# **Chapter 1 Animal Waste: An Environmentally Sustainable Management Approach**



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**Abstract** Some localities still use non-sustainable management techniques to deal with animal waste. Animal waste has the potential to be profitable if properly managed, but it can also pose severe risks to human health. The quality of the land, water and air may be threatened by improper animal waste handling. Animal manure can be adequately handled using a variety of approaches, ranging from simple, lowcost procedures to complex strategies. Microorganisms play a significant role in the multifaceted approach to sustainable animal waste management that benefits farmers, the general population and the environment. It is possible to efficiently revive contaminated areas by utilizing the unique characteristics of microorganisms. Microorganisms can be used as "miracle cures" for biodegradation and the remediation of contaminated sites. At different levels, rules and policies have been put in place in many countries to support sustainable animal manure treatment. Proper animal manure management not only reduces the amount of synthetic fertilizer required on fields, but it also contributes to lower net greenhouse gas emissions from livestock waste and has an impact on climate change. This chapter delves into the properties of various forms of animal waste and shows how microorganisms can be employed effectively for waste management and sustainability.

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#### **Graphical Abstract**



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### **1.1 Introduction**

Animal waste is defined as waste generated from livestock and meat production. When we think of animal waste, we usually think of the excreta of living animals. However, waste may also include wood crisps, hay, straw or other organic material, depending on the production process. The number of animal farms is growing yearly due to the increasing demand from the growing human population. In Europe, America, Australia, Africa and Asia, hectares of land are used to raise numerous herds of cattle, poultry, sheep and pigs for meat, milk, eggs and hides. Even though technological advances are mainly overtaking it, the ever-expanding agricultural industry continues to be an essential part of the global economy. Animal waste is generated in large quantities around the world every year, and if not properly collected, stored and treated, it can pollute soil, water and air. We can not only clean our environment but also save money on fertilizers if we adequately manage these animal wastes. A proper plan should be made to find a long-term solution to animal waste management (Malomo et al. [2018;](#page-29-0) Martinez et al. [2009a,](#page-29-1) [b](#page-29-2); Girotto and Cossu [2017;](#page-28-0) Arshad [2017\)](#page-26-0).

Animal waste has serious adverse effects on human health and the environment, and it also raises greenhouse gas emissions and lowers water and air quality. The spread of pathogens from livestock waste into water supplies can occur through direct leakage of waste in buildings or warehouses into sewage systems or indirectly through the spread of waste onto land if not adequately treated (Penakalapati et al. [2017\)](#page-31-0).

In addition, infections can enter the water phase from faeces deposited when animals graze on grasslands or dead animals. The pathway from soil to the water stream varies depending on soil type and conditions. Bacteria, protozoa and viruses are undoubtedly present in both aerosols and wastes, but how long they remain viable depends primarily on environmental conditions. Also, many livestock production practices often use antibiotics, which can enter the environment through waste and contribute to developing antibiotic-resistant microorganisms. Improper management of such waste can affect animal health, impacting disease transmission between animal production facilities and from animals to humans. The structure of the microbial population and the microbes participating in the degradation are both affected by antibiotic residues (Epps and Blaney [2016](#page-27-0); Tasho and Cho [2016\)](#page-32-0).

Composting is often an environmentally sound method of converting all animal waste into high-quality organic fertilizers for agriculture. However, the specific chemical composition of animal waste and its effects on the physicochemical and microbiological properties of compost are poorly understood. However, it is generally accepted that the type of animal waste affects microbial activity, metabolism and abundance, all of which depend on the physicochemical properties of the waste. The activity of a vast range of microorganisms that play a key role in the breakdown of organic material is required for microbial waste degradation. Bacteria and fungus are the most active and abundant microorganisms in waste degradation. Bacteria play key roles in the majority of the heat generated in compost and its breakdown, while fungi have the ability to decompose complicated polymers. While microbial populations evolving overtime during the various stages of composting has been thoroughly studied, there is little understanding of how the composition of the initial raw materials metataxonomy affects waste decomposition (Wan et al. [2021](#page-32-1); Fernandez-Bayo et al. [2020](#page-27-1); Akari and Uchida [2021\)](#page-25-0).

The metataxonomic composition of the waste at the initial time is vital because it influences the mesophilic microbiota proliferation, which is responsible for the quick rise in decomposition temperature and the establishment of a favourable environment for successive or secondary microbes throughout the decomposition process (Akari and Uchida [2021](#page-25-0); Sun et al. [2020\)](#page-32-2). Temperature, moisture content and *C*/*N* ratio are among the physicochemical properties that affect microbial degradation of animal waste. However, depending on the type of raw material in animal waste, it is still difficult to determine how these different properties affect the diversity, composition and structure of microbial communities (Sun et al. [2020](#page-32-2)).

In this chapter, we have discussed (Fig.  $1.1$ ) the factors affecting the decomposition of animal waste, the characteristics of different types of animal waste, microbial composition, microbial succession and how these microorganisms can be successfully used for waste management and sustainability.



<span id="page-3-0"></span>**Fig. 1.1** Some environmental problems linked to improper management of animal manure

### **1.2 Animal Waste**

#### *1.2.1 What Are Animal Wastes?*

Animal wastes are wastes generated during the production, processing, transportation and marketing of animals. They are used as a source for biomass-based conversion processes, especially in the production of biofertilizers and bioenergy. Feed waste or residues, effluents, wastes from hatcheries, slaughterhouses and manure are some possible sources of wastes generated during animal production. The most common sources of waste include effluents from dairy barns, which consist of urine, wash water, manure, feed residues and milk residues; poultry litter, which is a mixture of spilled feed, water, manure, litter material and feathers, and dairy manure, cleaning products and other wastes from animal finishing (Girotto and Cossu [2017;](#page-28-0) Girotto and Cossu [2017](#page-28-0)).

### *1.2.2 Characteristics and Composition of Animal Waste*

Numerous factors, including the environment, the age or growth stages of the animals, the type of animal, the digestibility of the ration or feed, productivity, the content of fibre and protein, waste collection and handling methods and the amount of water in the waste, affect the production and characteristics of the billions of metric tons of waste that are produced annually by the animal production industry. The wastes are categorized as solids, slurry (liquid) and wastewater (effluent), depending on the type of stock and their physical form (Table [1.1](#page-4-0)) (Martín-Marroquín and Hidalgo [2014](#page-29-3)). Solid waste (20–25% solids), which may include livestock manure, animal carcasses or the remains of the slaughter process in abattoirs, is primarily collected by dry mucking out the waste and stacking and picking it up with a forklift, and drying or composting it. Most liquid or slurry waste comes from the animals' urine, excreta or wastewater, as well as from residues generated by washing the stalls, cages and the

Waste form	Examples	Composition
Solid	Dung	Organic matter $(20\%)$ , moisture $(77\%)$ , nitrogen $(0.32\%)$ , phosphorous $(0.14\%)$ , calcium $(0.4\%)$ , potassium $(0.3\%)$
	Wasted feeding material	It includes food that is discarded or lost or uneaten
	Soiled bedding material	It includes wood shavings, straw, saw dust, paper-based bedding materials, etc.
Liquid	Urine	3–40 ml/kg bwt/Day
	Washed water	25–70 L/Animal/Day

<span id="page-4-0"></span>**Table 1.1** Forms and composition of animal waste

animals themselves with water. Converting the liquid waste to solid waste requires draining the liquids either by wet-mucking or dry-mucking, followed by drying or bedding. Stable waste treatment characteristics vary depending on the solids present. Wastes with a solids content of  $4-10\%$  can usually be disposed of as a liquid, although special pumping may be required. Wastes with a solids content of 0–4% are treated as a liquid with an irrigation or flushing consistency (Martín-Marroquín and Hidalgo [2014;](#page-29-3) Eliot [2015\)](#page-27-2).

