectrophotometer (FAAS)	Fe, Zn, Cu, Pb, Cd and Co	Cd levels were safe, while Fe, Pb, and Cu levels exceeded acceptable limits. Zn > Fe > Cu > Pb > Cd > Co.	Hasballah(2019)
2018	Northwest regions of Iran	Buffalos muscle (n = 30)	Atomic absorption spectrophotometer (AAS)	Pb	The lead levels in more than 3.33% of samples exceeded the	Mahmoudi & et al. (2018)

					acceptable threshold.	
2019	Iran, Birjand	Beef/ sheep	Inductively coupled plasma-optical emission spectrometry (ICP/OES)	Cd, Cr, Cu, Ni, and Pb	The most elevated target risk Pb quotients were discovered. Cadmium found in the kidneys of cows showed the highest cancer-causing rate.	Zeinali & et al. (2019)
2018	Iraq	meat products of sheep, cow, chicken, and fish (n = 20)	Atomic absorption spectrophotometer (AAS) and Nron Activation Analysis Technique (NAAT)	Cd, Pb	Gadeer sheep contained the highest levels of Cd, particularly in waterways close to Kufa cows..	Almayahi, Saheb & Abbood (2019)
2021	Lahore, Pakistan	poultry, cattle (mutton, beef), and fish (n= not stated)	Graphite Furnace Atomic Absorption Spectrometry (GFAAS)	Na, K, Fe, Zn, Cu, Ni, Mg, Co, Cd and Pb	The meat samples gathered found no measurable amounts of Co, Cd, or Pb. The levels of Fe and Ni were within acceptable limits. The highest concentratio	Arif & et al. (2020)

					n of Zn was present in beef liver.	
2020	Egypt	Sausage, pastirma, and luncheon (n = 20)	Atomic absorption spectrophotometry (AAS)	Pb, Cd	Pastirma had the highest Pb concentrations, while sausages had the lowest levels. Sausage samples displayed the highest Cd levels, while luncheon samples showed the lowest concentrations.	Maky, Abd-ElRasoul & Salah (2020)

6. Results and Discussion

6.1 Heavy Metal Contamination in Red Meat Across Various Regions

The reviewed studies provide critical insights into the elevated concentrations of heavy metals detected in red meat products across different regions worldwide. The primary toxic elements of concern identified include lead, cadmium, chromium, arsenic, nickel, mercury, copper, and zinc. Analytical methods for quantifying these contaminants predominantly utilize advanced spectroscopic techniques, such as Graphite Furnace Atomic Absorption Spectrometry (GFAAS), Inductively Coupled Plasma

Mass Spectrometry (ICP-MS), and Atomic Absorption Spectroscopy (AAS).

6.2 Regional Findings

Jordan (2006 & 2018): Massadeh et al. (2018) documented elevated concentrations of As, Cd, Cr, Ni, and Pb in canned beef samples from Irbid City, surpassing international safety standards. This indicates potential consumer health risks and underscores the need for stringent monitoring and regulation. another study was done in 2006. performed on sheep's kidneys, liver, and mutton (local Jordanian sheep and imported sheep from Australia and China). Australian mutton and liver had significantly higher lead levels than local and Chinese samples. Most mutton samples exceeded the international safe lead limit, posing health risks to animals and humans.

Türkiye (2017): Yayayürük & Erdem Yayayürük (2017) found that the levels of Pb and Cd were under-identified limits in liver samples from sheep, cows, and chickens. However, copper levels are notably high in the sheep and cow liver samples, suggesting differential accumulation of toxic metals in several organs of animals.

Saudi Arabia (2011): Alturiqi & Albedair (2012) identified meat products, especially sausages and luncheon meats, as having the highest values of heavy metals, especially mercury, lead, zinc, copper, iron, and mercury. Camel meat maintained the lowest levels, highlighting variability in contamination levels based on meat type.

Bangladesh (2024): Chowdhury & Alam (2024) found that (liver, brain, and muscle) from meat and poultry in Noakhali exceeded the maximum allowable heavy metal concentrations like Cadmium, Chromium, Lead, Nickel, Iron, and Copper. This poses significant health risks, necessitating robust consumer protection measures.

Kuwait (2020): Abd-Elghany et al. (2020) discovered that sheep samples, excluding Cr, had heavy metal concentrations exceeding allowed limits. This calls for improved regulatory enforcement and better contamination control in livestock rearing and meat processing practices.

Saudi Arabia (2015): Nasser (2015) reported high amounts of lead and cadmium in canned meat items, potentially endangering consumers. This highlights the need for better oversight and regular testing to ensure product safety.

Algeria (2020): Zenad et al. (2020) found the kidney and liver samples came from older cows and sheep had Pb and Cd levels exceeding the highest boundaries established by the European Commission. Such findings emphasize the risks associated with consuming organ meats from older animals.

Egypt (2019): Hasballah (2019) found that cow meat and chicken organs contained Fe, Pb, and Cu levels exceeding acceptable limits, with Zn being the most prevalent. This highlights the necessity for targeted measures to mitigate heavy metal exposure from dietary sources.

Iran (2018 & 2019): Mahmoudi et al. (2018) and Zeinali et al. (2019) found lead concentrations surpassing permissible limits in buffalo muscle, along with high toxicity ratios for lead and cadmium in beef and sheep meat. Cadmium in cow kidneys was linked to the highest carcinogenic risk.

Pakistan (2021): Arif et al. (2020) observed meat samples showed undetectable amounts of Pb, Cd, or Co. While maintaining Fe and Ni levels within acceptable limits. However, Zn levels were highest in beef liver, indicating specific heavy metal accumulation patterns.

6.3 Health Implications

High Contamination Regions: Jordan, Bangladesh, Kuwait, and Iran have reported heavy metal concentrations surpassing international safety standards, presenting considerable health risks, including cancer and other toxic effects.

Moderate Contamination Regions: Türkiye and Saudi Arabia (Riyadh City) showed varying contamination levels, with some heavy metals below detection limits while others exceeded safe thresholds.

Low Contamination Regions: Pakistan presented a relatively safer profile with undetectable amounts of cobalt, cadmium, or lead, suggesting better control and safety measures (Hassan Emami & et al., 2023).

6.4 Gaps and Suggestions for Future Studies

Lack of Standardized Methodologies: Different studies employ various measurement methods (e.g., AAS, ICP-MS, FAAS), making direct comparisons challenging. Standardized methodologies among studies would enable more accurate comparisons of contamination levels.

Intervention and Mitigation Strategies: Few studies provide solutions or strategies for mitigating heavy metal contamination. Research into effective intervention measures, such as soil remediation, cleaner feed alternatives, and improved waste management.

Insufficient Data on Long-term Health Impacts: Most research focuses on contamination levels without examining the long-term health impacts of chronic exposure to these metals through meat consumption. Longitudinal studies tracking health outcomes in populations consuming contaminated meat are needed.

7. Conclusion

Importance of Balancing Nutrition and Safety: Ensuring a diet rich in essential nutrients while minimizing exposure to harmful heavy metals is crucial. Red meat provides important minerals and serves as a substantial protein source, but it can also contain toxic levels of heavy metals, posing serious health risks. Balancing nutritional benefits with safety considerations is essential for protecting public health.

Consumers should diversify their diets and choose meat from regions with lower contamination levels. Regular monitoring and adherence to international safety standards by the meat industry are imperative. Better livestock rearing, meat processing, and environmental management practices can significantly reduce heavy metal contamination.

To enhance research on heavy metal contamination in meat, standardized measurement methods are essential for accurate comparisons. Additionally, more studies should propose effective mitigation strategies and investigate the long-term health impacts of chronic exposure through longitudinal studies tracking affected populations.

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CHAPTER II

Applications of Multi-Criteria Decision-Making Methods in Food Process Optimization

Mehmet GULDANE[1]

1. Introduction

In engineering practice, it is critical to identify and consider a range of potential solutions when developing proposals to address a specific problem (Güldane, 2023). This phenomenon also emerges in the selection of equipment necessary to fulfill technological requirements. When a single criterion is considered, the most preferred alternative can be easily selected. However, when multiple criteria of unequal importance are considered, choosing between alternatives with disparate performance characteristics becomes challenging. In such instances, decision-making methods designed to facilitate the process are essential (Liu, Eckert, & Earl, 2020).

The decision-making process involves the collection of data, the creation of alternatives, and the determination of the most appropriate alternative to achieve the desired outcome. This is accomplished through the application of scientific, logical, and

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systematic reasoning to the data collected. Multi-criteria decision-making (MCDM) can be described as a tool that allows the most suitable alternative to be selected from a set of options on the basis of the simultaneous application of multiple criteria (Parlar & Palancı, 2020). The steps involved in applying MCDM to solve a multi-criteria problem are shown in Figure 1.

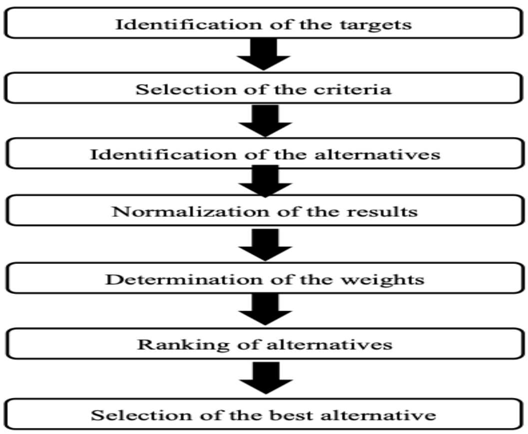

Figure 1. *A typical MCDM process (Amor* et al., *2023)*

MCDM methods were first developed in the 1960s to help decision makers. The aim of developing these methods is to provide faster and easier decision making in problems where there are many alternatives and criteria. MCDM techniques are employed to identify the optimal decision option among a set of alternatives, taking into account both quantitative and qualitative factors. The issues that MCDM techniques address typically consist of three main components: alternatives, criteria, and weights assigned to each criterion. The key advantage of MCDM approaches is their ability to evaluate a multitude of criteria and alternatives simultaneously (Özcan & Ömürbek, 2020).

The MCDM is a discipline that exemplifies an advanced area of operations research. It focuses on the development of mathematical tools and algorithms to objectively analyze many performance criteria and decision alternatives. The technique draws on disciplines such as mathematics, behavioral decision theory, economics, computer science, software and information systems. In the context of MCDM methods, the problem-solving process typically encompasses three distinct stages. Initially, the identification of a preferred alternative is undertaken. This is followed by the sorting of alternatives into groups and, finally, the ranking of alternatives according to subjective preferences (Behzadian, Khanmohammadi Otaghsara, Yazdani, & Ignatius, 2012). Several MCDM methods have been published in the academic literature. The most frequently used methods are the technique for order of preference by similarity to ideal solution (TOPSIS), gray relational analysis (GRA), analytical hierarchy process (AHP), simple additive weighed (SAW) and other MCDM methods (elimination et choix traduisant la realite-elimination and choice translating reality (ELECTRE), preference ranking organization method for enrichment evaluation (PROMETHEE), additive ratio assessment (ARAS), multi-objective optimization by ratio analysis (MOORA), data envelopment analysis based ranking (DEAR) etc.), all of which are generally employed in the field of food process engineering.

