BUKTI KORESPONDENSI

Sustainable Growth in Cattle: A Global Bibliometric Analysis of Physiological Research Trends

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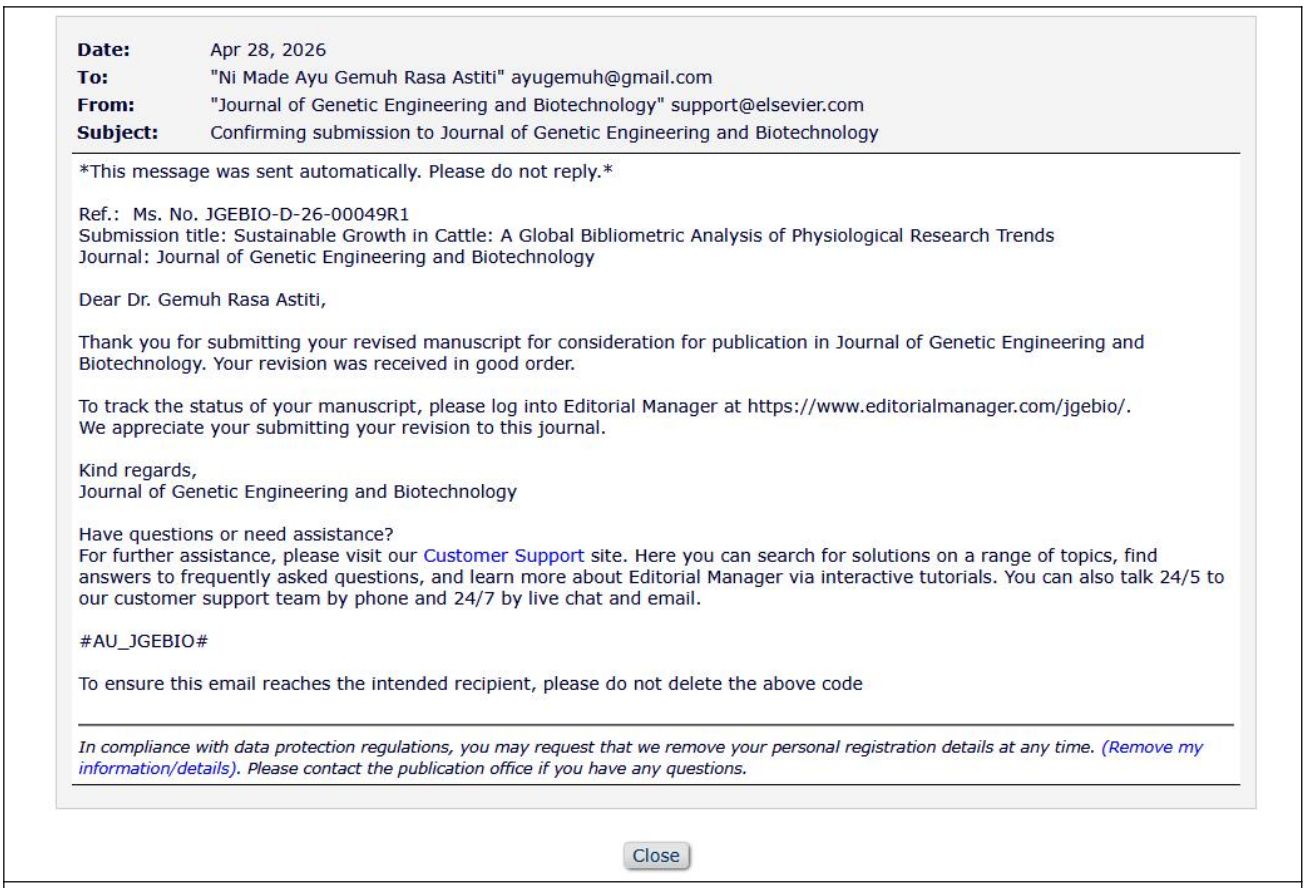
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Yours sincerely
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Journal: Journal of Genetic Engineering and Biotechnology