In addition to what has already been said, animal species, feeding management, production capacity, nutrient intake, digestion, absorption, feed wastage (especially in pigs and poultry), disposal systems, nutrient content, other additives and environmental factors all influence the composition of animal waste. The amount and type of structural carbohydrates, proteins, nitrogen and other indigestible materials (silica) in the rations of animals whose wastes are collected have a major influence. Some wastes contain about 70% total solids, of which 95% are volatile solids, and in wastes containing slightly more than 2% organic nitrogen, the crude protein value is nearly 13%. The amino acids contained in this material account for slightly less than 40% of the crude protein value, the remainder being accounted for by the other nitrogenous non-protein compounds. Some articles have convincingly discussed the composition of animal waste on the basis of animal species (Patton and Turner [2008](#page-31-1); Müller [1980](#page-30-0); Nimmi n.d.).

#### **1.3 Present-Day Environmental Problems**

Livestock farming constitutes one of the major drivers of environmental pollution in recent times. The discharge of animal wastes (manures), agrochemicals, toxic and odorous gases and dissemination of different populations of microorganisms in the form of aerosols are linked to the degradation of the quality of soils, air as well as surface and ground waters in many locations around the world. Interests created as a result of the contribution of anthropogenic activities to climate change have brought livestock farming into focus due to increase in the generation of several

greenhouse gases (GHG). GHG gases are known to be significantly connected to the steady decline in the global climatic and environmental conditions (Fig. [1.1](#page-3-0)). Presently, government guidelines are in force in many countries aimed at regulating livestock operations in order to be able to control the rate of emissions of environmental contaminants as a mitigation strategy. Equally, multiple streams of research are presently ongoing with efforts to characterize the emissions as well as identify their impacts on the health of man and animals in order to fully understand their chemistry and pathologies (Arshad [2017](#page-26-0); Arshad et al. [2022](#page-25-1)).

#### *1.3.1 Soil Pollution*

Manures were traditionally disposed of on agricultural fields without recourse to proper management plan pertaining to the amounts admissible in a space. This practice led to over-application in many areas leading to overfertilization of soils, run-off of toxic constituents, leaching of contaminants and accumulation of heavy metals and macronutrients, principally phosphorus (P) and nitrogen (N). Heavy metals [e.g. zinc  $(Zn)$  and copper  $(Cu)$ ] pose a significant health hazard to soil animals because they are passed through the food chain during grazing and also contribute directly to the causation of autosomal recessive diseases and to impaired metabolism and liver function (Giola et al. [2012;](#page-27-3) Maillard and Angers [2013](#page-29-4)). Endocrine disrupting compounds (EDC), e.g. steroids are another group of compounds found in animal wastes as residues. They originate from drugs administered animal feeds and have the tendency to trigger critical hormonal responses by mimicking normal androgenic and estrogenic signalling in man and animals. This condition could result in health and birth defects in the animals and their off springs (Combalbert et al. [2012\)](#page-26-1). One major apprehension in the application of this class of drugs is that they retain the capacity to display activity even at very minute (i.e. parts-per-trillion or nanogram-per-litre) concentrations.

#### *1.3.2 Water Pollution*

Water pollution caused by animal waste results from the leaching of minerals and runoff of nutrients from soils due to overfertilization with manure. It may also result from the direct discharge of animal wastewater into municipal waters. Stormwater run-off is the gateway through which leached nutrients, especially nitrogen and phosphorus, move from manure-saturated lands to surface waters, where they cause pollution. In the aquatic matrix, free ammonia  $(NH<sub>3</sub>)$  has been reported to be capable of causing higher levels of toxicity to much marine life than the salt compound ammonium (NH4); for example, as little as 5 mg/L of ammonia is known to cause detectable levels of lethality in salmon (Martinez et al. [2009a](#page-29-1), [b](#page-29-2)).

Surface waters are highly susceptible to contamination from manure and are potential sources of infection because they are contaminated with microorganisms found in livestock effluent. Microorganisms make their way through a combination of sorption and suspension (Edwards and Daniel [1992](#page-27-4)). There are three main pathways by which potential contaminants in manure enter surface waters from farmed areas. They can be bound or adsorbed to soil particles, transported in suspensions/solutions or carried in particulate form (Martín-Marroquín and Hidalgo [2014](#page-29-3)). Ammonia and phosphorus are bound to soil particles and can be transported by erosion, while carbon (C), phosphorus (P) and nitrogen (N) are transferred in particulate form. Pollutants that are transported in solutions include soluble forms of carbon, phosphorus, ammonium, nitrates and uric acid (Martín-Marroquín and Hidalgo [2014](#page-29-3)). Domestic use of such water without proper treatment could, therefore, inevitably lead to severe morbidity and mortality (Gilchrist et al. [2007\)](#page-27-5). There is, thus, a need to develop better management practices for manure application to protect streams and rivers from the reckless and unwarranted dumping of animal wastewater. The cooperation of all stakeholders, i.e. farmers, community leaders, opinion leaders, and policymakers, is critical in enforcing the appropriate legislation and ensuring compliance.

## *1.3.3 Air Pollution*

#### **Emission of ammonia**

Livestock farming contributes significantly to the generation and emission of odorous pollutants such as ammonia, methane and carbon dioxide. A significant proportion of gases that emerge from livestock farms are ammonia. It is a secondary particulate precursor that reacts with other compounds in the atmosphere, such as nitric and sulphate acids, to form ammonium salts, a deadly form of particulate matter. Hence, livestock farming is one most prominent contributors to ammonia outflows in the ecosystem. The gases are produced by microbial fermentation in stored mixtures of animal faeces and urine (Vanotti et al. [2009\)](#page-32-3). Under this condition, urea in urine is broken down by urease to liberate ammonia. However, the rate of emission varies from one facility to another because the conversion of liquid ammonium  $(NH<sub>4</sub>)$  to the gaseous phase (i.e. ammonia  $(NH<sub>3</sub>)$  is governed by a set of factors which include temperature, pH and wind speed (Martín-Marroquín and Hidalgo [2014\)](#page-29-3). Presently, manure on land is considered a nuisance, particularly in densely populated areas, due to the discomfort linked to the malodorous discharges from fertilized lawns and animal shelters. Other components in airborne emissions from manure and animal farm settings include hydrogen sulphide, volatile organic compounds, endotoxins and particulates. Many studies indicate that several pulmonary conditions are linked to the prolonged exposure of these compounds to individuals, particularly farm workers. They include bronchitis, mucus membrane irritation and asthma (May et al. [2012](#page-30-1)). In one report, endotoxins and organic aerosols were found to be behind the onset of

respiratory disorders among swine workers and neighbourhood residents (Leytem et al. [2011](#page-29-5)).

#### **Methane and nitrous oxide emissions and climate change**

Methane and carbon dioxide are greenhouse gases associated with the phenomenon of global warming. The increase in the concentration of these gases in the atmosphere is the cause of global warming. These gases inevitably cause global temperatures to rise, leading to economic and environmental disasters in some countries. Both gases originate from the metabolism of anaerobic microorganisms, whose activities dominate the digestive processes in ruminant diets. In addition, soils previously treated with livestock manure release nitrous oxide  $(N_2O)$ , another greenhouse gas. Methane and nitrous oxide are essential for regulating ozone concentrations in the atmosphere.

#### **Dusts, volatile organic compounds and particles**

Particulate emissions can occur through the aerosol-assisted movement of livestock manure during ammonia emission (Cambra-López et al. [2010\)](#page-26-2). They may also be propagated by the shaking up of litter or other materials during the movement of animals or equipment or through the exhaust system of the ventilation set installed in the animal shelters. Volatile organic compounds (VOC) are released mainly from fermented feeds and fresh faecal wastes of livestock (Martín-Marroquín and Hidalgo [2014\)](#page-29-3). VOCs contribute to the photochemical activities that lead to the production of ozone. In the presence of sunlight, VOCs drive the oxidation of NO to  $NO<sub>2</sub>$ , eventually culminating with the synthesis of ozone  $(O_3)$  (Ling and Guo [2014](#page-29-6)). Livestock rearing engenders the release of volatile odoriferous compounds due to the microbial modification of materials in their feed and excreta. However, the odorants released are not necessarily correlated to the presence or amounts of pathogens or indicator organisms but mainly promote the sensory recognition of the presence of the volatile organic compounds in any material or environment. VOCs can accumulate in confined spaces to pose health risks to animals and farm staff, particularly in settings where the stocking density of the livestock is relatively high (Schiffman et al. [2000](#page-31-2)).