2. Technique for Order of Preference by Similarity to Ideal Solution (TOPSIS)

The TOPSIS technique is based on determining the alternative that is closest to the positive ideal solution (PIS) and farthest from the negative ideal solution (NIS) among the alternatives (Behzadian et al., 2012). TOPSIS, which is a robust MCDM approach, was first proposed by Hwang & Yoon (1981). This method is one of the most preferred MCDM methods because of its ease of application and reliability. In this method, all alternatives are ranked on the basis of their geometric distances from PIS and NIS. While PIS represents the ideal solution, NIS represents the non-ideal solution. Therefore, the optimal solution alternative is the one that is closest to the PIS and farthest from the NIS (Falsafi et al., 2022). The TOPSIS method was performed in the following five steps:

1. First, the decision matrix (D_{mxn}) consisting of alternatives (m) and criteria (n) generated via Equation (1).

$$D_{mxn} = \begin{Bmatrix} X_{11} & x_{12} \dots & x_{1n} \\ X_{12} & x_{22} \dots & x_{2n} \\ \vdots & \vdots & \vdots \\ X_{m1} & x_{m2} \dots & x_{mn} \end{Bmatrix} \tag{1}$$

2. The decision matrix is normalized using Equation (2).

$$\mathrm{x_{ij}} = \frac{\mathrm{a_{ij}}}{\sqrt{\sum_{\mathrm{i=1}}^{\mathrm{m}} \mathrm{a_{ij}^2}}}\ , \mathrm{i} = 1, \dots, \mathrm{m\ and\ j} = 1, \dots, \mathrm{n}$$

(2)

where x_{ij} and a_{ij} are the normalized value and the real value of the corresponding criteria, respectively.

3. The third step is to multiply the normalized decision matrix values (x_{ij}) by the weight factor values (w_{ij}) to obtain the weighted normalized decision matrix (Equation (3)). Subjective weighting methods, including the simple multiattribute rating technique (SMART), AHP, pairwise comparison, the Delphi method, and others, may be employed to assign relative importance to each criterion. Furthermore, objective weighting techniques, such as entropy, least mean square (LMS), and principal component analysis, may be employed in this process. Finally, combination weighting methods, including multiplication synthesis and additive synthesis, can be utilized to synthesize the results of the aforementioned techniques (Wang, Jing, Zhang, & Zhao, 2009).

$$v_{ij} = x_{ij} \times w_{ij}$$

(3)

4. The distance of each alternative from the PIS (Si^+) and NIS (Si^-) is estimated according to Equations (4) and (5), respectively.

$$S_i^+ = \sqrt{\sum_{j=1}^{n}(v_{ij} - v_j^+)^2}$$

(4)

$$S_i^- = \sqrt{\sum_{j=1}^{n}(v_{ij} - v_j^-)^2}$$

(5)

5. Finally, the performance score (Pi) for each alternative is calculated via Equation (6). The values of P_i are then ranked from highest to lowest to obtain the optimal solution.

$$P_i = \frac{S_i^-}{S_i^+ - S_i^-}.$$

(6)

In a study conducted by Güldane (2024), the TOPSIS method was employed for the optimization of a foam mat drying process utilized for cranberry pulp. The optimization study, which considered the drying characteristics and properties of the dried product, revealed that a drying temperature of 70°C was the optimal temperature for the process.

TOPSIS was employed to optimize the sensory properties of gluten-free baton cakes produced from 25% seed flour samples (hemp, okra, mustard or coriander) instead of rice flour. As a result of the analysis, the cake formulation containing hemp seed flour was found to be closest to the ideal formulation (Dedebas & Cebi, 2024).

In the ultrasound-assisted hot air drying technique, the entropy-weighted TOPSIS method was applied to determine the optimum drying parameters by considering the effects of the ultrasound frequency, ultrasound power and hot air temperature variables on the physicochemical properties of cherries (Lu et al., 2024).

In a recent study, Cingöz and Güldane (2023) employed the TOPSIS method to optimize the sensory preference process involved in the production of gluten-free biscuits from chickpea species.

Hedayati, Ansari, Javaheri, Golmakani, & Ansarifar (2022) used the TOPSIS method to optimize the product formulation of cakes obtained from different sugar sources (sucrose, date syrup, fig syrup) and hydrocolloids (*Alyssum homolocarpum* seed gum and basil seed gum). Considering the physical and sensory properties, the product obtained with fig syrup and basil seed gum was determined to be the most ideal product.

The cookie formulation containing resistant starch species was optimized via TOPSIS. The findings indicated that cookies containing 15% resistant starch were the best samples from both physicochemical and organoleptic perspectives (Falsafi et al., 2022).

In a recent study, Ozkaya, Gecgel, & Durak (2022) employed TOPSIS to assess the microbiological quality of salad samples procured from diverse restaurant outlets across the districts of Istanbul, namely Esenler, Fatih, Beşiktaş, Üsküdar, Kadıköy, and Ümraniye.

The TOPSIS technique was utilized to determine the most ideal sample in terms of hardness, the observed spring value and the weight loss properties of gluten-free cakes produced via the partial vacuum baking technique (Tuta Şimşek, 2019).

The effects of ultrasound-pulsed electric field and hydrodynamic-pulsed electric field systems on microorganism inhibition and product quality in sour cherry juice were determined. TOPSIS was applied to determine the ideal method among alternative pasteurization techniques (Hosseinzadeh Samani, Behruzian, Khoshtaghaza, Behruzian, & Ansari Ardali, 2020).

Gul, Atalar, Mortas, Saricaoglu, & Yazıcı (2018) used the TOPSIS method to optimize hazelnut milk production from cold pressed hazelnut oil cake, which is considered a waste of the hazelnut oil production process.

The optimal protein and glycerol concentration parameters (4% protein and 40% glycerol) that most affect the quality characteristics of films obtained from anchovy (Engraulis encrasicholus) by-product proteins were determined via the TOPSIS method (Tural & Turhan, 2017).

3. Gray Relational Analysis (GRA)

The GRA is an efficient methodology for identifying the optimum process parameters for engineering problems with multiple variables. The objective of this MCDM method is to define the gray relational grade (GRG) for the purpose of optimizing multiobjective problems into single-objective problems. The GRG is employed to assess the influence of variables on overall performance while simultaneously evaluating the degree of alignment between each alternative and the optimal solution. This approach offers a valuable tool for decision-making in uncertain and multidimensional contexts. The GRA provides an impact assessment model that measures the degree of similarity of candidate solutions to the reference solution. Solutions with a higher relational degree should be retained, as they are more similar to the ideal solution. Therefore, GRA can be used as a method for analyzing the relational degree of discrete datasets (Sankar, Umamaheswarrao, Srinivasulu, & Chowdari, 2015; Zhai, Khoo, & Zhong, 2009). The method basically consists of four stages:

1. A decision matrix was constructed comprising a set of alternatives (m) and a set of criteria (n) (Equation (7)).

$$D_{mxn} = \begin{Bmatrix} X_{11} & x_{12} \cdots & x_{1n} \\ X_{12} & x_{22} \cdots & x_{2n} \\ \vdots & \vdots & \vdots \\ X_{m1} & x_{m2} \cdots & x_{mn} \end{Bmatrix} \tag{7}$$

2. To prevent confusion between criteria that are composed of different elements, it is necessary to normalize the results using Equation (8).

$$N_{y_i}(k) = \frac{x_i(k) - \min x_i(k)}{\max x_i(k) - \min x_i(k)} \tag{8}$$

where $N_{y_i}(k)$ represents the normalized value and x_i (k) is the test result. The minimum and maximum experimental values are represented by min x_i (k) and max x_i (k), respectively.

3. Determination of the gray relational coefficient (GRC) and GRG.

- To describe the correlation between ideal and actual experimental scores, the GRCs are computed according to Equation (9).

$$GRC\big(X_0(k), X_i(k)\big) = \frac{\Delta_{min}+\varphi\Delta_{max}}{\Delta_{0i}+\varphi\Delta_{max}} \tag{9}$$

- The value of φ, which is referred to as the coefficient of discrimination, ranges from 0 to 1. A lower value of φ corresponds to a higher degree of discrimination. However, in many studies cited in the literature, the value of φ is set at 0.5.
- The difference between the reference ($x_o(k)$) and comparison ($x_j(k)$) values is represented by Δ_0i. The calculations are performed with Equation (10).

$$\Delta_{0i}(k) = \left|X_0(k) - X_j(k)\right| \tag{10}$$

- Notably, the minimum value of $\Delta 0_i$, represented by Δ_{min} (Equation (11)), and the maximum value of $\Delta 0_i$, represented by Δ_{max} (Equation (12)), are derived from the respective equations.

$$\Delta_{min} = min_j min_k |X_0(k) - X_j(k)| \tag{11}$$

$$\Delta_{max} = max_j max_k \left|X_0(k) - X_j(k)\right| \tag{12}$$

4. The GRG revealed a linear relationship between the reference and analyzed sequences. Accordingly, it was hypothesized that higher GRG values (approaching 1) would be observed for the responses in question. In contrast, the lower GRG values indicated inconsistencies between the data sequences. The weighted GRG was calculated via the weighted factors specified in Equation (13). As mentioned

before, subjective, objective or combination weighting methods can be used to determine the relative weight value for each alternative (Wang et al., 2009).

$$GRG\ (X_0, X_i) = \frac{1}{n}\sum_{k=1}^{n} w_k \varphi_i(k) \tag{13}$$

In this study, the number of trials (n) and the weighting value for the k^{th} observation (w_k) represent the variables (Arce, Saavedra, Míguez, & Granada, 2015).

The Taguchi-GRA hybrid optimization technique was employed to determine the optimal mixing parameters for ensuring homogeneous mixing in V-type mixers utilized for powder material mixing in the food industry (Gürmeriç & Doğan, 2024).

In a recent study, Zhang et al. (2023) applied citric acid, $Ca(OH)_2$, $CuSO_4$, and α-cyclodextrin to turbid kiwifruit juice to minimize the loss of color and odor during thermal sterilization. Following the optimization study with GRA, the sample treated with 6 g/kg α-cyclodextrin was identified as the ideal juice sample.

Guldane & Dogan (2022) used the PCA-weighted GRA method to optimize the foaming process by transforming the multi response problem into a single response in a model food foam system containing milk proteins and saponins.

In one study, Zhao et al. (2022) conducted GRA for comprehensive sensory analysis results of 26 distinct mung bean (*Vigna radiata* L.) varieties.

Salacheep et al. (2020) employed a Taguchi-GRA hybrid approach to determine the optimal conditions for the extraction of bioactive components (anthocyanins, antioxidants, and phenolic compounds) from butterfly pea petals via an ultrasound-assisted extraction method, with the objective of achieving maximum yield.

Chung, Liaw, Gavahian, & Chen (2020) employed the Taguchi-GRA hybrid optimization method to identify the optimal process parameters and baking formulation to produce sourdough bread with red quinoa (*Chenopodium formosanum*).

The GRA was used to investigate the effects of sourdough on the nutrient profile of steamed potato bread (Z. Zhao, Mu, & Sun, 2019). In addition, Chen et al. (2005) applied the GRA method for the classification of dried roselle (*Hibiscus sabdariffa* L.) samples.