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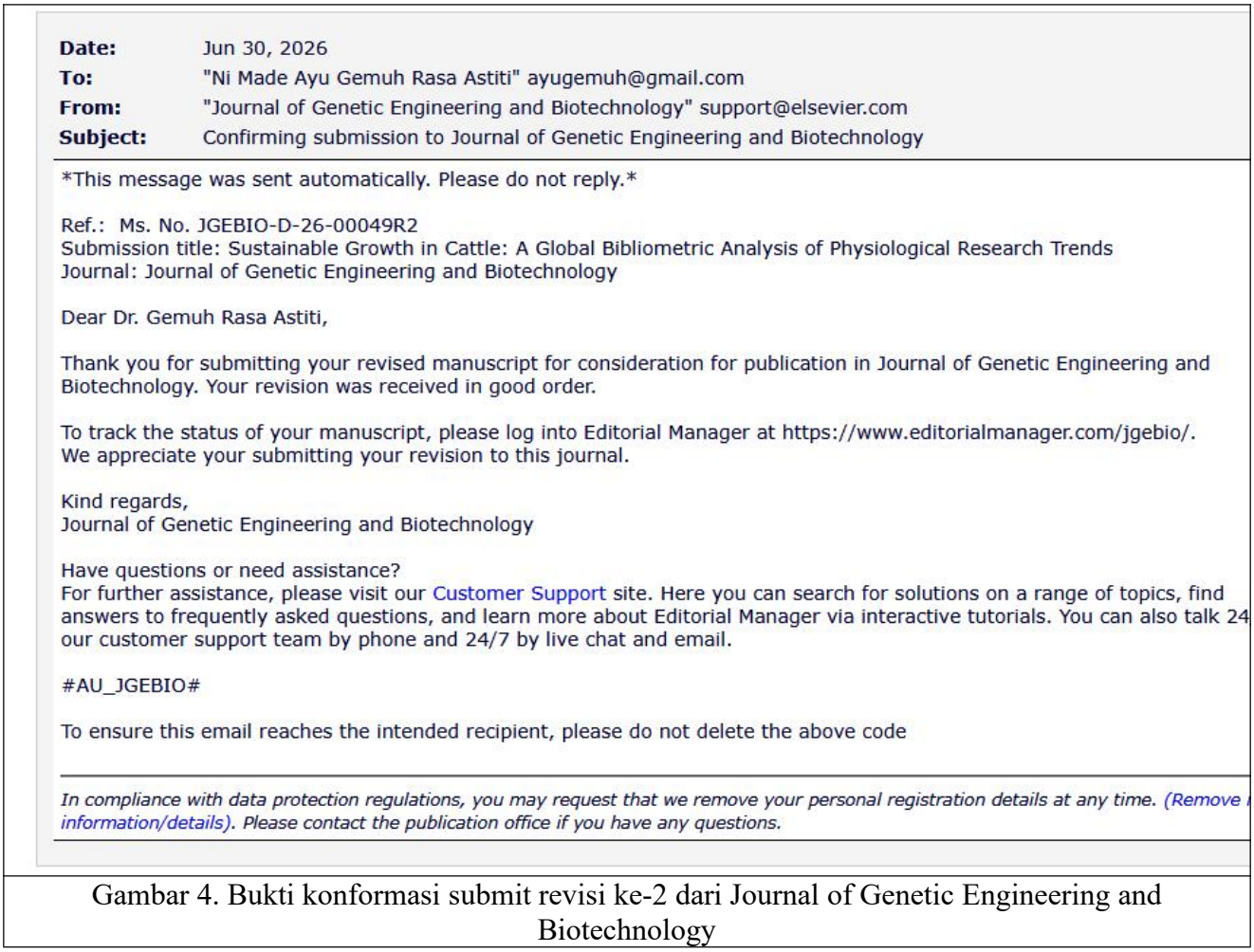
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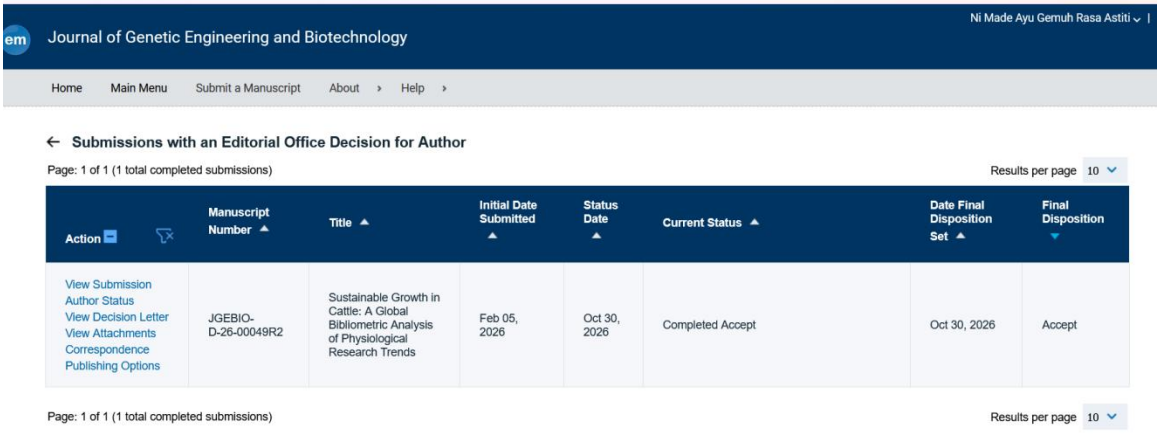
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Mahmoud Mohamed Sakr, PhD
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Comments from the Editors and Reviewers:
Reviewer #2: N/A