#### **Source of disease causing agents**

Many types of pathogenic organisms including bacteria, viruses and parasites are present in livestock wastes and could potentially constitute hygiene risks during collection, packing and subsequent dispersal on agricultural fields. Although biological agents such as obligate parasites do not pose significant dangers outside of their hosts, bacteria and viruses are capable of surviving for extended periods in the fields. Some confirmed cases indicate that while the risk of zoonotic infections is low, it is the transmission of infection to other livestock that accounts by far the most significant numbers of confirmed cases of disease outbreaks (Burton [2009\)](#page-26-3) often spreading to nearby farms.

of infections because they harbour pathogens related to the application of livestock manures in soils during farming (Bezanson et al. [2014;](#page-26-4) Blaiotta et al. [2016](#page-26-5)). Common enteric pathogens such as campylobacter and salmonella are often implicated, although reported cases of food poisoning by the pathogens are comparatively low. However, efforts to protect the retailers and the public from a potential full outbreak are driving the enforcement of certain regulations on the use of animal wastes as manure in several countries. The health of farm workers is equally exposed due to frequent direct contact with the wastes as well as the dusts and gaseous emissions spewing out from the confined spaces of the animal enclosures (Burton [2009](#page-26-3)). Equally, the threat of transmission of zoonotic diseases is potent because run-offs usually carry materials from manure-dosed farms into surface waters which serve the domestic needs of many people in the locality. Zoonoses may also be transmitted when manure comes into contact with food or contaminate water used for irrigation or washing crops like leafy vegetables which are consumed raw (Cliver [2009\)](#page-26-6).

### **1.4 Brief Background of Animal Waste Treatment Systems**

Animal waste treatment system is a process used to reduce biomass, manage pathogens, concentrate nutrients and generate by-products like fertilizer or energy (Sobsey et al., [2006](#page-31-3)). Before disposal, a robust waste gathering and storing system is unavoidable. In most European and North American countries, these processes have simplified by using mixing and separation methods, which reduces clogging problems and ease carriage. These approaches can help to reduce environmental effect in some circumstances by resulting in a more consistent application of nutrients (Vanotti et al. [2009](#page-32-3); Arshad et al. [2021\)](#page-25-2).

Unlike direct application to land, animal waste treatment currently uses technology to alter its chemical or physical properties. This can be achieved by biological, chemical, physical or mechanical methods or their combinations. The major options of animal waste treatment include solid–liquid separation, nutrient partitioning, composting and digestion (missing citation). While sieving works well for cattle slurry containing 30–40% solids, centrifugation works better for poultry and pig slurry containing finer particles. Gravity sedimentation in large, shallow bins results in sludge with a dry solid concentration of 5–10%. With the right C/N ratio, moisture content, aeration and time, composting can produce an environmentally stable byproducts using oxygen-consuming bacteria and fungi (missing citation). Digestion methods (aerobic/anaerobic) can be used for the removal of nitrogen and organic load from animal waste (Vanotti et al. [2009](#page-32-3)). In aerobic treatment, for example, aerobic microorganisms oxidize bioavailable oxygen-consuming compounds such as nitrogenous and organic compounds, which is a means of reducing odour and ammonia emissions. Nitrogen removal is accomplished through the processes of nitrification and denitrification. Microbial activity is expected to break down organic material and reduce the biomass load, producing carbon dioxide and water. However, this method has rarely been used for the treatment of slurry or manure, mainly because of the costs associated with the operation of the machine required to supply sufficient oxygen to the aerobic microorganisms. Under anaerobic conditions, acetic acid is formed, which is then utilized by methanogens to produce energy, mainly biogas  $(CH<sub>4</sub>)$ , the yield of which varies according to animal waste. Digestates from animal waste can be a valuable fertilizer, but this may require additional technology and cost due to its high moisture content. Anaerobic digestion of animal wastes is mostly popular in Europe because it benefits biogas production, which is used to generate heat and electricity (Arshad et al. [2021](#page-25-2)).

Concentration, separation and exportation are other strategies for removing ineradicable components of animal manure, such as heavy metals and phosphorus. If there are defined, accepted levels for these constituents, this process may be the efficient method to remove surplus nutrients, including nitrogenous and organic compounds. These methods yield dry solid products that can be utilized, blended with other products, or composted to create valuable natural ingredients that can occasionally be sold (Vanotti et al. [2009\)](#page-32-3). Precipitation of some animal waste components can be done with some chemicals such as flocculants or lime, but their use alone is not often sufficient or sustainable (Vanotti et al. [2009\)](#page-32-3).

### **1.5 Microorganisms in Animal Waste Recycle**

#### *1.5.1 Microbes Found in Animal Waste*

Animal manure contains a variety of bacteria that change organic materials through various chemical processes in addition to disease microbes. The physical factors surrounding microorganisms, particularly the humidity, temperature and oxygen content, impact the chemical reactions. The metabolic activity of bacteria alters these conditions (Wan et al. [2021](#page-32-1)). The most prevalent and active microbes participating in the process are bacteria and fungi. Bacteria carry out the majority of decomposition and heat production, but fungi are also capable of degrading complex polymers (Akdeniz [2019](#page-25-3)). For instance, Proteobacteria are more prevalent in cattle manure, but Firmicutes frequently predominate in pig manure. Basidiomycota and Ascomycota are the main phyla of fungus found in chicken and cow manures. Such variations may result from the decomposition process. Still, they may also result from initial variations in the waste microbiota composition, which is influenced by the nutrition and microbiota of the animal's gut (Teira-Esmatges and Flotats [2003](#page-32-4)).

Animal wastes frequently carry high levels of disease-causing microbes from humans, spilled feed, bedding material, fur, process-generated wastewater, undigested feed leftovers, faeces, as well as urine. These microorganisms are also involved in the degradation processes. The amounts and kinds of disease-causing agents seen in animal wastes differ depending on the animal species, state of health, animals'

age, physical/chemical features of the dung generated and the manure's storage installations (Burkholder et al. [2007](#page-26-7); Hutchison et al. [2005\)](#page-28-1).

#### *1.5.2 Nitrogen Cycle and Microorganisms*

Microbes (bacteria and fungi) play crucial functions in the nitrogen cycle in the natural environment. Nitrogen is the nutrient most susceptible to changes that increase the likelihood of wasteful losses. Mineralization to ammonium, immobilization, oxidation (nitrification) and denitrification are among the changes. It has commonly been recorded that total nitrogen is typically conserved amid the process of anaerobic digestion (Schievano et al. [2011](#page-31-4)). On the other hand, researchers compared biogas digesters' nutritional inputs plus outputs and discovered gross nitrogen depletion of 18% (Möller [2015\)](#page-30-2). Net nitrogen losses of 5–10% were also recorded by Schievano and co researchers (Schievano et al. [2011\)](#page-31-4). The biogas stream's nitrogen content of the ammonium ion flux, which comprises methane, carbon (iv) oxide, water vapour, minimum amounts of ammonium ion, hydrogen sulphide, as well as other elements, accounted for only about 10% of the depletions; other factors like incomplete sedimentation of organic or inorganic matter, formation of struvite, precipitation, as well as final reservation in the digesters, are ascribed to the remainder (Massé et al. [2007](#page-30-3); Möller and Müller [2012\)](#page-30-4). Moreover, following anaerobic digestion, animal manures slurry that has been digested rarely forms a "natural" top crust by suspended fibre particles in manure depots, as it does in undigested slurry reserves. Ammonia losses from the slurry that has been digested were comparable to those from the slurry that hasn't been treated over the winter, according to Clemens and other scholars (Clemens and Huschka [2001](#page-26-8)).