4. Analytical Hierarchical Process (AHP)

The AHP is a widely recognized MCDM tool that is utilized by researchers and decision-makers for the establishment of criteria and the assessment of their relative weights. The AHP, proposed by Satty (1980), has been gained extensively applied because of its effectiveness in addressing complex decision problems characterized by multiple criteria and subjective assessments. Additionally, its capacity to integrate with other MCDM techniques has contributed to its widespread usage. A major advantage of the AHP is its capacity to decompose decision problems into manageable components, thereby creating a hierarchical structure that clarifies the relative importance of each criterion. Furthermore, it reduces the influence of bias in decision-making by assessing the consistency of priorities assigned by decision-makers to each criterion. However, this approach may prove inadequate when decision-makers present incomplete, ambiguous, or fragmented information, and it can become complex when numerous criteria are involved. The AHP organizes complex decision problems hierarchically, with the primary objective at the top level, followed by evaluation criteria, subcriteria at subsequent levels, and alternatives at the lowest level (Beeram, Srinivas, Raj, & Reddy, 2020). The following stages are employed in the application of the AHP (Satty, 1980).

1. The initial step in the process is to define the decision problem and establish the main objective clearly.
2. Draw a hierarchy process constituting the aim, criteria and alternatives, as shown in Figure 2.

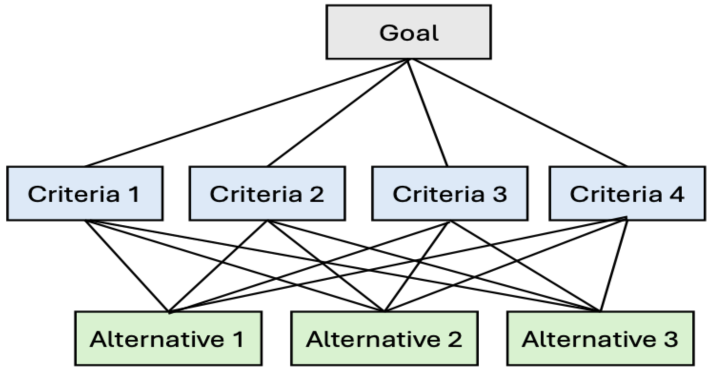

Figure 2. *Hierarchy drawing for AHP optimization*

3. Construction of a pairwise comparison matrix (Equation (14)).

$$\begin{Bmatrix} 1 & a_{12} \dots & a_{1n} \\ a_{21} = 1/a_{12} & 1 \dots & a_{2n} \\ \vdots & & \vdots \\ a_{n1} = 1/a_{n1} & x_{n2} \dots & 1 \end{Bmatrix} \tag{14}$$

These matrices are constructed via the comparative scale proposed by Satty (1980), which varies from 1 (equal importance) to 9 (extreme importance).

4. Normalize the comparison matrix via Equation (15).

$$X_{n,ij} = \frac{X_{ij}}{\sum_{i=1}^{n} a_{ij}} \tag{15}$$

where, $X_{n,ij}$ represents the normalized value, X_{ij} denotes the original value, i is the row number, and j is the column number.

5. The weights for each criterion are determined using Equation (16).

$$W_{ij} = \frac{1}{n} \sum_{j=1}^{n} X_{n,ij} \tag{16}$$

6. The consistency index (CI) is calculated via Equations (17) and (18).

$$CI = \frac{\lambda_{max} - n}{n-1} \tag{18}$$

$$\lambda_{max} = \frac{1}{n}\sum_{i=1}^{n}\left(\frac{\sum_{j=1}^{n} x_{ij}w_j}{w_i}\right) \quad (18)$$

To assess consistency, it is necessary to define the "random index" (RI) value (Satty, 1980):

To ensure the reliability and consistency of the data, the consistency ratio (CR) of each matrix is less than 0.1. This can be calculated using the following formula (Equation (19)):

$$CR = \frac{CI}{RI} \quad (19)$$

Yazici et al. (2023) employed an AHP–TOPSIS hybrid optimization method to assess the potential of aquafaba derived from various legumes, including kidney beans, chickpeas, dried beans, and cowpeas, as gluten-free cake ingredients.

In a recent study, the AHP method, which employs a hierarchical structure comprising 11 criteria and 6 alternatives, was utilized to identify the optimal juice extraction technique for non-centrifugal sugar extraction, a conventional sugar production process in India (Beeram et al., 2020).

The optimal osmotic dehydration conditions (30 minutes and 37 kHz) for golden strawberries exposed to sonication (37 and 80 kHz) for different durations (20-40 minutes) were determined using the AHP–TOPSIS hybrid method (Noshad, Savari, & Roueita, 2018).

In another study, a sensory panel was conducted to determine the optimal fat content in a model hot chocolate beverage formulation. In this study, the optimal formulation of chocolate-based beverages was evaluated by optimizing consumer preference results with AHP (Dogan, Aslan, Aktar, & Goksel Sarac, 2016).

5. Simple additive weighted (SAW)

The SAW technique is widely preferred as a simple MCDM method for solving engineering problems. This approach mainly targets the benefit criterion. First, the cost criteria are converted into benefit criteria. The lowest and highest cost criteria take the largest and smallest values respectively. The experimental data for each criterion are then divided by the sum of all the criteria to obtain a new normalized experimental matrix. Finally, the total score of each alternative is multiplied by the weight value determined by the previously mentioned methods. As a result, the alternative with the highest score is identified as the optimal choice (Lee & Chang, 2018).The SAW method is conducted in the following 4 steps:

1. The initial stage of the process is the formation of the decision matrix (D_{mxn}), which comprises a set of alternatives (m) and a set of criteria (n) (Equation (20)).

$$D_{mxn} = \begin{Bmatrix} x_{11} & x_{12} \cdots & x_{1n} \\ x_{12} & x_{22} \cdots & x_{2n} \\ \vdots & \vdots & \vdots \\ x_{m1} & x_{m2} \cdots & x_{mn} \end{Bmatrix} \tag{20}$$

2. The experimental results are normalized via Equation (21).

$$n_{ij} = \frac{r_{ij}}{\max(r_{ij})} \tag{21}$$

   where r_{ij} is the value of alternative j for variable i; max (r_{ij}) is the highest value for variable i.

3. Calculation of the weighted decision matrix using the formula provided in Equation (22). The weight value of each criterion can be calculated via several weighting methods mentioned previously.

$$A_j = \sum w_i x_{ij} \tag{22}$$

   where "w_i" represents the weight associated with variable "i," and "x_{ij}" denotes the normalized value of variable "i" with respect to parameter "j."

4. The sample with the highest score is identified as the optimal one.

Güldane & Cingöz (2023) optimized the process of determining the optimal process parameters for ultrasound-assisted extraction of bioactive components from onion peel by employing a Taguchi-SAW hybrid method.

In a study conducted by Dogan, Aslan, & Ozgur (2018), the SAW and TOPSIS methods were used to optimize the physicochemical, bioactive, and sensory properties of milk-based herbal tea (*Rumex crispus* L.)

The SAW, AHP, TOPSIS, and ELECTRE methods were applied to determine the most suitable flavoring agent (vanilla, strawberry or cocoa) for prebiotic pudding production (Gurmeric, Dogan, Toker, Senyigit, & Ersoz, 2013).

6. Other MCDM methods

The SWARA–TOPSIS method was applied to measure the quality parameters of gluten-free products obtained by adding okra seed flour at different ratios to muffin formulations (Sahan & Capraz, 2024).

Volatile aroma components were evaluated via PROMETHEE and cluster analysis methods in the production of fermented probiotic fruit puree for lactose intolerant people (Ucak-Ozkaya, 2024).

The best-worst method was applied to rank fruit juice products in Iran on the basis of the quality parameters of alcohol content, sugar content, Brix degree and pH value (Pirkhah & Hosseini, 2022).

In a recent study, Göksel Saraç (2021) employed the ELECTRE method to optimize the sensory properties of Turkish-type noodles produced with apple, carrot, inulin, and pea fibers.

The optimal levels of process parameters (cooking time, temperature and fan speed) were determined by using the attractiveness function, MOORA and ARAS methods while considering the quality characteristics (microbial load, center temperature and weight performance) of nugget coated products produced in a steam cooking oven in a food business (Kuvat, 2020).

ELECTRE III was used to determine the optimal production conditions for the production of functional pasta with Opuntia

(*Opuntia ficus-indica* (L.) *Mill.*) (Micale, Giallanza, Russo, & La Scalia, 2017).

7. Conclusion

The optimal solution to a multivariate problem in an engineering process can be determined via a multi-criteria decision-making process. A review of the literature reveals that multi-criteria decision-making methods are not yet widely employed in food processing. However, the technique for order of preference by similarity to ideal solution (TOPSIS) and gray relational analysis (GRA) methods are frequently used to identify the optimal production formulation or to optimize extraction conditions. In practice, combining multi-criteria decision-making methods with other optimization techniques is common. It is anticipated that multi-criteria decision-making methods will become more prevalent in food processing.

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BÖLÜM III

The Relationships Between Dietary Polyphenols and Gut Microbiota: Health Benefits

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1. Introduction

The delicate interplay between gut microbiota and dietary components has become one of the focal points of interest, which can have huge potential implications for human health, especially when polyphenols are involved. The microflora and the gut microbiota, which is the contingent of microorganisms that exists from the upper part of the large intestine of the human small intestine colon terminal, are incredibly vital for metabolism and the functions of the body's immune system and digestion (Catalkaya et al., 2020). At the same time, polyphenols are bioactive compounds in plants

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that are mainly found in fruits, vegetables, and some beverages such as tea and wine and have, in recent years, been touted for their potential health-enhancing attributes (Xie et al., 2023).

The human gut microbiota consists of diverse communities of microbes that exist in symbiotic relationships with the human body. The essence and constitution of gut microbiota depend on the host's genetics and the lifestyle that the host offers to the microbes to share. Gut microbiota and the gut bacteria contribute to nutrient utilization and several metabolic processes (pathways such as bile acid metabolism, choline metabolism, and tryptophan metabolism, which is important for several homeostatic developments) and the protection of the host's immunological and physiological well-being (Baky et al., 2022).

On the other hand, understanding the relationship between gut microbiota and polyphenols with glycolipid metabolism would have health effects such as the level of zinc and iron, intestinal permeability, and cognitive performance (Kennedy, 2014; Xie et al., 2023). The further objectives are to investigate all these aspects in question and elucidate them to disclose the intricate connection of diets, gut microbiota, and human health. This essay aims to analyze and define the intricate network of associations between gut microbiota and polyphenols with a focus on their roles in glycolipids metabolism and health stability. This work will, therefore, be instrumental in providing further understanding of the interplay between human health and the gut microbiota, which is considered insignificant.

2. Understanding Gut Microbiota and Polyphenols

2.1. Gut Microbiota

The gut microbiota is a microbial-based ecosystem that comprises microorganisms, including bacteria, viruses, and fungi, that are in the gastrointestinal tract (Wang et al., 2021). An especially organized form of bacteria, or a consortium, that participates in various functions within the human body, and its most vital roles include digestion, nutrition assimilation, immune regulation, and calorific expenditure (Sallam et al., 2021). It has been estimated that the gut has numerous factors, which include diet, genes, age, lifestyle, and the environment, which are all responsible for the microflora that comprises all the microorganisms that are found within the gut (Mithul Aravind et al., 2021).