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Gambar 5. Bukti accepted dari Journal of Genetic Engineering and Biotechnology

6. Comments and answer Revisi Ke-1

No.	Comments Reviewer	Answers
1.	**Bibliometric Analysis and Data Visualization** 1. **Investigate Publication Spikes:** The publication spikes observed in 2021 and 2025 may have been influenced by the COVID-19 pandemic. It would be beneficial	1. In line 145-155 : The surges in publications observed in 2021 and 2025 can be partially attributed to the indirect effects of the COVID-19 pandemic on scientific research and agricultural systems. During the pandemic, disruptions to global food supply chains heightened concerns about food security, efficiency, and resilience in

	to check if other bibliometric studies show similar trends and discuss this potential impact. 2. **Improve Figure Descriptions:** There is a need for more descriptive text for the VOSviewer network visualizations (Figure 2) and the country-based output (Figure 4). 3. **Justify Figure 4:** This figure is currently not referred to in the text; its inclusion must be justified or it should be removed. 4. **Citation Formatting:** An error in the citation format was noted on page 11.	livestock production, prompting increased research attention toward cattle growth physiology, productivity, and resource optimization. In addition, lockdowns and reduced field activities in 2020 allowed researchers to focus more on data analysis and manuscript preparation, contributing to the spike in publications observed in 2021. The subsequent rise in 2025 likely reflects post-pandemic recovery, renewed research funding, and the accelerated adoption of advanced tools such as genomics, precision nutrition, and growth modeling, as research priorities shifted toward sustainable and efficient animal production systems informed by lessons learned during the pandemic [10]. 2. In line 179-195: The VOSviewer network visualization in Figure 2 illustrates how research themes surrounding the physiological processes of growth in cattle are intellectually organized and interconnected based on keyword co-occurrence patterns. Node size reflects the frequency of terms in the literature, while the distance and connecting lines indicate the strength of their conceptual relationships, allowing dominant and emerging themes to be easily identified. The central positioning of the term "cattle" confirms its role as the unifying research subject, linking multiple clusters that represent complementary dimensions of growth physiology. Dense linkages within the red and blue clusters indicate well-established research areas, where growth is closely associated with reproduction, metabolic regulation, milk production, feed efficiency, and environmental stress adaptation. Surrounding clusters, such as those focused on lactation, endocrine regulation, pregnancy, and molecular approaches, add biological depth by highlighting developmental, hormonal, and omics-driven perspectives. More peripheral clusters, including cell culture and apoptosis, suggest specialized mechanistic studies that contribute foundational knowledge but are less frequently integrated into applied research. Overall, the visualization demonstrates that cattle growth physiology research is highly multidisciplinary, with VOSviewer effectively capturing both the core themes and their supporting subfields within a coherent and interconnected research network. 3. In line 338-353: Figure 4 illustrates a clear geographic concentration of Scopus-indexed research output on the physiological processes of