Nitrification has been observed in bacteria, archaea and fungi (autotrophs) (Laughlin et al. [2008;](#page-29-7) Leininger et al. [2006\)](#page-29-8). Heterotrophic nitrification, on the other hand, occurs when  $NH<sub>3</sub>$  is directly oxidized or organic materials decompose to nitrate by heterotrophic bacteria. This procedure is known to occur in a variety of bacteria, and some, like *Paracoccus denitrificans* and *Pseudomonas putida*, have amoA sequences that differ from autotrophic nitrifiers (Maeda et al. [2011\)](#page-29-9). Normally, heterotrophic denitrifiers convert  $NO_2^-$  or  $NO_3^-$  produced by nitrifiers into nitrous oxide, dinitrogen, or just nitrogen gas before releasing it into the environment. Despite the fact that nitrous oxide depletion is thermodynamically advantageous and nitrous oxide is a good electron acceptor, certain denitrifiers create nitrous oxide as an end product. This could be due to the fact that nitrous oxide is nontoxic to some microbes but may be poisonous to some bacterial cells (Schneider and Einsle [2016](#page-31-5)).

### *1.5.3 Systems of the Manure Recycle and Treatment*

Indiscriminate disposal of manure may result in pollution of surface and groundwater. In the light of the above, various manure recycling and treatment systems, including activated sludge systems, lagoons, compaction, composting and other methods, are required for the recycling and treatment of animal manure before its use in the soil (Malomo et al. [2018\)](#page-29-0).

An activated sludge system is one of the most predominant approaches to waste treatment. In the activated sludge, microbes absorb and assimilate nitrogen, phosphorus compounds as well as other nutrients in the wastewater. They as well nitrify as well as denitrify nitrogen compounds to nitrogen gas. The  $H_2O$  can be recycled for agricultural or domestic usage, whereas sludge deposited in the system which is a biomass of microbial cells is recycled as the fertilizer (Waki et al. [2018](#page-32-5)). Physical techniques such as pelletizing and baling can help to improve the storage as well as management of heap solid manures. These approaches are aimed at delivering manure's nutrients in a more cost-effective and dust-free manner, and dung conditioning before bio-energy transformation. Compacting a loose material into pellets like poultry litter enhances its consistency dramatically (McMullen et al. [2005](#page-30-5)).

The widely accepted standard practice for recycling waste is composting. It eliminates raw waste from areas where it could contaminate streams and groundwater. Pathogens are eliminated, and a safe soil amendment is produced by effective composting (Teira-Esmatges and Flotats [2003\)](#page-32-4). When a heap of garbage is created, composting begins. Microbes begin to decompose by consuming oxygen as well as transforming it to  $CO_2$ , water vapours, plus heat (Sorathiya et al. [2014\)](#page-32-6). It is possible to have an open or closed composting system, and compost can be piled or stacked in rows or deposited in a closed reactor or container (Haug [2018\)](#page-28-2). Because of its technical complexity, the open system is seldom employed in low-income nations. The waste should ideally be piled and left for the same period of time in a four-pole fence that is surrounded by boards or chicken wire. This creates a rich compost that can be applied as a fertilizer for fields as well as gardens (Akdeniz [2019](#page-25-3)). Sanitation, odour elimination and safe storage are among the benefits of composting animal dungs over manure that has not been processed applied directly to the soil. On the other hand, the cost of installation and management, as well as the need for vast storage and operation spaces, is potential downsides of composting (Narula et al. [2011\)](#page-30-6).

### *1.5.4 Microbial Flora of Animal Faeces After Excretion*

The microbial flora of fresh faeces from animals has been extensively studied. For example, the most common faecal bacteria in pigs include Bacteroidaceae, Peptococcaceae, Eubacteria, Lactobacilli, Bifidobacteria, Spirillaceae and Enterobacteriaceae (Cox et al. [2005;](#page-27-6) Dowd et al. [2008;](#page-27-7) Lim et al. [2018](#page-29-10)). In the

rectum of chickens, Bacteroidaceae, Lactobacilli, Enterobacteriaceae and Streptococci predominate (Nodar et al. [1990\)](#page-30-7). Similarly, Bacteroidaceae, Spirillaceae, Enterobacteriaceae and Streptococci are the most common microbial groupings found in bovine faeces (Dowd et al. [2008\)](#page-27-7). Despite the fact that the microbial flora in faeces has been extensively studied, little research has been done on how the microbial flora alters after expulsion. Animal excretion microbial flora may affect the performance of microbiological treatment systems for animal wastes (Hagey et al. [2019](#page-28-3)).

# *1.5.5 Microorganisms and Their Function in the Animal Waste Lagoon*

In animal waste lagoon that operate normally, acid formers as well as methane formers, are two noticeable types of bacteria. Biodegradable organic matter is transformed to volatile acids by acid formers while methane and carbon dioxide are produced by converting these volatile acids by methane formers. Moreover, a level of equilibrium of biological responses by the two types of bacteria is attained under optimum conditions. This balance will be disturbed, and overweening odour and sludge accumulation are produced due to environmental variations (e.g. temperature fluctuations), indecorous design and lousy management. Consequently, anaerobic digestion is employed to stabilize manure, diminish pathogens plus emanations of odour and as well generate energy via production of biogas. The primary mechanism for natural animal waste treatment is anaerobic digestion, in open anaerobic digesters as well as anaerobic lagoons (MacSAFLEY et al. [1992;](#page-29-11) Nakai [2001](#page-30-8)). Anaerobic lagoons are typically designed for a storage period of twenty to one hundred and fifty days and for the treatment of wastewater. They're normally eight to fifteen feet deep and function similarly to septic tanks. The effluent from an anaerobic lagoon will need to be treated further (Leffert et al. [2008](#page-29-12)).

The lagoon system uses a combination of physical, biological as well as chemical approaches to treat waste. Although a few approaches employ aeration devices to provide  $O_2$  to the wastewater, the majority of the treatment is done organically. Aeration enhances treatment effectiveness and reduces the amount of ground area required. Soil type, size of available land, as well as weather have an impact on the layout of the system. Waste from a lagoon may require additional treatment or "polishing" to remove pathogens or nutrients before it is released into the environment (Deviney et al. [2020\)](#page-27-8).

### *1.5.6 Microorganisms in the Composting Process*

An aerobic method of converting organic waste into a humus-like substance through microbial activity is termed composting. Composting is as well an approach to

produce soil conditioner or fertilizer. In a normal composting process, bacteria as well as fungi exist and function (Jusoh et al., [2013](#page-28-4)). Researches beforehand have unveiled that mesophilic organic acid-generating bacteria like *Lactobacillus* species as well as *Acetobacter* species are the considerable groups of bacteria in the baseline of the composting process (Pan et al.  $2011$ ). Thereafter, in the thermophilic stage, bacterial species (e.g. Bacillus species and Actinobacteria) predominate. However, it has been suggested that the most effective composting process is achieved by mixed communities of bacteria and fungi (Malinska and Zabochnicka-Świtek [2013;](#page-29-13) Zhang et al. [2010](#page-32-7)).

Furthermore, composting is a three-phase process that involves microbes (e.g. bacteria and fungi), as well as mesophiles such as *Streptomyces rectus* and thermophiles such as *Actinobifida chromogena* (*Thermomonospora fusca*), etc., ultimately, transforming organic waste into humus. The substrate is depleted amid the first phase because of sugar as well as protein degradation by the mesophilic microbes' activity, as well as a rise in carbon dioxide levels in tandem with a rise in temperature (Novinscak et al. [2008](#page-30-9); Zeng et al. [2011\)](#page-32-8). In the second phase, the temperature of the compost heap increases from 45 to 70 °C, and thermophilic microorganisms replace mesophilic microbes. Several harmful individuals are minimized at this moment. The third process begins with the lowering of the temperature of the compost heap (Schloss et al. [2003\)](#page-31-7).

# **1.6 The Microbial Community Profiles of Different Animal Waste**

Animal wastes are home to a diverse spectrum of microbial communities, including both beneficial and pathogenic microorganisms (Mawdsley et al., [1995](#page-30-10)). Despite its extensive usage in agriculture, there is a variation in microbial diversity as a result of various treatment processes, which also vary based on the waste source (Table [1.2](#page-14-0)). For example, at various handling stages, manure from a dairy farm in the California Central Valley was sampled for 16S rRNA study of composition and diversity of microbial communities. The study revealed that there are variations in microbial population between the solid and liquid waste. For example, the bacterial genus *Thermos* was only present in the solid samples, while *Sulfuriomonas* was only observed in liquid samples. The genus *Clostridium* was abundant in both liquid and solid samples (Pandey et al. [2018\)](#page-31-8).