The earliest segment of the small intestine, the duodenum, expands the gut microbiota composition to be like that of the stomach due to chyme and biliary and pancreatic secretions. This place, from the duodenum to the ileum, is characterized by an increased number of bacterial diversities along with an increase in pH. In this sector, major *Lactobacillus* and *Clostridium* belong to *Firmicutes*, *Escherichia coli* belong to *Proteobacteria*, *Bacteroidetes*, and facultative gram-negative anaerobes (Singh et al., 2019).That is, the conditions in the large intestine, namely the colon with a more favorable nutrient environment and pH (5.7-6.8) conducive to bacterial growth, it is possible to have a higher bacterial density of diverse, complicated, and dense microbial community, which is primarily composed of obligate anaerobes which can metabolize at low oxygen tension. *Firmicutes* such as *Ruminococcus*, *Lactobacillus,* Clostridium, and *Bacteroidetes* such as *Bacteroides* and *Prevotella* are the most abundant bacteria in the colon. Other relatively less diverse phyla exist in the adult gut microbiota, including *Actinobacteria*, *Fusobacteria*, *Proteobacteria*, *Verrucomicrobi*a, and facultative anaerobes. The composition and functions of bacteria are also not similar in the intestinal lumen and mucus layer of the intestinal mucosa; the ratio of anaerobes and aerobes, for example, differs significantly (Singh et al., 2019)

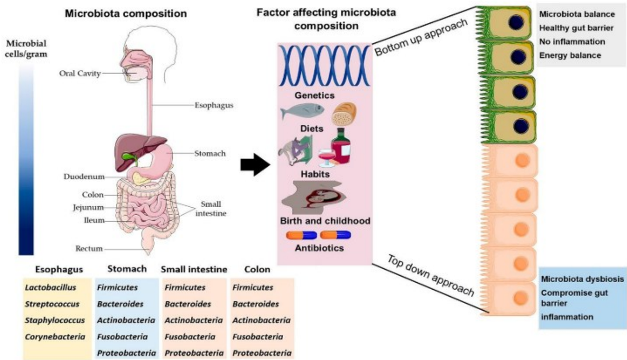

Figure 1: Microbiota composition and factors affecting its balance (Rajoka et al., 2021).

Findings suggest that gut microbiota is integral in the preservation of the physiological integrity of the host's health and the development of numerous diseases, including obesity, diabetes, inflammatory bowel disease, and possibly even neurodegenerative disorders. Certain foods, drinks, and supplements can act on the gut microbiota, with subsequent consequences on host metabolism. The concept of changing the composition of the targeted microbiota after the administration of probiotics, prebiotics, or fecal microbiota transplantation is already proven. Nevertheless, the role of polyphenols in modulating the gut microbiota is still puzzling. However, there is emerging data that indicates that dietary polyphenols may act in a direct manner on the gut microbiota; that is, it may stimulate specific beneficial microbial or inhibit undesirable microbial species in the gut microbiome (Kalita et al., 2022).

2.2. Polyphenols

Polyphenols, a kind of biologically active component in plant foods and beverages with diverse chemical structures like flavonoids, phenolic acids, and polyphenolic polymers, constitute a cohort that is very large, microbial, and metabolic synthesis (Ma & Chen, 2020). Polyphenols give fruits and vegetables various colors and the aroma and flavor typical of certain foods (Kasprzak-Drozd et al., 2021). Polyphenols can be found in fruits, vegetables, grains, tea, coffee, and wine (Zhu, 2018; Table 1). Upon digestion, the polyphenols experience the metabolic process, which encompasses ingestion, biotransformation, and excretion, and it depends on these that their bioavailability as well as physiological effects were influenced within the body (Tomás-Barberán et al., 2016).

Table 1: Different classes of polyphenols and their sources

Polyphenol Class	Examples	Dietary Sources
Flavonoids	Flavonols (quercetin, kaempferol), Flavanones (hesperidin, naringenin), Flavones (apigenin, luteolin), Flavan-3-ols (catechins, epicatechins), Anthocyanidins (cyanidin, pelargonidin)	Citrus fruits, onions, apples, berries, tea, cocoa, red wine, soy products, legumes
Phenolic Acids	Hydroxybenzoic acids (gallic acid), Hydroxycinnamic acids (caffeic acid, ferulic acid)	Coffee, tea, whole grains, fruits, vegetables, nuts
Stilbenes	Resveratrol	Red grapes, red wine, peanuts, berries, cocoa
Lignans	Secoisolariciresinol, Matairesinol	Flaxseeds, sesame seeds, whole grains, legumes
Tannins	Hydrolysable tannins (gallic acid), Condensed tannins (catechins)	Tea, red wine, cocoa, berries, nuts, legumes, grains
Polyphenolic Polymers	Proanthocyanidins (procyanidins, prodelphinidins)	Cocoa, red wine, apples, berries, nuts, seeds

Source: Mithul Aravind et al., 2021

2.3. Gut Microbiota-Polyphenols Interaction

The gut microbiota and polyphenols relationship, as well as the intestinal bioavailability, metabolism of polyphenols, and their biological activity, is a set of dynamic, interconnected processes (Molinari et al., 2022). In the alimentary canal, polyphenols undergo enzymatic metabolism and microbial biotransformation mitigated by gut microbiota with an outcome of the derivation of a variety of metabolites that have distinct physiological functions (Wang et al., 2023). In addition, the gut microbiota influences the process of polyphenol metabolism and effectiveness by enzymatic decomposition, fermentation, and biotransformation (Ozdal et al., 2016).

The dynamics between gut microbes and polyphenols can cause important consequences for human health, creating a path for disease prevention (Z. Zhao et al., 2023). Polyphenols show several bioactive properties among which are the prevention of oxidation, the regulation of inflammation, and the protection against carcinogenesis as well as cardiovascular disease (Wang et al., 2022b). They achieve this through microbiota-mediated metabolism. In contrast to a healthy situation, dysbiosis, defined as microbiome changes in the gut's composition and function, could negatively impact the phenolic compounds metabolism and, therefore, result in a reduction in the health benefits that could arise from their consumption (Moorthy et al., 2020). The complex relationships between gut microbiota and polyphenols need to be extensively studied for scientists to know how it is possible for these compounds to promote health and fight disease.

3. Gut Microbiota Dysbiosis and Consequential Diseases

3.1. Gut Microbiota Dysbiosis

In the middle of the twentieth century, Metchnikoff described the term as dysbiosis and attempted to link it to a shift in intestinal bacteria and immune balance and the genesis of an intestinal disease. In general terms, dysbiosis refers to the following: (I) Decrease in the density of symbionts; (II) Increase in pathobionts; (III) Loss of species diversity and equitability. And it has been written that these three types of change can occur together and that is more likely the situation. Diet, perceived physical activity, age factors, stress, medications, and other chemicals, also known as xenobiotics, are the causes of impaired gut microbiota composition and/or function – dysbiosis (Singh et al., 2019).

There are studies showing that significant changes in gut microbiota occur at early developmental stages, especially during the first years of life and regarding an increase in number and variety. Ecological successions may be illustrated by the maturation and evolution of human gut microbes (An et al., 2018). Initially, its colonization during the early days may be highly heterogeneous depending on new colonization success, but after undergoing several changes in composition and function, gut microbiota becomes more stabilized, and climax communities are formed. However, different data has been received depending on the geographic World regions of adults, which can be depended on various factors, such as genetic and environmental ones, including diet, hygiene, antibiotics, and other medicines usage. Thirdly, aging alters the number of gut microbiota and the structure, especially by down-regulating the Firmicutes/Bacteroidetes (F/B) ratio, which could partly be due to immunosenescence and modification of the immune-inflammatory system due to aging (Fernandes et al., 2019). Additional reasons explaining the aging-related change in gut microbiota are a decline in physical health, toothlessness, impaired function of salivary glands, digestion, and gut transit time, and atypical nutrient intake causing malnutrition (Conlon & Bird, 2015).

Diet is undeniably among the primary determinants of gut microbiota responsible for composition and function management aspects of health vs disease states. For instance, human milk oligosaccharides are particular to encourage the growth of Lactobacillus and Bifidobacterium that imprint the neonate’s gut and may form the immune system. As has been observed before for the demographic and dietary factors, they differentially shift the gut microbiota. This means that children consuming plant polysaccharides from rural Africa had reduced fecal and over *Bacteroidetes*, especially *Prevotella* and *Xylanibacter*, compared to Italian kids with a higher probability of *Enterobacteriaceae*, particularly *Shigella* and *Escherichia*, as observed in Singh et al. (2019). *Prevotella* and, to some extent, *Xylanibacter*, consequently, enhance beneficial SCFAs or the capacity for breaking down cellulose/xylenes, which underpins an adaptation toward an enhanced ability to extract energy from a fiber-rich diet. *Ruminococcus bromii* and *Eubacterium rectal* in the human gut which is associated with fiber fermentation rises with the increase in resistant starch in the diet of many people. The findings drawn from both pre-clinical studies in animal models and cross-sectional and interventional human studies depict that high fat, high sugar consumption causes alteration of the gut microbiota on the other hand, a vegan diet and especially inulin and or with added probiotics have been demonstrated to positively influence gut microbiota composition and functionality reduce adiposity and inflammatory molecules including LPS (lipopolysaccharide) and other physiological enhancement in metabolic regulation (Fernandes et al., 2019).

It has also been seen that several non-dietary environmental factors can influence the human gut microbiota toward dysbiosis; stress, smoking habits, and lack of exercise practice could possibly be attributed to many factors related to the pro-oxidative and pro-inflammatory environment. Fourthly, medication forms an integral part of the modulator of the gut ecology. Depending on the definition, antibiotics change the functions and composition of gut microbiota, and the absence of colonization resistance is one of the first things antibiotics do to the gut. This loss led to a significantly enhanced rate of colonization by Salmonella after antibiotics (Sauceda et al., 2017).

3.2 Diseases Caused by Dysbiosis

As mentioned above, the components of microflora in the intestine depend on some factors, including lifestyle practices, diet, and exercise, which are major determinants of cardiometabolic diseases, for example, obesity and type 2 diabetes. They have been considered as outcomes of an interaction between the host genetic factors, the environmental factors, such as the diet plan, and the gut microbiota (Figure 1). Growing data from the preclinical and clinical studies provide evidence of dysbiosis in obesity and type 2 diabetes, which is associated with reduced richness and stability. The postulated link between dysbiosis and the pathogenesis of obesity, type 2 diabetes, and its severe chronic microvascular complications has been hypothesized by several mechanisms (Fernandes et al., 2019). To summarise, dysbiosis of the gut microbiota leads to a decreased integrity of the gut barrier, alterations in the expression of tight proteins, increased permeability, and consequently the translocation of bacteria fragments including LPS and PG (porphyromonas gingivalis) and uremic toxins from the gut lumen to the bloodstream which results in endotoxemia or a state of low-grade inflammation. The so-called microbe-associated molecular pattern (MAMP) triggers inflammation response through (TLR) toll-like receptors, TLR4 specifically, these stimuli release a series of signals which at some point issue pro-inflammatory molecules, which will affect glucose and/or insulin in respectively signaling or metabolism (Singh et al., 2019). This is compounded by the increased production of advanced glycation end products as well as other oxidative processes that are commonly implicated in the metabolic dysfunction evident in both obesity and diabetes.

In the same way, several observations suggest that the signals arising from gut microbiota dysbiosis change the immunometabolic reprogramming of epithelial and immune cells and define the correct immunoinflammatory environment for diabetes and its complications. However, diabetic gut dysbiosis seems to be involved not only in obesity or diabetes development but also in the progression of some of the most severe microvascular complications of diabetes like DR (diabetic retinopathy) and DN (nephropathy). According to the present data, the increase in circulating bacterial endotoxin, and especially LPS, may play a role in the essential pathophysiology of MS, obesity diabetes, and the complications of diabetes shifting towards low-grade inflammation. These bacterial components and other microbial-derived products that reached the circulating system through a leaky gut in DN and DR can in part account for the increased pro-inflammatory and pro-oxidative status and heightened innate and adaptive immunity in DN and DR. Overall, these mechanisms may be critical for enhancing the metabolic and vascular diabetes-related complications (Wang et al., 2022c).