		growth in cattle, highlighting the dominant role of a small group of leading countries. The United States emerges as the most prolific contributor, accounting for just over one-quarter of the total publications, reflecting its strong research infrastructure, extensive cattle industry, and sustained investment in animal science. China follows closely, contributing more than one-fifth of the documents, which underscores its rapidly expanding focus on livestock productivity, food security, and modernized agricultural systems. Brazil, Germany, and Canada form a second tier of contributors, together reinforcing the importance of both emerging and well-established cattle-producing nations in advancing growth-related research. Contributions from countries such as India, France, the Russian Federation, the United Kingdom, and Australia further demonstrate the global relevance of cattle growth physiology, although at more moderate output levels. Collectively, the dominance of the top five countries responsible for nearly three-quarters of all publications indicates that research activity is highly centralized in regions with strong scientific capacity and significant livestock sectors, while also suggesting opportunities for broader international collaboration and increased contributions from underrepresented regions. 4. We have deleted the name of author
2.	**Technical Precision and Definitions** 1. **Define Gestational Stages:** The manuscript would be improved by clearly defining the three trimesters of gestation in cattle at the start of Section 3.1. Furthermore, terms like "early" and "last" gestation used later in the text should be applied more precisely. 2. **Clarify Growth Concepts:** When discussing "growth," it is important to specify whether the focus is on a particular life stage or lifetime growth. 3. **Clarify Table 1 Data:** It should be made clear if the historical averages in Table 1 refer specifically to the 1970 timeframe.	1. In line 359-373: Prenatal development plays a critical role in establishing the foundational structure of muscle, adipose, and bone tissues in cattle, and these processes are best understood within clearly defined gestational stages. Bovine pregnancy is conventionally divided into three trimesters: the first trimester (conception to ~95 days of gestation), the second trimester (~96–190 days), and the third trimester (~191 days to parturition). Skeletal muscle fiber number is determined entirely before birth, with primary and secondary myogenesis occurring predominantly during the first and second trimesters (early to mid-pregnancy) under the regulation of conserved myogenic regulatory factors, including MyoD, Myf5, Myogenin, and MRF4 [34], [35]. Because the quantity of postnatal muscle fiber cannot be increased, nutritional, hormonal, or environmental perturbations during these early and mid-gestational windows can have lasting consequences for muscle growth potential and carcass traits. Adipogenesis follows a more staggered timeline, with adipoblasts emerging