#### *1.6.1 Cow Waste*

Cow waste, particularly dung, contains a diverse group of bacteria including *Kluyvera sp., Bacillus sp., Klebsiella pneumoniae, Lactobacillus sp., Corynebacterium sp.,*

Waste source	Type of microbes	Microorganisms	References
Cow	Bacteria	Bacillus sp., Lactobacillus sp., Corynebacterium sp., Bacteroides, Paludibacter, Alistipes, Anaerovorax, Ruminococcus, Turicibacter, Lysinibacillus, Stenotrophomonas	Randhawa and Kullar (2011), Girija et al. (2013), Mao et al. (2012)
	Fungi	Candida, Saccharomyces cerevisiae, Aspergillus, Thermomyces, Myriococcum, Fusarium oxysporum, Alternaria, Ascobolus sp.	Randhawa and Kullar (2011), Jiang et al. (2020), Thilagam et al. $(2015)$ , Tan and Cao (2013)
	Archaea	Methanobrevibacter, Methanocorpusculum, Methanosphaera	Cendron et al. (2020)
Poultry	Bacteria	Bacillus, Lactobacillaceae, Brachybacterium, Azomonas agilis, Streptococcus sp., Proteus vulgaris, Aeromonas hydrophila, Proteus vulgaris, Echerichia coli, Sarcina maxima, Lactobacillus sp., Staphylococcus aureus	Lovanh et al. $(2007)$
	Fungi	Candida sp., Mucor sp., Cladosporium spp., Aspergillus sp., Penicillium sp., Saccharomycopsis, Sporendonema sp., Kloeckera sp., Zygosaccharomyces sp.	Adegunloye and Adejumo (2014), Emmanuel-Akerele and Adamolekun (2021)
Swine	Bacteria	Clostridium, Bacillus, Lactobacillus, Novibacillus, Planifilum, Corynebacterium, Virgibacillus, Terrisporobacter petrolearius	Lim et al. (2018), Chen et al. (2017), Kumar et al. (2020)
	Fungi	Aspergillus, Melanocarpus, Debaryomyces hansenii, Geotrichum sp., Acremonium strictum, Fusarium, Geotrichum sp, Mucorales, Wallemia	Wan et al. (2021), Kumar et al. (2020), Kristiansen et al. $(2012)$ , Kim $(2009)$
	Archaea	Methanobrevibacter, Methanosarcina, Methanobacterium, Methanothermobacter, Methanocorpusculum, Methanofollis	Tuan et al. (2014), Qin et al. (2013)
Sheep	Bacteria	Lysinibacillus, Clostridium, Enterococcus, Escherichia, Streptococcus, Bifidobacterium, Anaerocolumn, Tissierella, Anaerocolumna, <b>Muricomes</b>	Shabana et al. (2020)
	Fungi	Ascobolus, Preussia, Mortierella	Tan and Cao $(2013)$
Goat	Bacteria	Escherichia, Anaerotignum, Ruminococcus, Prevotella, Butyrivibrio	Shabana et al. (2020)
	Fungi	Neocallimastix, Caecomyces, Piromyces	Peng et al. (2021)
	Archaea	Methanobrevibacter sp., Methanosphaera stadtmanae	Peng et al., 2021

<span id="page-14-0"></span>**Table 1.2** Some dominant microorganisms found in different animal wastes

*Pseudomonas sp., Citrobacter koseri, Providencia stuartii, Staphylococcus sp., Klebsiella oxytoca, Morgarella morganii, Enterobacter aerogenes, Providencia alcaligenes, Pasteurella sp.,* and *Escherichia coli* (Sawant et al. [2007](#page-31-13); Randhawa and Kullar [2011;](#page-31-9) Gupta and Rana [2016\)](#page-28-9). About 60 bacterial species are found in dung, generally dominated by *Bacillus sp*., *Lactobacillus sp*., and *Corynebacterium sp*. A culture independent 16S rDNA techniques identified dominant genera in cow dung as *Bacteroides, Paludibacter, Alistipes* (Bacteroidetes), *Bacillus, Clostridium, Anaerovorax, Ruminococcus* (Firmicutes), *Pseudomonas, Acinetobacter, Rheinheimera, Rhodobacter, Stenotrophomonas* (alpha- and beta-Proteobacteria), and *Akkermansia* (Verrucomicrobia). About 87.5% of Firmicutes and 83.3% of Bacteroidetes constituted the unculturable bacteria (Girija et al. [2013](#page-27-9)). Mao et al. [\(2012](#page-29-14)) reported the abundance of Firmicutes, Proteobacteria, Actinobacteria, Bacteroidetes and Tenericutes in cow faecal bacterial community. The most dominant groups are T*uricibacter, Lysinibacillus, Stenotrophomonas, Solibacillus silvestris* and the family Lachnospiraceae.

It also contains other microorganisms, such as yeast (*Candida* and *Saccharomyces cerevisiae*), about 100 species of protozoa (Randhawa and Kullar [2011](#page-31-9)), fungi (*Trichoderma, Actinomycetes* and *Aspergillus*) (Munshi et al. [2019\)](#page-30-11) and archaea (Cendron et al. [2020\)](#page-26-9). Jiang et al. ([2020\)](#page-28-5) identified *Aspergillus*, *Thermomyces, Myriococcum*, *Mycothermus, Cladosporium, Scedosporium* and unclassified Microascaceae as fungal communities in cow manure using high-throughput sequencing. Of all the 25 fungal species belonging to 20 genera recorded in dung samples from the Lawspet area of Puducherry Union Territory of India, *Aspergillus fumigatus* was the dominant species by *Fusarium oxysporum*  and *Alternaria alternata*. Other species include Aspergillus *clavatus, Penicillum sp., Cladosporium cladosporioides, Scopulariopsis sp., Arthrinium sp., Acremonium sp., Arthrobotrys sp., Cephaliophora sp., Myrothecium sp., Trichoderma sp., Fusarium oxysporum, Drechslera sp., Pithomyces sp., Nigrospora oryzae, Paecilomyces sp., Phialophora sp.* and *Oidiodendron sp* (Thilagam et al. [2015](#page-32-9)). Tan and Cao ([2013\)](#page-32-10) also reported that the fungal diversity in cow faeces is dominated by the phylum Ascomycota (*Ascobolus* sp. and *Candida*) followed by Basidiomycota, and Chytridiomycota.

Various groups of archaea and methanogens belonging to the Methanomicrobiaceae have been detected in cattle manure (Kim et al. [2014\)](#page-28-10). Cendron et al. ([2020\)](#page-26-9) reported archaeal phylum Euryarchaeota which includes five genera, *Methanobrevibacter, Methanocorpusculum, Methanosphaera*, unclassified Methanobacteriaceae and uncultured Methanomethylophilaceae.