4. Benefits of Polyphenols on Gut Microbiota and Metabolism

4.1. Modulation of Gut Microbial Composition

It has been found that most of the dietary polyphenols never enter the circulation but remain in the small intestine, while the unabsorbed fractions may be redistributed within the large intestine and are subjected to a significant microbial metabolism (Sallam et al., 2021). Thus, the intestinal microbiota is responsible for the biotransformation and metabolism of the initial polyphenolic structures into low molecular weight metabolites that can be absorbed and provide health-beneficial effects to the host. Although, it is still not well understood, approximately to what extent the possible mechanism exists between the consumption of dietary polyphenols, gut microbes, and host health (Wang et al., 2022c).

Polyphenols were known to have unique and very significant effects on the microbiota composition and the overall microbial density by changing the quantities of the existing microbial species and encouraging diversification of the microbial community (Prasain & Barnes, 2020). Polyphenols, due to the antimicrobial action and the prebiotic effect, select beneficial gut bacterium types, as shown in Table 2, such as Bifidobacteria and Lactobacilli, which enjoy favorable stimulation while the proliferation of pathogenic bacterium is checked. After that, the commensal gut bacteria that ferment these polyphenolic compounds resulted in SCFAs having a feedback inhibition effect for immune cells and low profiles of inflammation (Song et al., 2022). As presented in Table 1, the various polyphenols and their sources and their effect on the beneficial gut bacteria also some harmful bacteria can be promoted through the same polyphenols, and the previous study revealed that polyphenols enhance the good bacteria and suppress the formation of bad bacteria (Wang et al., 2022c).

Table 2: Overview of polyphenols effect on gut microbiota composition

Beneficial Bacteria	Harmful Bacteria	Polyphenol Increasing Beneficial Bacteria	Polyphenol Inhibiting Harmful Bacteria
Lactobacillus spp.	Clostridium difficile	Resveratrol: Found in red wine, grapes, and berries. Supports the growth of Lactobacillus spp. by promoting their proliferation and adhesion to the intestinal mucosa.	Catechins: Abundant in green tea, cocoa, and various fruits. May inhibit the growth of Clostridium difficile, thereby reducing the risk of dysbiosis and associated infections.
Bifidobacterium spp.	Escherichia coli	Quercetin: Found in onions, apples, and citrus fruits. Stimulates the growth of Bifidobacterium spp. by enhancing their metabolic activity and colonization in the gut.	EGCG (Epigallocatechin gallate): Predominantly found in green tea. Exhibits antimicrobial activity against Escherichia coli, thus reducing its abundance in the gut microbiota.

Enterococcus faecium	Salmonella spp.	EGCG (Epigallocatechin gallate): Predominantly found in green tea. Enhances the growth of Enterococcus faecium, contributing to gut health and immune modulation.	Procyanidins: Found in cocoa, apples, and grapes. Inhibit the growth of Salmonella spp. and other Enterobacteriaceae, reducing the risk of gastrointestinal infections.
Akkermansia muciniphila	Helicobacter pylori	Curcumin: Active compound in turmeric. Supports the proliferation of Akkermansia muciniphila, associated with improved gut barrier function and metabolic health.	Ellagic Acid: Found in various fruits like pomegranates and berries. Exhibits antimicrobial activity against Helicobacter pylori, reducing its colonization in the gut and associated risks of gastritis and peptic ulcers.

Sources: Baky et al., 2022; Mithul Aravind et al., 2021; Singh et al., 2019

3.2 Microbial Metabolism of Polyphenols

Among the members which are the products of the digestive tract, gut microbiota is a life-long partner that helps in converting dietary polyphenols into bioactive metabolites with a better ability to maintain physiologic effects (Iqbal et al., 2020). Microorganismal enzymes such as β-glucosidases, esterases and reductases are responsible for the breakdown of the polyphenol molecules by cleaving the bond, conjugating the molecules, and thus facilitating their absorption and distribution (Ray & Mukherjee, 2021). Throughout the process of intestinal microbiota transformation of polyphenols, numerous phenolic acids, polyphenol alcohols, and other compounds having a plethora of bioactivities will be produced.

3.3. Impact on Gut Barrier Function

The gut microbiota-phenolic interactions help regulate intestinal barrier integrity, which is important in the development of the gut and immunological functions. Polyphenols accelerate the tight junction protein expression at the intestinal barrier, including occludin and claudins, and this event slows down gut mucosa passing (Mithul Aravind et al., 2021). That performs the avoidance of translocation of bacteria and toxins through the gut mucosa. On the other hand, the polyphenols decrease the levels of pro-inflammatory cytokines synthesized locally under the gut mucosa and alter the course of immune reactions, as well (Wang et al., 2022a).

3.4 Implications for Metabolic Health

The great importance of gut microbiota with polyphenols interactions is the metabolic health management and the processes associated with glucose and lipid metabolisms (Toney et al., 2021). Polyphenols affect lipid metabolism by their mediation of the activity of the enzymes crucial to lipid synthesis, storage, and oxidation (Chan et al., 2023). Microorganisms from the gut do this to polyphenols, which enforce insulin sensitivity, lead to less fat, and improve the relationship between lipids, with overall effects of trimming down the risk of obesity, insulin resistance, and cardiovascular disease (Tomás-Barberán et al., 2016).

3.5 Regulation of glycolipid metabolism

Glycolipids perform vital functions during metabolic stability by being pivotal parts of cellular membranes and molecules involved in the signaling of lipid metabolism and insulin sensitivity (Xie et al., 2023). As representatives of the glycolipid family, they regulate the proliferation, apoptosis, and differentiation of the cell. Meanwhile, they also change cellular reactions to stress and inflammation with the modification of cell membranes (Wang et al., 2022c). The misregulation of glycolipid metabolism is reported to be a cause of the development of metabolic disorders such as obesity, diabetes, and cardiovascular disease.

It has been revealed that the interplay of microbiota in the gut and polyphenols has pronounced consequences in glycolipids metabolism, which may influence lipid absorption, synthesis, and storage in adipose tissue & liver (Man et al., 2020). Polyphenols control the level of various enzymes that function in lipid oxidation, such as lipoprotein lipase (LPL), Hormone-sensitive lipase (HSL), and Fatty acid synthase (FAS). This results in changed storage and use of lipids by the body (Lippolis et al., 2023). The gut microbiome increases glycolipid metabolism via microbial metabolites like SCFAs linked to hepatic lipogenesis interference, adipocyte differentiation influence and insulin sensitivity regulation.

Regulation of glycolipids metabolism, which can be triggered by both the gut microbiota and polyphenol derivatives, gives rise to treatment perspectives for obesity and diabetes management (Song et al., 2022). Polyphenol-rich diets (such as Mediterranean ones) show lower levels of inflammation, and enhanced lipid profiles (including insulin sensitivity) are likely to be partly because of gut microbiota and glycolipid metabolism (Zhao & Jiang, 2021). The evidence that probiotics and prebiotics can target the gut microbiota-specific populations, as shown in Table 2, directly leading to the modulation of the glycolipid metabolism and metabolic health as an actual therapeutic tool, is very promising (Katsagoni et al., 2018).

4. Polyphenols Maintaining Health Beyond Microbiota

4.1. Zinc Homeostasis

Fruits, vegetables, and beverages rich in polyphenols contribute much to the favorable condition of gastrointestinal flora, achieving great effects on the balance of zinc concentration (Sorita et al., 2023). The presence of gut microbiota in the proper balance promotes the efficacious consumption of zinc. Zinc assists immunity, DNA synthesis, and the healing process (Ashwin et al., 2021). It is possible that this balance might be disrupted, and if this happens, impaired zinc absorption, what comes to the fore in this case, would certainly include weakened immunity, delay in the wound healing processes, and compromised DNA synthesis (Islam et al., 2023).

Consequence of Imbalance: Zinc deficiency, caused through dysfunctional microbiota-gut junctions, might contribute to rising incidences of infections, delayed healing of wounds, and weakening of DNA repair systems (Ray & Mukherjee, 2021).

4.2. Iron Homeostasis

The synergistic relationship between polyphenols and intestinal microbiota involves iron homeostasis too (Garzarella et al., 2022). Polyphenols induce influence on iron absorption, and the microbiome regulates the expression of metal transporters. These two systems must work well together to deliver oxygen, enable metabolism, and make red blood cells (Rana et al., 2022).

A consequence of Imbalance: Disruptions of end products of polyphenols by microbiota controlling iron compartmentation may cause the iron deficit, trying to bring on an anemic state, alopecia, and fatigue as well as tissue hyperoxygenation (Wan et al., 2020).

4.3. Polyphenols, Gut Microbiota, and Brain Health

Polyphenols and their interrelation with a healthy gut microbiome and brain health have great intricacy. Therefore, the networks of interactions between these elements are quite complex (Song et al., 2022). Polyphenols have neuroprotective functions; in the meantime, gut microflora are engaged in the process of generating neurotransmitters and metabolites linked to the memory process. This interdependence is imperative to the rejuvenation of healthy brain functions (Wang et al., 2021).

Consequence of Imbalance: Differences or changes in gut microbiota-polyphenol connections may cause neurodegenerative disorders that present with declines in cognitive functions and many times lead to Alzheimer’s and Parkinson’s diseases (Kalita et al., 2022).

5. Conclusion

The microbiota-polyphenol correlation emphasizes the crucial role of diet in human health and comfort. Gut microbiota, polyphenols, and health are related in a multi-directional fashion, a common theme that is explored in this paper. A more in-depth examination of the complex mechanisms through which that relationship occurs and the implication for human health is unraveled.

The uptake of polyphenol-rich foods contributes to the development of a diverse and durable gut cohabitation, particularly for preserving zinc and iron balance, resisting the damage of the intestinal barrier, stabilizing the working, and blunting the chance for cancer development. Polyphenols play, on account of the relationship they so often establish with the gut microbiota, the role of controller, moderator, and protector vis-à-vis metabolic processes, immune reactions, and free radicals, in this way promoting health and overall disease resilience.

On the contrary, the breakdown of the microbiome-polyphenols interaction prevents the vital biochemical reactions from occurring that are necessary to regulate the homeostasis of micronutrients, maintain the functionality of the intestinal barrier, improve cognitive abilities, and protect from developing cancer and other chronic diseases. We need to comprehend the intricate relation between dietary polyphenols, gut microbiota, and health directly to ensure prevention and minimizing the risk of metabolic, gastrointestinal, neurological, and oncologic diseases. The latest dietary trends and the influence of the environment pose new challenges that cannot be ignored by the proponents of modern preventive healthcare. In this context, a diet rich in polyphenols and a thriving gut microbiota are two fundamental components.