		primarily during the second trimester (mid-pregnancy) and differentiating into mature adipocytes during the third trimester (late pregnancy), a phase particularly sensitive to maternal nutrition and endocrine signals that influence adipose precursor proliferation and differentiation [36], [37]. 2. In line 462-478: When discussing cattle growth, it is essential to clarify whether growth is assessed within a specific life stage or across the entire lifespan, as tissue deposition patterns and underlying controls change markedly with physiological maturity. Lifelong growth follows a sigmoidal trajectory, in which early stages emphasize organogenesis and skeletal expansion, followed by a muscle- dominant phase, and ultimately a shift toward adipose deposition as animals near maturity, in line with classical allometric growth models [45]. Serial harvest studies demonstrate that during the finishing phase, skeletal and lean tissue accretion decline while fat becomes the primary contributor to weight gain, with adipose tissue accruing at rates disproportionate to empty body weight [47]. This transition reflects a metabolic reprioritization toward lipid storage once structural growth plateaus. Growth-modifying interventions further illustrate stage-specific growth dynamics, as anabolic implants such as trenbolone acetate and estradiol-17β can extend the muscle-dominant growth phase by sustaining protein accretion and suppressing adipogenesis [48], whereas advancing age and estrogenic influences accelerate fat deposition [43], [44]. Collectively, these findings indicate that "growth" cannot be treated as a uniform process; rather, its interpretation and management must be aligned with the animal's developmental stage, endocrine status, and production objective, underscoring the importance of using stage-specific references appropriately when evaluating growth biology and performance outcomes. 3. In line 547-559: Table **1** shows the biological types of cattle weaning weight and carcass composition. The combined evaluation of breed type, sex class, and modern production strategies emphasizes that carcass performance results from the interaction of genetic predisposition, endocrine influences, and environmental management. Continental breeds exhibit superior lean growth capacity, but British

		breeds remain advantageous for marbling-driven quality grades. Sex hormones modulate these genetically defined growth patterns, resulting in distinct deposition trajectories for heifers, steers, and bulls. Continuous genetic improvement, coupled with optimized DOF and implant technologies, has produced progressively heavier and more muscular carcasses across the U.S. beef industry, as reflected in national records from the 1970s to 2023 [49], [51]. These findings highlight the importance of integrated management strategies that account for biological constraints and production goals. Aligning breed selection, sex class management, nutritional strategies, and GET protocols enables producers to strategically optimize both yield and quality outcomes in contemporary beef systems
3.	**Critical Content Additions and Discussions** 1. **Incorporate Marker-Assisted Selection:** Information should be added regarding beef breeds specifically Angus seedstock incorporating marker-assisted selection into their breeding programs. 2. **Deepen the Multi-Omics Discussion:** There is currently limited discussion of multi-omics. The manuscript would be more compelling if it included specific examples of how multi-omics provides advantages over more traditional investigations of individual molecules or traits. 3. **Address Practical Constraints:** A potential contradiction exists in the recommendation for "personalized nutrition". Consider explaining how such tailored nutrition could practically be delivered to beef cattle in a group or herd setting.	1. In line 217-226: Significant progress has been made in identifying genes linked to feed efficiency. For instance, Abo-Ismail et al. have developed a single-nucleotide polymorphism (SNP) panel tailored for beef cattle, facilitating genetic evaluation of feed efficiency traits across populations [12]. This SNP panel, validated in **Angus** and Hereford breeds, is crucial for breeding programs focused on improving feed efficiency. Additionally, extensive genome-wide association studies (GWAS) have been conducted, identifying numerous genetic markers associated with feed efficiency traits, including RFI and ADG. Seabury et al. highlighted the potential for integrating these markers into breeding programs, thereby enhancing both feed efficiency and growth traits [13]. Identifying significant SNPs associated with RFI can lead to more precise breeding strategies that increase productivity while minimizing resource use. 2. In line 278-287: Genetic factors also contribute significantly to the differences observed in metabolic profiles among cattle breeds. Genomic studies in conjunction with metabolomics have begun to uncover how specific genetic markers influence metabolic pathways associated with growth and adaptation [25]. Research efforts are increasingly employing **multi-omics** approaches that integrate genomics, transcriptomics, and metabolomics to provide a holistic view of the metabolic processes underlying growth traits in cattle [23]. Such comprehensive methodologies enable the