### *1.6.2 Poultry Waste*

Poultry waste contains a wide range of intestinal microbiota, primarily Proteobacteria-derived species, which may contain pathogens that pose a health risk. A taxonomic analysis of the 16S rRNA sequences showed that it is

dominated by Firmicutes followed by Proteobacteria and Bacteroidetes (Zhang et al. [2018](#page-32-12)). The 16S rRNA sequencing identified *Bacillus, Lactobacillaceae, Brachybacterium sp., Arthrobacter sp., Corynebacterium sp*., *Enterococcaceae*, *Brevibacterium sp.*, *Staphylococcus, Corynebacteriaceae*, *Aerococcaceae* and *Actinomycetes* (Lu et al. [2003;](#page-29-16) Lovanh et al. [2007\)](#page-29-15). *Bacillus cereus, Azomonas agilis, Streptococcus sp., Proteus vulgaris, Escherichia coli, Staphylococcus aureus, Sarcina maxima, Thiocapsa lumicola, Xanthomonas fragariae* and *Enterococcus sp*. were isolated from turkey faeces. Other species found in duck samples included *Bacillus cereus, Aeromonas hydrophila, Proteus vulgaris, Echerichia coli, Sarcina maxima, Lactobacillus sp., Streptococcus sp., Streptobacillus moniliformis, Enterococcus sp.* and *Staphylococcus aureus*. Fungal species present in both samples were *Candida sp., Mucor sp., Cladosporium spp., Aspergillus fumigatus, Penicillium sp., Aspergillus flavus, Alternaria sp., Fusarium sp.* and *Varicosporium elodea* (Adegunloye and Adejumo [2014\)](#page-25-4). Characterization and identification of bacteria from poultry droppings showed the presence of *Pseudomonas picketti, Streptococcus pluranimalium, Micrococcus holobium, Cellobiococcus sciuri, Enterobacter agglomerans, Bacillus pumilus, Staphylococcus aureus, Staphylococcus alrettae, Salmonella enteritidis* and *Staphylococcus saprophyticus.* The identified fungal species were *Saccharomyces sp., Candida tropicalis, Aspergillus fumigatus, Aspergillus niger, Saccharomycopsis, Sporendonema sp., Kloeckera sp., Fusarium oxysporum, Candida sp., Zygosaccharomyces sp.* (Emmanuel-Akerele and Adamolekun [2021\)](#page-27-10). Nauanova et al. ([2020\)](#page-30-12) also reported cellulose-degrading bacteria from poultry manure, such as *Bacillus megaterium*, *Lentzea chajnantorensis*, *Burkholderia xenovorans*, *Enterobacter hormaechei* and *Sphingomonas trueperi*.

#### *1.6.3 Swine Waste*

Pig waste contains a diverse group of microorganisms that play an important role in the waste decomposition, including *Clostridium, Bacillus* and *Lactobacillus*. Firmicutes (*Clostridium*, *Lactobacillus, Streptococcus and Turicibacter*) and Actinobacteria (*Corynebacterium*) have been found to be the most abundant phyla in swine manure at different temperatures and storage times (Lim et al. [2018;](#page-29-10) Chen et al. [2017\)](#page-26-10). According to most studies (Wan et al. [2021;](#page-32-1) Kumar et al. [2020](#page-28-6)), Firmicutes are commonly the most abundant phylum in pig and chicken waste. The bacterial genera profile of pig manure showed the presence of *Bacillus, Novibacillus* and *Planifilum*. In the same samples, the fungal group was dominated by *Aspergillus* and *Melanocarpus*. In another pig manure, *Bacillus, Corynebacterium*, Virgibacillus, *Actinobacteria, Pseudomonas*, *Pediococcus and Lactobacillus* were the predominant genera (Chen et al. [2017](#page-26-10)). A compositional analysis of swine slurry at different times using 16S rRNA metagenomic sequencing approach identified *Clostridium saudience, Clostridium leptum*, *Terrisporobacter petrolearius*, *Butyrivibrio hungatei and Lactobacillus ultunensis* as the most significantly abundant bacteria (Kumar et al. [2020](#page-28-6)).

Similarly, a liquid swine manure studied using DGGE/PCR of 16S rDNA identified *Clostridium disporicum, Clostridium butyricum*, two *Rhodanobacter* sp., a *Pedobacter* sp., a spirochete and seven uncultured eubacteria (Leung and Topp [2001\)](#page-29-17). The microbial composition analysis of the pig particulate matter (faeces, hair, bedding particles, feedstuff, and animal skin) also showed that *Clostridium* was the most predominant followed by *Bacillus* and *Terrisporobacter. Other abundant species were Lactobacillus, Turicibacter, Prevotella, Curvibacter, Staphylococcus, Blautia, Weissella, Roseburia* and *Sediminibacterium* (Hong et al. [2021\)](#page-28-11).

The archaeal community commonly found in swine wastes are members of the genera Methanobrevibacter, *Methanosarcina*, M*ethanobacterium* and *Methanothermobacter* (Tuan et al. [2014](#page-32-11)). Qin et al. ([2013](#page-31-10)) reported the detection of *Methanocorpusculum, Methanofollis, Methanogenium, Methanoculleus, Methanocorpusculum labreanum* Z, *Methanosaeta concilii*, *Methanosarcina siciliae* and *Methanofollis ethanolicus* in swine manure.

Fungi are also part of the microbial communities in swine waste and a diverse species have been identified, including *Debaryomyces hansenii, Geotrichum sp., Acremonium strictum, Fusarium sporotrichioides, Fusarium sporotrichioides, Monographella nivalis, Cladosporium sphaerospermum, Acremonium alternatum, Pleurotus eryngii, Malassezia globosa, Myriangium durosai, Rhodotorula glutinis*  and *Malassezia restricta. Geotrichum sp. (Saccharomycetes)* was the most abundant species, followed by *Acremonium strictum, Monographella nivalis* and *Pleurotus eryngii* (Kim [2009](#page-28-8)). Kristiansen et al. [\(2012](#page-28-7)) also identified *Mucorales, Wallemia and Russulales* as the most abundant fungal.

## *1.6.4 Sheep Waste*

Firmicutes and Bacteroidetes have been found to be the most prevalent bacterial phyla in sheep faecal matter, accounting for 80% of the total population (Mamun et al. [2019](#page-29-18)). From a taxonomic standpoint, the sheep faecal bacteria appear to be comparable to that of other ruminants, with Firmicutes as the dominant phylum (Tanca et al. [2017\)](#page-32-13). Instead of Bacteroidetes, Shabana et al. ([2020\)](#page-31-11) found Proteobacteria to be the second most abundant core bacterial phylum in sheep 6 months after birth, with *Lysinibacillus* being the most abundant genus, followed by *Clostridium*, *Enterococcus, Escherichia, Streptococcus, Bifidobacterium, Anaerocolumn, Tissierella*, *Anaerocolumna* and *Muricomes.* In ITS, 28S and 18S study of fungal community composition of sheep faeces, Tan and Cao ([2013\)](#page-32-10) reported that Ascomycota, Basidiomycota and Chytridiomycota are the most abundant phyla. The most detected genera were *Ascobolus* (ITS, 28S and 18S), *Preussia* (ITS and 28S) and *Mortierella* (ITS and 18S).

# *1.6.5 Goat Waste*

The phylum Proteobacteria was discovered to be the most dominant community in goat faeces 6 months after birth, with *Escherichia* and *Anaerotignum* being highly prevalent. The goat faeces share the same core bacteria genera with sheep. At one year of age, goats had significantly higher abundance of the phylum Firmicutes than sheep, but sheep had higher abundance of the phylum Proteobacteria than goats. (Shabana et al. [2020\)](#page-31-11). A metagenomic analysis of goat faecal microbial communities revealed that about 33.3% of the constructed metagenome-assembled-genomes (MAGs) were Firmicutes and Bacteroidetes, with more than half belonging to the Ruminococcaceae and Rikenellaceae families. *Ruminococcus*, *Prevotella* and *Butyrivibrio* are among the most abundant genera. The archaeal MAGs recovered were dominated by the genus *Methanobrevibacter sp.* as well as the class *Thermoplasmata* and the species *Methanosphaera stadtmanae*. The fungal MAGs studied in this research are members of the subphylum Neocallimastigomycota, with the majority belonging to the genus *Neocallimastix*. Other MAGs recovered from only the first generation of enrichment cultures are from the *Caecomyces* and *Piromyces* genera (Peng et al. [2021\)](#page-31-12).

#### **1.7 Composting Process**

Composting simply enhances the process of decomposition by creating an ideal environment (nutrients, warm temperatures, moisture and sufficient oxygen) for bacteria, fungi and other decomposers (such as worms, nematodes, and sow bugs) (Bernal et al. [2009](#page-26-11)). Mesophilic bacteria (*Bacillus sp., Streptococcus, Pseudomonas, Streptosporangium sp, Proteus, Seratia, Streptomyces, Actinomyces, Methylomonas sp*  and some faecal coliforms) and fungi (*Rhizopus* and *Trichothecium sp*) that flourish in temperatures of 20–45 °C begin physical breakdown of biodegradable materials a few days after composting begins (Chinakwe et al. [2019](#page-26-12)). These mesophiles are supersede by thermophilic bacteria (*Bacillus sp, Seratia sp, Methylomonas sp, Streptosporangium sp*) and fungi (*Aspergillus fumigatus*) after a few days and can last for some days or even several months (Taiwo and Oso [2004\)](#page-32-14). At this point, temperatures have dropped sufficiently for mesophiles to reclaim dominance of the compost pile and complete the breakdown of the remnant organic materials into useful humus (Neher et al. [2013;](#page-30-13) Mingyan [2011](#page-30-14)).