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BÖLÜM IV

Antibacterial Properties of Plant-based Kefir

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Introduction

Cow's milk has played a significant role in human nutrition for many years and is considered a complete food. It consists of macro- and micro-nutrients such as proteins, fats, lactose, vitamins, and minerals, which are crucial for human growth and development (Reyes-Jurado & et al., 2023). The studies reported that the consumption of milk and dairy products may play a protective role

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against the most common chronic diseases and have very few side effects. However, the scientific community is increasingly questioning and examining the role of milk and dairy products in human nutrition (Antunes & et al., 2022). Currently, cow milk allergy, lactose intolerance, calorie considerations, and the prevalence of hypercholesterolemia have led consumers to choose plant-based milk alternatives (Sethi, Tyagi & Anurag, 2022). The preference for plant-based products is due to factors such as health awareness, environmental concerns, sustainability, and the importance of animal welfare (Aydar & et al., 2020). Plant-based sources such as cereals and legumes are considered functional foods and nutraceuticals due to their content of minerals, vitamins, and antioxidants as well as their content of prebiotic compounds like inulin, making them suited to the development of synbiotic products (Bernat & et al., 2015; Sethi, Tyagi & Anurag, 2022). Plant-based milks may be used as raw materials for yoghurt and kefir (Gocer & Koptagel, 2023).

Kefir is a fermented dairy product known as a source of probiotic microorganisms, containing lactic acid bacteria, acetic acid bacteria, and yeasts (Kadıoğlu, 2017; Yılmaz & et al., 2022). Kefir could be produced from the milk of animals such as cows, goats, sheep, camels and buffaloes, however nowadays it can also be produced by fermenting extracts obtained from cereals, cereal-like products, legumes, fruits, vegetables or nuts (Sethi, Tyagi & Anurag, 2022; Al-Mohammadi & et al.2021). The nutritional value of plant-based milks and products varies depending on the raw materials. During fermentation, kefir microorganisms produce bioactive compounds such as organic acids, bioactive peptides, bacteriocins and exopolysaccharides. These compounds improve several health benefits of kefir including antihypertensive, hypocholesterolemic, antidiabetic, anticarcinogenic, anti-inflammatory, antioxidative, antiallergic, immunomodulatory, antiviral, and antimicrobial properties (Kadıoğlu, 2017; Koyu & Demirel, 2018; Reyes-Jurado & et al., 2023). For example, lactic acid, acetic acid, citric acid, malic acid, and succinic acid, increase the acidity of the kefir, and this high acidity has been associated with the antimicrobial efficacy. The high acidity creates an unfavourable environment for pathogenic or spoilage microorganisms in kefir (Egea & et al., 2022). Moreover, Al-Mohammadi & et al. (2021) reported that alkaloids, phenols, esters, steroids, polyalkenes, heterocyclic compounds, and aromatic aldehydes inhibit bacterial pathogens by different mechanisms of action. The antibacterial effect of kefir has been observed against bacteria such as *Salmonella*, *Shigella*, *Staphylococcus*, *Helicobacter pylori*, *Escherichia coli*, *Enterobacter aerogenes*, *Proteus vulgaris*, *Bacillus subtilis*, *Micrococcus luteus*, *Listeria monocytogenes*, *Streptococcus pyogenes* as well as *Candida albicans* yeast (Rosa & et al., 2017; Koyu & Demirel, 2018). In this study, plant-based kefir was produced from milk extracted from chickpea, lentil and bean. Anibacterial effects of cow milk kefir and plant-based kefirs against *Escherichia coli*, *Enterococcus faecalis*, *Staphylococcus aureus*, and *Bacillus cereus* were investigated.

Material and Method

Material

The legumes (white beans, lentils, chickpeas) and pasteurised milk were purchased from the local market. Commercial kefir starter culture was obtained from Türker Industry Technic Machine Ltd. Co. (İstanbul, Türkiye). Nutrient Broth, Nutrient Agar and other chemicals were purchased from Sigma Aldrich (MO, USA). Plant-based kefir production carried out in the laboratories of Food Engineering Department, Akdeniz University.

Kefir samples production

Legume milk obtained with the modified method described by Costa & et al. (2018). Raw dried legumes were soaked in mineral water for 24 h. After boiled, white bean and chickpeas peeled. The legumes crushed in distilled water and homogenized with blender (Bosch, Mixxo Quattro MSM 7700, Jesenice, Slovenia). The legumes-water mix was used to produce kefir. A legume-water mix and cow milk were inoculated with commercial kefir starter culture (0.15%) and incubated at 25°C until the pH reached 4.6 (Gocer & Koptagel, 2023). The kefir samples were stored at 4°C for a day to determine antibacterial activity.

Methods

To determine the antibacterial activity, *Escherichia coli* (ATCC 35218), *Enterococcus faecalis*, *Staphylococcus aureus* (ATCC 25923), and *Bacillus cereus* 2248 were used as test bacteria. The pathogenic test bacteria were activated in Nutrient broth (NB) by incubating at 37°C for 24 hours, and their density was adjusted to 0.5 OD with McFarland using fresh NB. Nutrient agar (15 ml) was poured into each sterile Petri dish (90 mm diameter). Subsequently, each bacterial suspension cultured for 24 h were spread on the plates. Wells with a diameter of 1 cm was created on the agar using a sterile rod. To determine the pH effect on antibacterial activity, the pH of kefir samples was adjusted to 7.0 with 1 M NaOH. Each kefir sample (100 µl) was then filled into the wells of agar. The plates were incubated at 37°C for 24 hours. The diameters of the inhibition zones formed around each well were measured using a calliper, and the results were recorded in millimetres (Reinheimer & et al., 1990).

Result

Table 1 is shown inhibition zone values of kefir produced from cow's milk and plant-based milk against pathogenic bacteria at pH 4.6. The highest and lowest inhibition zone diameter was determined against *S. aureus* (27.4±0.6 mm) and *B. cereus* (19.9±0.2 mm), respectively, in kefir produced from cow milk. The study conducted by Ulusoy & et al. (2007) determined that kefir had inhibition zones with diameters of 18.3 mm, 21.4 mm, and 19.6 mm against *Escherichia coli*, *Staphylococcus aureus*, and *Bacillus cereus*, respectively. Our result agreed with Ulusoy et al. (2007) who found the highest antibacterial effect against *S. aureus* in kefir samples. Kefir produced from bean milk exhibited the highest and lowest inhibition zone diameter against *E. coli* (24.6±0.4 mm) and against *E. faecalis* (15.0±0.0 mm), respectively. Kefir produced from lentil and chickpea milk had the highest antibacterial activity against *E. coli* with 27.1±0.4 mm and with 24.7±0.4 mm, respectively. Antibacterial activity against *B. cereus* was not determined in kefir obtained from bean milk. In the present study, kefir produced from cow milk had higher antibacterial activity than those produced from legume milk.

Kefir exhibits both bacteriostatic and bactericidal effects against gram-positive and gram-negative bacterial pathogens as well as spoilage fungi. The antimicrobial activity of kefir is attributed to various factors such as proteolytic enzymes, organic acids, carbon dioxide (CO_2), bacteriocins, bioactive peptides, and hydrogen peroxide. Additionally, the reduction in pH of kefir, caused by the accumulation of organic acids, results in broad-spectrum inhibitory activity against both gram-positive and gram-negative bacteria (Gonzalez-Orozco & et al., 2022). Moreover, our results demonstrated that kefir with high pH (7.0) values had a lower antibacterial effect against all pathogenic bacteria compared to kefir samples with 4.6 pH values (Table 2). Al-Mohammadi & et al. (2021) also observed that antimicrobial activity is higher in kefir than neutralized ones.

Table 1: Inhibition zone values (mm) of kefir samples that pH adjusted at 4.6.

pH 4.6	***E. coli***	***B. cereus***	***S. aureus***	***E. faecalis***
Kefir	25.8±0.1	19.9±0.2	27.4±0.6	21.0±0.2
Bean	24.6±0.4	ND	16.4±0.0	15.0±0.0
Lentil	27.1±0.4	16.6±0.3	20.7±0.1	13.4±0.7
Chickpea	24.7±0.4	18.2±0.3	17.2±0.0	19.9±0.0

ND: Not determined

Table 2 is given inhibition zone values of kefir samples that pH adjusted at 7.0. The highest and lowest inhibition zone diameter was determined against *E. coli* (28.3±0.0 mm) and *B. cereus* (19.6±0.0 mm), respectively, in kefir produced from cow milk. Kefir produced from bean milk exhibited the highest and lowest inhibition zone diameter against *E. faecalis* (18.6±0.3 mm) and *S. aureus* (12.7±0.1 mm), respectively. Kefir produced from lentil milk exhibited the highest and lowest inhibition zone diameter against *E. coli* (14.5±1.1 mm) and *S. aureus* (12.9±0.1 mm) respectively. Kefir produced from chickpea milk exhibited the highest and lowest inhibition zone diameter against *E. faecalis* (17,3±0.7 mm) *E. coli* (12.17±0.0 mm) respectively. Antibacterial activity against *B. cereus* was not determined in kefir produced from bean, lentil, and chickpea milks. Figure 1 shows the antibacterial effect of chickpea and bean milks against *B. cereus*.

Table 2: Inhibition zone values (mm) of kefir samples that pH adjusted at 7.0.

pH 7	***E. coli***	***B. cereus***	***S. aureus***	***E. faecalis***
Kefir	28.3±0.0	19.58±0.0	27.9±0.4	19.7±0.9
Bean	13.3±0.2	ND	12.7±0.1	18.6±0.3
Lentil	14.5±1.1	ND	12.9±0.1	13.6±0.2
Chickpea	12.2±0.0	ND	12.5±0.1	17.3±0.7

ND: Not determined

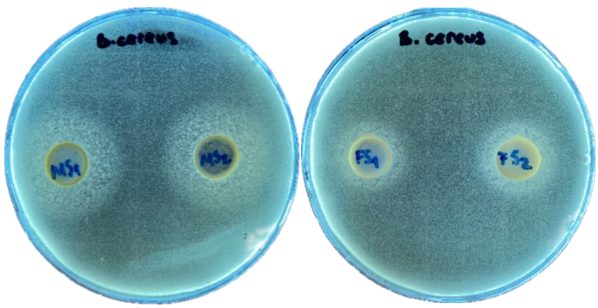

Figure 1: Antibacterial effect of chickpea and bean milks against B. cereus

Conclusion

Legumes such as lentils, peas and chickpeas are an important source of protein, carbohydrates, vitamins and minerals and are widely consumed. The health effects of legumes are related to the potassium, magnesium, soluble fiber, flavonol, flavone, flavone, isoflavone compounds and bioactive compounds such as glycosides, tannins, polyphenols, saponins, alkaloids (Atalay & Gökbulut 2021). However, this study showed that kefir produced from cow milk had a more antibacterial activity than kefir produced from legumes milk.

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BÖLÜM V

Determınatıon Of Fatty Acıd Composıtıons Of Some Raısın Cultuvars In Turkey

Özcan Barış ÇİTİL[1]

1. Introduction

Grapes (Vitis vinifera L.) are known as one of most important fruit crops in the world, with an approximate annual production of 68 million tons. Because Turkey is located between 36o and 42o north latitudes providing a suitable geographic position, its climate is very convenient to grape growing. Raisins are an important agricultural product with 300,000 tons produced in the Turkey in 2008. Turkey, U.S.A., Chile, Iran, South Africa and Greece seedless grape producing countries in the world are most important(Özden, 2008).
In general, the composition of grapes are water, sugar, minerals, organic acids, nitrogenous agents, flavoring agents, enzymes, vitamins and phenolic compounds(Fidan & Yavaş, 1986). Food value of raisins lies chiefly in their sugars, fruit acids and mineral

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salts(Winkler, 1974). Raisins are rich in point of potassium, calcium, magnesium and phosphorus minerals(Kavas, 1990; Winkler, 1974). On the other hand, raisins are rich also on account of vitamin A, thiamin, ribofilamin, niacin, vitamin C, pyridoxine vitamins (Kavas, 1990). The sugars glucose and fructose found in grapes, and via direct diffusion bleeding, particularly because of pass-quality infant and children nutrition is important(Cabaroğlu & Yılmaztekin, 2006). These species are known to have antiinflammatory, antispasmodic, carminative, analgesic nervous system stimulant, sedative, antitussive, stomachic, anticonvulsant, and antifeedant activities (Cabaroğlu & Yılmaztekin, 2006).