		identification of candidate genes that can be leveraged in breeding programs to enhance growth performance and disease resistance in cattle. This genetic information, when analyzed alongside metabolomic data, reveals potential pathways that could be targeted for improving growth efficiency in livestock [26]. 3. In line 590-607: Addressing the apparent contradiction between recommendations for "personalized nutrition" and the realities of group-fed beef production requires reframing personalization as biologically informed, cohort-based management rather than individual-animal feeding. Extensive evidence from backgrounding and growing-phase studies demonstrates that cattle respond predictably to differences in nutritional plane, growth rate, and timing of energy restriction or provision, with measurable downstream effects on finishing performance and carcass traits [59,60]. In practice, this enables producers to implement personalized nutrition by sorting cattle into groups based on weight, age, sex, growth system (e.g., calf-fed vs. yearling), or expected maturity pattern, as is already common in backgrounding and system-level comparisons [61,62]. Such grouping aligns nutrient supply with shared physiological stage and growth potential, effectively tailoring nutrition at the pen or cohort level. Moreover, recognition that growth capacity is influenced by earlier developmental factors, including prenatal muscle development and environmental constraints such as drought, further supports the need for flexible, stage-specific nutritional strategies that account for starting biological variation without requiring individual feeding [63,64]. Thus, personalized nutrition in beef systems is most realistically achieved through strategic sorting, phase-feeding, and system-specific ration design, allowing nutrition to be matched to biological need within herds while remaining compatible with large-scale, group-based management.
4.	**Structural and Formatting Revisions** • **Sentence Relocation:** A sentence on page 10 regarding proteomics appears out of place and should be moved to the beginning or end of a more relevant paragraph. • **Referencing Gaps:** There is a significant lack of references in several key sections, particularly	We have revised the structural and formatting by proofreading check.

	regarding the regulation of developmental phases, muscle/bone development, genetic selection, and the composition of gain. • **Formatting Errors:** Paragraph indentation needs correction on pages 14, 15, and 26. Certain inserted text factors on page 7 also require review for clarity.	

7. Comments and answer Revisi ke-2

No.	Comments Reviewer	Answers
1.	The underlying descriptive analysis accompanying the core statistical and bibliometric outputs requires stronger justification.	In line 157-169: Figure 2 shows the PRISMA diagram. The data were retrieved from the internationally recognized Scopus database on February 3, 2026, using the search keyword "Physiological Processes of Growth in Cattle." The initial search yielded 470 publications published between 2015 and 2026. To ensure the relevance and quality of the dataset, a multi-stage screening procedure was implemented. During the first screening stage, the titles, abstracts, and conclusions of all retrieved records were systematically examined, resulting in the selection of 155 relevant publications. Subsequently, a more rigorous inclusion process was conducted by selecting studies that aligned with three emerging research themes identified through the overlay visualization generated using VOSviewer: feed efficiency, metabolomics, and proteomics. This final screening produced a refined dataset of 23 publications, which served as the foundation for the subsequent bibliometric and thematic analyses. The complete study selection process, together with the identification of the emerging research themes, is presented in Figure 4 (Overlay Visualization in VOSviewer)
2	Specifically, the authors must provide a much deeper explanation of the mathematical layout and similarity metrics defining the VOSviewer network visualizations (Figure 2),	In line 175-187: Although both the network visualization and overlay visualization in VOSviewer are derived from the same keyword co-occurrence dataset, they provide complementary insights into the research field. The network visualization reveals the conceptual structure by illustrating the relationships, co-occurrence strength, and clustering of keywords, thereby identifying the major research themes and their interconnections. In contrast, the overlay visualization incorporates

		a temporal dimension by assigning colors to keywords based on their average publication year, enabling the identification of emerging research trends. In this study, the network visualization highlights the conceptual relationships among keywords related to the physiological processes of growth in cattle, whereas the overlay visualization identifies feed efficiency, metabolomics, and proteomics as emerging research themes, reflecting a recent shift toward molecular, metabolic, and precision-livestock approaches to understanding cattle growth. Together, these visualizations provide a comprehensive understanding of both the knowledge structure and its temporal evolution.
3.	And they must explicitly address why the country-based output (Figure 4) is entirely omitted from the text narrative despite its inclusion as a visual data point.	We have removed or omitted the country-based output (Figure 4) based your advices