# *1.7.1 Types of Composting*

Depending on the nature of decomposition process, composting can be divided into two types.

#### **Aerobic composting**

Aerobic composting occurs when there is adequate oxygen in the system. Aerobic microorganisms decompose organic matter, producing ammonia, carbon dioxide, water, heat and humus in the process (Kim et al., [2015\)](#page-28-12). These microorganisms continue to break down intermediate compounds such as organic acids, despite the fact that aerobic composting produces them (Cai et al. [2018\)](#page-26-13). The intermediate products are relatively unstable, and the compost is completely safe. The heat generated in the process accelerates the degradation of complex carbohydrates (cellulose and hemicellulose), proteins and lipids. As a result, processing time is shorter and many pathogenic microorganisms that may infect humans and plants are killed, as they are not adapted to these environmental conditions (Millner et al., [2014\)](#page-30-15). The heat also aids the growth of beneficial bacterial species such as mesophiles, psychrophiles and thermophiles. Although aerobic composting leads to more nutrient loss from the waste, it is considered more efficient and beneficial for agricultural production than anaerobic composting (Cai et al. [2019](#page-26-14); Mehta and Sirari [2018\)](#page-30-16).

#### **Anaerobic composting**

In anaerobic composting, decomposition occurs in the absence of or with a limited supply of oxygen. Anaerobic microorganisms thrive and take control of the community in this situation, resulting in the production of chemical intermediates such as carboxylic acids ( $-COOH$ ),  $CH_4$ ,  $H_2S$  and other toxic pollutants. In the absence of oxygen, these compounds build up and are not digested. Most of these compounds have a foul odour, and some of them may be harmful to animals and plants. Because anaerobic composting is a low-temperature process, organic materials and pathogens do not decompose. Moreover, the procedure usually takes longer than aerobic composting. These drawbacks typically overshadow the method's advantages (Eze and Okonkwo [2013;](#page-27-11) Mehta and Sirari [2018\)](#page-30-16).

# *1.7.2 Factors Affecting the Animal Waste Composting Process*

The composting of animal waste is influenced by a number of parameters, each of which has the potential to significantly affect the process. Such parameters (Fig. [1.2\)](#page-20-0) include the size of the feedstock, pH, temperature, C/N ratio, moisture, the interaction of oxygen and aeration and other parameters (Bernal et al., [2009](#page-26-11); Guo et al. [2012;](#page-28-13) Ameen et al., [2016](#page-25-5); Chen et al. [2020\)](#page-26-15). Controlling these elements helps speed up the natural composting process.



<span id="page-20-0"></span>**Fig. 1.2** Some parameters that affect animal waste composing process

## **1.8 Animal Waste Biodegradation**

#### *1.8.1 Bacterial Degradation Potential*

Animal wastes include organic materials, decomposing animal body parts, urea (in the case of mammals), uric acid (in the case of birds), faeces and waste feed (Dinh Tuan et al. [2006\)](#page-27-12). These components of organic wastes can be broken down by anaerobic and or aerobic bacteria such as *Escherichia coli* and *Salmonella spp*., and there are three ways to introduce microorganisms to the waste for degradation processes (Jang et al. [2017\)](#page-28-14). The first method involves spreading an isolated bacterium over the accumulated animal excreta. Animal wastes will be combined with soil and broken down by soil microorganisms if there is no microbial isolate available for this purpose (Briški and Domanovac [2017\)](#page-26-16). This soil is best obtained from a moist, shaded area, such as beneath trees, as moist soil has more microorganisms than dried dirt (Hoitink and Boehm [1999](#page-28-15)). To save time, money and effort, the wastes should be stacked adjacent to the organic matter source, such as a field or a harvesting area (Dobermann et al. [2000\)](#page-27-13). The final method uses bacteria linked to animal faeces. Animal faeces are a source of varying-quality organic nutrients, which puts microbial communities in a resource-contest and changes the structure and makeup of the soil microbiome. This is achieved by the excretion of specialized enzymes that convert complex polysaccharides, proteins and fats, such as cellulose, into simple nutrients that are ingested, such as sugars, amino acids and fatty acids. The heat produced by the biological process also aids in the stability and biodegradation of animal manure as the temperature rises. The other elements of animal manure are also taken into consideration. For example, the enzyme urease catalyzes urea hydrolysis, which is typically finished

within one day of urine output, as opposed to the enzyme uricase, which takes longer to catalyze uric acid breakdown (Rastogi et al. [2020\)](#page-31-14).

It is feasible to use these species for biological stabilization and treatment to produce valuable end products by altering the ambient and physio-chemical conditions (Brandelli et al. [2015\)](#page-26-17). Anaerobic bacteria have been found to be useful in the production of value-added products from the processing of animal waste, including minerals, volatile fatty acids, fertilizer, biogas and feedstocks. In contrast, Anaerobic Digestion (AD) is also helpful in the biological treatment of animal wastes using outdoor anaerobic ponds or bioreactors, allowing for the sustainable utilization of animal wastes (Li et al.  $2021$ ). In the absence of oxygen and in the presence of nutrient-rich medium, anaerobic digestion converts organic matter into volatile organic molecules, such as methane, ammonia, hydrogen sulphide and carbon dioxide. Around the world, AD is used to stabilize animal wastes like manure, lower pathogen and odour emissions and produce energy through biogas (Durán-Lara et al. [2020\)](#page-27-14). The energy in the biogas produced is substantially greater than what is needed, even though additional heat may be needed to maintain the proper temperatures (Chibuike [2013\)](#page-26-18). The biogas synthesized from animal waste can be processed and utilized as fuel, injected into the transmission lines or used to produce heat and/or power.

# *1.8.2 Degradation by Plant and Animal Feed-Associated Bacteria*

The environmentally responsible treatment of animal manure has benefited from plants. Animal faeces, which are a source of nutrients for plants, really promote plant growth far more than synthetic fertilizer does. Through their roots, plants primarily take up nutrients from animal waste and transform the soluble chemical components into plant tissues. Considering this, it is feasible to use plants to treat animal waste, which would have the twofold advantages of accelerating development and biochemical transformation while also recycling necessary animal wastes into plant feed, berries or dry materials. Based on the plant's species, growth stage, root length and dispersion, soil moisture, temperature and a variety of other parameters, the proportion of total absorbed by the roots varies (Ramachandra et al. [2018](#page-31-15)). In contrast, decomposers, which are often found in animal feed, absorb simple sugars and easily digested carbon compounds. They also bind soluble chemicals like nitrogen in their cell membranes, which helps with the organic recycling of carbon (Jambon et al. [2018\)](#page-28-16).

#### *1.8.3 Microfungal and Mycorrhizal Degradation*

Roots of vascular plants and fungi have a symbiotic interaction known as mycorrhiza (Al-Maliki and AL-Masoudi [2018](#page-25-6)). The plant gives the fungi glucose, and the mycorrhizal fungi increase the roots surface area, enabling plant roots to absorb more water and nutrients from the soil and boosting the plant's resistance to disease (Jacoby et al. [2017\)](#page-28-17). Free-living saprophytes and ectomycorrhizal or arbuscular mycorrhizal (AM) fungi are both well known for their substantial degradative abilities and effects that promote plant growth, making them appealing candidates for use in organic matter degradation (Jansa et al. [2013\)](#page-28-18). AM fungus assists in the decomposition of animal dung by enhancing the activity of bacteria. Based on their capacity to stimulate the creation of bio-catalysts like pectinases, cellulases and hemicellulases, which are in charge of the breakdown process, mycorrhizal fungal species can decompose animal waste (Toljander et al. [2008\)](#page-32-15). Because AM fungi lack saprotrophic abilities and depend on saprotrophic microorganisms to digest organic materials like animal wastes, this demonstrates that the breakdown of organic wastes by AM fungus is not considered direct (Etesami et al. [2021\)](#page-27-15). As a result, there is a greater amount of organic nitrogen available for AM fungi to absorb (Wilkes [2021](#page-32-16)).