Among the polyunsaturated fatty acids, linolenic acid (C18:3 n-3), EPA (eicosapentaenoic acid, C20:5 n-3) and DHA (docosahexaenoic acid, C22:6 n-3) are the dominant n-3 fatty acids in sunflower oil(CİtİI, Sezgin, Guler, & Aktumsek, 2010). These fatty acids are of great importance to humans for the prevention of coronary heart disease(Kinsella, 1987). ω-3 PUFA have been shown to have positive effects on cardiovascular diseases(Connor, 1997).

Most of the studies on Vitis vinifera L. varieties comprise their fatty acid composition. There is no work on the drying of Vitis vinifera L. cultuvars. Therefore, the aim of this study was to determine the total fatty acid composition, ω3/ω6 fatty acids ratio and SFA/PUFA ratio of some raisin samples in eating.

2. Materials and Methods

2.1. Collection of Samples

Three raisin samples were collected from the Eastern Mediterranean Region of Anatolia in order to determine the fatty acid compositions for 7 samples from each of the 3 most widespread Ekşi Kara, Gök Üzüm and Kara Dimrit. were dried. Identification of the varieties of grape collected was carried out according to the usual procedures, based on methods suggested by the method(Sezik & Ozer, 1983), at the Herbarium of the Department of Biology at Selcuk University. These samples were frozen and stored at -27 ºC until analyzed.

2.2. Fatty Acid Analysis

The resultant fatty acid methyl esters were separated and stored at -20 oC. At the beginning of each analysis, the samples were allowed to equilibrate to room temperature and analysed by gas liquid chromatography (Shimadzu 15-A), equipped with dual flame ionisation detector and a 1.8 m × 3 mm internal diameter packed glass column containing GP 10 % SP–2330 on 100/120 Chromosorb WAW, cat no: 11851. Column temperature was 190 °C for 31 min., and then rose progressively at 30 oC/min up to 220 °C where it was maintained for 10 min at 220 °C. Carrier gas was nitrogen (2 ml/min). The injector and detector temperatures were 225 and 245 °C respectively. Conditions were chosen to separate fatty acids of carbon chain length from 8 to 24. The fatty acids were identified by comparison of retention times with known external standard mixtures (Alltech), quantified by a Shimadzu Class-Vp software were expressed as percentage distribution of fatty acid methyl esters. Each of the experiments was repeated three times.

Identification of fatty acids was carried out comparing sample FAME peak relative retantion times with those obtained for Alltech standarts. Results were expressed as relative percentages. All solvents and reagents were analytical grade.

2.3. Statistical Analysis

Three raisin samples were analyzed for each parts of varieties were analyzed in triplicate. The average results of peak area are offered as means ± SD. The statistical analysis of the percentages of fatty acid was tested by analysis of variance (ANOVA) and comparisons between mean values were performed Duncan's test. Differences between means were reported as significant if $P < 0.05$.

3. Results

Table 1. *Fatty acid profiles of raisin (%, w/w).*

Fatty acids	Ekşi Kara	Gök Üzüm	Kara Dimrit n
C 8:0	0.00±0.00a	0.00±0.00a	0.00±0.00a
C 10:0	0.00±0.00a	0.00±0.00a	0.01±0.00a
C 12:0	0.01±0.00a	0.01±0.00a	0.01±0.00a
C 14:0	0.66±0.07b	0.55±0.07b	1.03±0.07a
C 15:0	0.03±0.01a	0.01±0.01b	0.02±0.01ab
C 16:0	18.91±0.2b	15.84±0.26c	24.23±0.26a
C 17:0	0.01±0.00a	0.03±0.00a	0.03±0.00a
C 18:0	2.84±0.11c	3.51±0.11b	4.09±0.11a
C 20:0	0.03±0.00a	0.00±0.00a	0.02±0.00a
C 21:0	0.28±0.03a	0.32±0.03a	0.29±0.03a
C 22:0	0.00±0.00a	0.00±0.00a	0.01±0.00a
C 24:0	0.38±0.04ab	0.33±0.04b	0.48±0.04a
∑SFA	**23.15**	**20.60**	**30.22**
C 14:1 ω5	0.17±0.01a	0.15±0.01a	0.16±0.01a
C 16:1 ω7	3.43±0.15a	2.12±0.15c	3.05±0.15b
C 18:1 ω9*	9.72±0.23c	16.01±0.23a	12.68±0.23b
∑MUFA	**13.32**	**18.28**	**15.89**
C 18:2 ω6*	60.74±0.69a	56.65±0.69b	47.80±0.69c
C 18:3 ω3*	1.00±0.12c	2.88±0.12b	3.27±0.12a
C 20:2 ω6	0.01±0.00a	0.01±0.00a	0.02±0.00a

C 20:3 ω3	0.00±0.00a	0.00±0.00a	0.00±0.00a
C 20:4 ω6	0.00±0.00a	0.00±0.00a	0.00±0.00a
C 20:5 ω3	0.39±0.04b	0.32±0.04b	0.85±0.04a
C 22:3 ω3	0.03±0.01ab	0.02±0.01b	0.04±0.01a
C 22:4 ω6	0.01±0.00a	0.02±0.00a	0.02±0.00a
C 22:5 ω3	0.35±0.03b	0.32±0.03b	0.64±0.03a
C 22:6 ω3	0.60±0.08a	0.55±0.08a	0.60±0.08a
∑PUFA	**63.13**	**60.77**	**53.28**
∑ ω 3	2.37±0.12c	4.09±0.12b	5.40±0.12a
∑ ω 6	60.76±0.41a	56.68±0.41b	47.84±0.41c

[* a – c] Mean values within the same row sharing a common superscripts are not significantly different at $P<0.05$.

The raisin included in this study were contained fatty acids of 8-24 carbon chain lengths. Total lipid contents of the raisins investigated in Hadim district of Konya province in Turkey. The lipid of raisin was found to be 1.90%, 2.50% and 2.75%, Kara Dimrit, Gök Üzüm and Ekşi Kara, respectively. Similarly, Gallendar and Peng(Gallander & Peng, 1980) found that contents of raisin was between 0.15% and 0.25. For total lipid contents in Ekşi Kara were determined higher than other samples.

In the present study, the most abundant fatty acids in Ekşi Kara were linoleic (C18:2), palmitic (C16:0), oleic (C18:1), palmitoleic acid (C16:1), stearic acid (C18:0) and linolenic acid (C18:3), at 60.74%, 18.91%, 9.72%, 3.43%, 2.84%, 1.00%, respectively. These six fatty acids represented about the 96.64 % of total fatty acids. Similar results were observed by Guler et al. (Guler, Aktumsek, Citil,

Arslan, & Torlak, 2007) for 22:6 (DHA), 16:0, 18:1 ω9, 16:1 ω7, 20:5 ω3 (EPA) and 18:0 in zander.
Similarly, Parlat et al. (Parlat, Çitil, & Yıldırım, 2010) found that linoleic acid was the predominant fatty acid (69.08%) in sunflower meal and corn oil (56.89%). Fatty acid composition of total 3 raisin in eating is shown in Table 1. In the present study, palmitic acid was the major SFA (15.84- 24.23 % of total fatty acids) in all samples Similar results were obtained by Akin et al (Altındişli & Yağcı, 2009) with 15.24% for Ekşi Kara.
The highest value of the saturated (SFA) to polyunsaturated (PUFA) fatty acids ratio was in Kara Dimrit. The SFA/PUFA value in Kara Dimrit was around 0.57. The highest total saturated fatty acid content (30.22 %) was found in Kara Dimrit. Similar results obtained by Tangolar et al.(Tangolar, özoğul, Tangolar, & Torun, 2009) for Razakı, Öküzgözü, Horoz karası, Narince; 0.21, 0.22, 0.23, 0.19, respectively.
Oleic acid was identified as the major MUFA (9.72- 16.01% of total fatty acids) in all samples (Table 1). Tangolar et al. found smilar results for Razakı (19.06%), for Öküzgözü (19.33), for Horoz Karası (20.13%), for Narince (20.53), Navas(Navas, 2009) for syrah (22.2%), for Tintorera (24.9%)
Linoleic acid (LA) was the most abundant PUFA (47.80-60.74%) in all samples. Similar results were obtained by Demir and Namli (Demir & Namli, 2006) in Mazmura varieties. Navas (Navas, 2009) for Syrah (64,5 g/100g of fatty acids), for Tintorera (61.4%), Pardo et al. (Pardo, Fernández, Rubio, Alvarruiz, & Alonso, 2009) for Syrah (64.53%) and Monastrell (66.84%), respectively.
Consumption of n-3 fatty acids may prevent the devolepment of coronary heart disease(Schmidt, Arnesen, de Caterina, Rasmussen, & Kristensen, 2005). In the present study, Ekşi Kara Gök Üzüm and Kara Dimrit contained the highest levels of ω-6 fatty acids. These

concentrations found were 60.76%, 56.68 and 47.84% for Ekşi Kara, Gök Üzüm and Kara Dimrit, respectively. In the present trial, the values for ω-6/ω-3 ratio were higher than 4. This ratio was 25.64, 13.82 and 8.84, in Ekşi Kara, Gök Üzüm and Kara Dimrit, respectively.

4. DISCUSSION

In conclusion, it was determined that fatty acid compositions varied between raisin samples. While Kara Dimrit variety contents the least ∑ω 6, the same variety contents the most ∑ω 3 among the other cultuvars. When Ekşi Kara variety contents the most ∑ω 6, the same variety contents the least ∑ω 3 among the other cultuvars. Unsaturated fat content was determined the highest level (%79.05) in Gök üzüm variety. Further researches are needed to determine fatty acid composition of human fed this raisin.

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BÖLÜM VI

Parameters affecting the presence and formation of biogenic amines in cheese

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The global population is expanding at a rapid rate, with projections indicating that it will reach 10 billion by 2050. In this context, the accessibility of food is becoming increasingly challenging. For millennia, humans have been compelled to ingest sustenance to sustain their existence, facilitate growth

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and development. Dairy products, which are a vital component of a balanced diet, contain macronutrients such as protein, fat and carbohydrates, as well as micronutrients such as vitamins and minerals (Demir & Gürses, 2022; Savaş, 2024; Savaş & Binici, 2024; Binici & Savaş, 2024).

Cheese, which constitutes a significant portion of this food group, is a vital component of the dairy product category.

Cheese is a dairy product that is defined by its distinctive organoleptic characteristics, flavour and aroma. These properties are the result of a series of biochemical processes, including glycolysis, proteolysis and lipolysis (McSweeney, 2017; Galli et al., 2019). In particular, proteolysis plays a significant role in the formation of the distinctive aroma and texture of cheese. It is responsible for imparting the cheese with its unique characteristics and contributes to the formation of bioactive peptides, which have gained popularity due to their potential to positively influence body functions (Galli et al., 2019). During the process of cheese ripening, the decomposition of casein results in the accumulation of free amino acids. These can be converted into a range of sensory bioactive substances by the action of the microflora present, or alternatively, they can be converted to biogenic amines by decarboxylation (Adamek et al., 2021). Furthermore, biochemical, physical and microbiological alterations take place throughout the maturation process. It is evident that this process is influenced by a multitude of factors.

These factors include the activity of microorganisms developing during cheese production, the type of starter used, the pH value of the milk, environmental conditions, technological processes, and storage conditions (Adamek et al., 2021; Adamek et al., 2024).

In the present era, there is a growing interest in matters pertaining to health and nutrition. It is evident that while our diets contribute to the development of numerous ailments, they also possess vital functional attributes that can avert the onset of many diseases. These properties have been revealed by in vivo, in vitro and epidemiological studies. In this context, the present review study provides information about the effect of biogenic amines, which have various effects on human health, on cheese.

Effects of biogenic amines on human health and legal limits

Biogenic amines are defined as organic, basic, low molecular weight nitrogenous compounds with biological activity, formed mainly by decarboxylation of amino acids. The formation of BAs is subject to variation depending on a number of factors, including the availability of free amino acid precursors, the presence of decarboxylase-producing bacteria and the pH value, ripening temperature and salt concentration for the growth of these bacteria. The ingestion of small quantities of BAs via food sources does not have an adverse impact on human health. Intestinal amine oxidase enzymes are capable of rapidly metabolising and detoxifying small amounts of BAs. Nevertheless, elevated levels of BAs may exceed the detoxification capacity of amine oxidases, potentially leading to minor allergic reactions and, in some cases, more serious health complications (Turna, Chung & McIntyre, 2024; Ramos et al., 2024).

BAs are commonly found in raw and fermented food products, including cheese, wine, sauerkraut, cured meats, and fruit juices (Ganjeh et al., 2024). The most common BAs are histamine, tyramine, putrescine, cadaverine and phenylethylamine. These are formed by decarboxylation of precursor amino acids, including histidine, tyrosine, ornithine, lysine and phenylalanine. The respective processes are illustrated in figure 1. It is established that the levels of BAs exhibit considerable variation depending on the specific type or variety of food, with notable differences observed between different types of fish or cheese. Moreover, the concentration of BAs is subject to influence from a number of factors, including the composition of the food in question, the raw materials used in its production, food hygiene practices, the microbial composition of the food, and the manner in which it is processed, fermented and stored (Doeun, Davaatseren & Chung, 2017; Dos Santos et al., 2023).

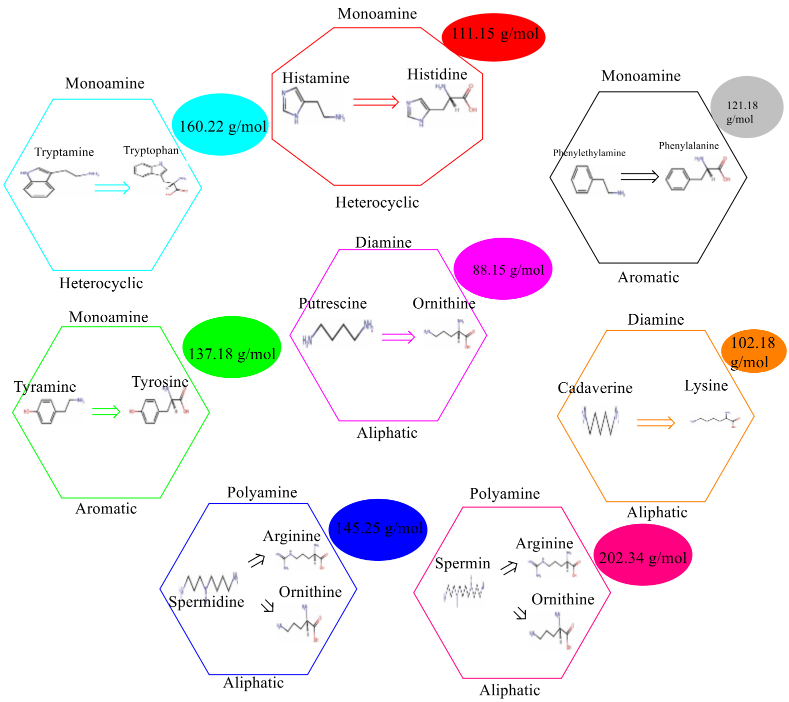

Figure 1. Biogenic amines commonly found in foods, their precursor amino acids and chemical classification (Dos santos et al., 2023; Ganjeh et al., 2024)

BAs are classified according to a number of different criteria. The chemical structure of these compounds allows for their classification into two main groups: aliphatic amines and aromatic amines. The latter are further divided into two subcategories: aromatic amines with benzene and those with heterocyclic nuclei. In terms of the number of amino groups they possess, they can also be classified as monoamines and diamines. Although spermidine and spermine are traditionally considered to be biogenic amines (BAs), their biosynthesis and physiological functions are markedly distinct. Consequently, they are now regarded as constituting an independent group. Spermidine and spermine are not considered to pose a risk because they are present at very low concentrations in foods (Kalac, 2014; del rio et al., 2024).

In addition to their impact on human growth and development, biogenic amines have the potential to induce a range of health issues when consumed in quantities exceeding certain thresholds (McCabe-Seller, Staggs & Bogle, 2006). The ingestion of elevated levels of BAs through foodstuffs can have toxic effects, contingent on the composition of the food, quantitative and qualitative factors, individual susceptibility and health status. Exposure to high levels of BAs can result in a range of adverse effects, including nausea, respiratory distress, gastric distress, headache, sweating, heart palpitations and hypotension (histamine) or hypertension (tyramine). Additionally, there is a risk of developing various foodborne illnesses, such as histamine poisoning (scombroid poisoning) and tyramine toxicity (cheese reaction). Of particular note is the accumulation of biogenic amines, particularly histamine and tyramine, during the ripening process of cheese (Yıldız et al., 2010; Adamek et al., 2021). Although histamine has more research in the literatüre due to its higher toxicity, there are studies and concerns about other biogenic amines, including, tyramine, putrescine, phenylethylamine, and cadaverine

(Turna, Chung & McIntyre, 2024). Table 1 illustrates the tolerable levels of biogenic amines and the quantities that may exert a toxic effect.

Table 1. Recommended and reported threshold values for biogenic amines in foods. (Durak-Dados, Michalski & Osek, 2020; Turna, Chung & McIntyre, 2024).

Biogenic amines	Recommended dose in foods (mg/kg)	Toxic dose per meal in healthy individuals (mg)	Toxic dose per meal in sensitive and non-sensitive groups individuals at risk (mg)
Histamine	100	>50	5-10
Tyramine	100-300	>600	>6
β-phenylethylamine	30	N.E	N.E
Putrescine, cadaverine spermidine, tryptamine, spermine	N.E		N.E

N.E: None established

The determination of biogenic amines is of significance not only from a toxicological perspective, but also as a means of assessing the quality of food products. The presence of these compounds is frequently indicative of a range of quality parameters, including a lack of freshness, inadequate hygienic storage conditions or the spoilage of processed or fermented products (Herrero et al., 2016).

At the time of writing this article, to our knowledge, there is no legal regulation defining the limits of biogenic amine tolerance in fermented foods in Turkey. It has been established that cheese is a dairy product with a high concentration of biogenic amines (Renes et al., 2014). It is therefore important to control the biogenic amine values in milk and its products, which occupy a significant position in particular with regard to the nutrition of children. It has been demonstrated that histamine, tyramine, putrescine and cadaverine, which are biogenic amines, should not exceed 900 mg/kg in cheese (Valsamaki, Michaelidou & Polychroniadou, 2000). Furthermore, given the inter-individual variability in detoxification mechanisms and capacity for biogenic amines, it is important to recognise that sensitivity to biogenic amine levels may also differ between individuals (Bozkurt, 2019).

The European Union Food Safety Authority (EFSA), a preeminent organization in the field of food safety, has established permissible levels for certain biogenic amines. The

European Food Safety Authority (EFSA) has published recommendations for tolerable levels of histamine (50 mg) and tyramine (600 mg) per person per meal. No recommendations were made for putrescine, cadaverine and other biogenic amines due to the absence of sufficient scientific data (EFSA, 2011). The Turkish Food Codex establishes legal limits for histamine in fish species (200 mg/kg) and wines (10 mg/kg).

A review of the literature reveals numerous studies investigating the biogenic amine content of cheese, a fermented milk product. Durlu-Özkaya (2002) conducted an analysis of the biogenic amine levels present in a selection of cheeses produced in Turkey. The highest levels of histamine (94.76 mg/100 g) and tyramine (138.16 mg/100 g) were observed in Civil cheese, which also exhibited the highest average biogenic amine content (349 mg/100 g) among the cheese types (Kashar, Mihaliç, Van Herb, Braided, Urfa).

In their study determining the biogenic amine contents in mold-ripened blue cheeses, Reinholds et al. (2020) stated that putrescine, cadaverine, histamine and tyramine were at the levels of 1.3-45.5 mg/kg, cadaverine 1.7-131.0 mg/kg, 0.2-186.0 mg/kg and 1.1-717.0 mg/kg, respectively.

In a study published in 2021, Kandasamy and colleagues investigated the biogenic amine contents of various cheese types. The highest biogenic amine contents were observed in Gouda cheese, with histamine levels reaching 9.66-111.18 mg/kg, cadaverine levels at 17.68-92.47 mg/kg, and spermidine levels at 141.33 mg/kg. Tyramine levels were 82.63 mg/kg, tryptamine levels were 65.19 mg/kg, phenylethylamine levels were 11.89-22.57 mg/kg, and spermidine levels were 69.86 mg/kg in Cheddar cheese.

Mayer & Fiechter (2018) conducted a study to determine the biogenic amine contents of hard and semi-hard cheeses sold in Austria. The results indicated that the mean histamine value was 4.63 mg/100 g, the tyramine value was 8.30 mg/100 g, and the putrescine value was 5.13 mg/100 g. The cadaverine value was 4.23 mg/100 g, the tryptamine value was 1.31 mg/100 g, and the total biogenic amine content was 23.60 mg/100 g.

In a study conducted by Ramos, Brandão & Rodrigues (2020), the biogenic amine contents in Gouda cheese were determined. The researchers indicated that the concentration of putrescine was 7.1 ± 1.3 mg/kg, cadaverine was 3.4 ± 1.0 mg/kg, and tyramine was 24.7 ± 1.3 mg/kg.

It has been demonstrated in previous studies that the ripening stage of cheese generally results in an increase in the concentration of biogenic amines. Nevertheless, it has been established that hard cheeses contain a higher concentration of biogenic amines than their soft or semi-hard counterparts (Botello-Morte et al., 2022).

Conclusion

Consumers' awareness of access to healthy and safe food has led to an increase in studies on the detection of compounds harmful to human health. This review study provides a brief perspective on biogenic amine formation, health effects and contents of cheeses, which have an important place in milk and milk products. Milk and milk products are consumed by individuals from all segments of society, particularly more children. The formation of biogenic amines is a process that occurs during the processing and storage of a variety of foods, including fermented foods, fish products, and particularly protein-rich foods. Cheese is a significant component of the dairy product category and is a rich source of protein. Given the potential risks to human health and the possibility of nutritional quality losses, it is important to consider the presence of biogenic amines in food products. It is therefore essential to ascertain the potential risks associated with biogenic amines during the production and storage of cheese, and to implement measures to prevent or detoxify them. In light of the potential health implications of biogenic amines, there is a need for further scientific investigation into the prevention and detoxification of their formation in milk and dairy products.

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