Furthermore, the AM fungus may indirectly affect the decomposition process by producing significant amounts of bio-compounds that aid the soil's microbial community in degrading organic waste. The bacterial population in soil is increased by low molecular weight carbohydrates and organic acids released by AM fungi, according to prior research (Jdruchniewicz [2018](#page-28-19)). However, Filion et al. found that some soil microbes were stimulated while others were inhibited by the hyphal exudates of AM fungi (Batstone et al. [2002](#page-26-19)). This suggests that instead of seeding microorganisms, earth could be used as the source of microorganisms for treating animal waste with microfungi.

# *1.8.4 Degradation by Algae*

Algae and other aquatic plants' photosynthetic ability has proved successful in recycling carbon and other nutrients from animal wastes, as well as in environmental bio-remediation. According to this theory, diluted nutrients from animal excreta are converted into higher and lower plants by photosynthetic processes (Fernández et al. [2018\)](#page-27-16). Animal waste can be effectively reused or converted into usable products and energy through the process of algal degradation. Algae could help people economically by using the energy and chemicals in animal waste (Puyol et al. [2017\)](#page-31-16). Despite decades of algal seeding on animal waste effluent, just a few projects have reached commercial scale (Shah et al. [2014](#page-31-17)). Methane biosynthesis is the end product of several biological breakdown processes, including hydrolysis, acidogenesis, acetogenesis and methanogenesis. The products from previous phases are transformed into

methane and carbon dioxide through the hydrogenotrophic and acetotrophic pathways (Phillips et al. [2017\)](#page-31-18). Algae's capacity to break down animal waste can result in the production of significant biofertilizers in addition to methane. Additionally, a pilot plant that can transform pig poo into single cell protein has been created. It consists of a group of bacteria and algae. A high-temperature strain of *Chlorella vulgaris* was utilized the generating organism. According to research, 30–35% of the nitrogen waste from animal waste can be converted into single-cell protein. Algae biomass production, on the other hand, is more difficult than bacterial biomass production. This is due to the fact that algae biomass production necessitates control over culture depths, retention time and the amount of nutrients in the solution (Ozi et al. [2022](#page-31-19)).

### **1.9 Recovery of Nutrients and Energy from Animal Waste**

There are many strategies or new technologies to recover high-value products and low-value by-products from animal waste in terms of environmental sustainability, which can also be incorporated into the value chain (Table [1.3](#page-23-0)). The anaerobic digestion can be used to convert waste into biogas for energy production and into a nutrientrich digestate for use as fertilizer. Microbial technologies have the ability to convert waste into animal feed. Currently, processes such as anaerobic digestion, composting, worm culture and lime stabilization are used to process waste as well as to recycle and recover nutrients from the waste, and these can establish supply chains that are part of the bioeconomy. The use of treated digestate or organic waste as fertilizer and the CH4 produced by anaerobic digestion for energy is considered waste recycling methods.

By products	Description
<b>Biogas</b>	It is produced through anaerobic digestion of animal waste. It has various applications in cooking, drying, cooling, heating, electricity generation, etc.
Digestate	It is a nutrient-rich material left at the end of anaerobic digestion and can be used as a fertiliser
Animal feeds	Animal wastes can be used as source of feed nutrients for, aquaculture, livestock, pig and poultry. To maintain the nutrient composition and increase the palatability and feeding values of the waste, dehydration, ensiling, chemical and physical treatments can be used. With proper treatment, animal waste is rich in nutrients and the worms can be the source of proteins

<span id="page-23-0"></span>**Table 1.3** Beneficial high- and low-value by-products of animal wastes

### *1.9.1 Recovery of Energy from Animal Waste*

Animal waste with a high organic content is degraded by microbes in both natural and artificial environments. These methods stabilize the waste, reduce pathogens and odours and convert waste streams into biogas, which are rich in methane. In the context of the circular economy, the biogas produced can be used to generate heat or electricity (Arshad et al. [2022\)](#page-25-1). The economic worth of biogas is mainly determined by its ability to produce heat. The biogas produced by a biodigester can be combusted on-site in a low-treatment processing plant to offset the plant's heat and energy needs. According to Fredheim et al., biogas produced at an animal processing plant can offset on-site heating needs (20–50%). This equates to an 83% reduction in carbon emissions and savings in energy costs (Fredheim [2017\)](#page-27-17). A modelled scenario for producing biogas from swine wastewater resulted in a comparable reduction in fossil fuel use (25%) (Wiedemann et al. [2016](#page-32-17)). The uses of biogas are not limited to on-site energy production, as we have described in other chapters. Biogas can be upgraded to increase CH<sub>4</sub> content and injected into flexible and easily storable fuel as biomethane, or it can be stored in cylinders as an alternative to liquefied natural gas (Wiedemann et al. [2016](#page-32-17); Malomo et al. [2018;](#page-29-0) Girotto and Cossu [2017](#page-28-0)). In addition, biochar, a valuable soil conditioner, can be produced as a by-product of waste treatment processes such as pyrolysis and liquefaction (Maroušek et al. [2019](#page-29-20)).

### *1.9.2 Animal Waste as a Source of Animal Feeds*

As mentioned earlier, anaerobic digestion of waste is not only an effective treatment method and fertilizer source, but it can also be used to propagate microorganisms to produce nutrient-rich biomass. Slaughterhouse waste, including blood, can also be used as animal feed. The market for microbial-based proteins is growing due to the protein-rich biomass from microbes, which can be used as high-protein livestock feed or as high-performance feed additives for livestock (Ramirez et al. [2021\)](#page-31-20). Microbes are chosen based on their lipid and protein contents, ability to thrive, productivity and efficiency in extracting nutrients from wastes. In addition to microbes such as *Chlorella* sp., *Lemna minor, Cladophora* sp., *Scenedesmus*  sp., *Rhizoclonium* sp., *Rhodopseudomonas* sp., *Rhodobacter* sp. and *Ulothrix* sp., rumen microorganisms from rumen wastes rich in lignocellulosic plant fibres could be used in solid-state fermentation as a substrate to produce a product rich in protein that can be used directly in animal feed (Ramirez et al. [2021](#page-31-20); Vadiveloo et al. [2019](#page-32-18); Nwoba et al. [2017](#page-30-17)). According to studies, microbial biomass products are superior to both animal and plant feeds in terms of probiotic potential, protein content, essential vitamin or amino acids content, conversion efficiency and land footprint in different climates. The use of animal waste as feed for livestock and aquaculture has been shown to be cost-effective and straightforward and can meet the nutritional needs of animals (Delamare-Deboutteville et al. [2019](#page-27-18); Ramirez et al. [2021;](#page-31-20) Matassa

et al. [2015](#page-30-18)). Enzymatic digestion of solid animal waste such as cattle hair or wool residues has been shown to provide amino acids or peptides that can be used as feed supplement. In the animal production cycle, fermentation of waste materials to produce the required amino acids is an important method of recovering nutrients from waste (Navone and Speight [2018;](#page-30-19) Ramirez et al. [2021\)](#page-31-20).

### **1.10 Conclusion**

Scientists are focusing much of their attention on the current challenge of environmental sustainability. It is recognized as necessary at the highest levels and requires urgent attention at the global level because it is essential for progress. Animal waste management is a critical issue that requires the most incredible attention if sustainability is to be ensured. As society struggles to find a sustainable way to remediate polluted environments and wastes, interest in using various microorganisms has recently increased and gained importance. The potential of microbes for specific applications has attracted more attention and speculation with the development of biotechnology. The nature of microorganisms is unusual and even unpredictable. Diverse microorganisms can effectively solve numerous environmental problems. They can help decompose animal manure and return nutrients to the soil. The primary nutrients and vital components for plant health—nitrogen, potassium and phosphorus—are released through nutrient recycling. The successful development and application of microbiological waste management techniques are essential for environmental remediation and value creation.

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