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Visualisation analysis of research frontiers, hotspots and trends in Fleckvieh breeding based on CiteSpace knowledge graph

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Abstract: This study investigates advancements and trends in Fleckvieh breeding research using the Web of Science Core Collection database to collate articles published since 1994. Through CiteSpace 6.4.R1, we conducted systematic analyses to visualise research trajectories, identify seminal domains, and delineate emerging patterns. Our methodology encompassed publication profiling, scientific collaboration network mapping, co-citation analysis, and keyword co-occurrence/clustering techniques. The findings reveal that the current research frontiers focus on: Genomic applications in genetic selection, Reproductive efficiency optimisation, Environmental adaptability mechanisms, Thermotolerance management strategies, Cross-disciplinary methodological integration. Germany, Czech Republic, Austria, and Switzerland emerged as leading contributors, with institutions including the Technical University of Munich and University of Natural Resources and Life Sciences, Vienna, demonstrating a particular scholarly influence. Knowledge mapping effectively delineated thematic concentrations and temporal evolution patterns, providing actionable insights for future research prioritisation. The field is progressing towards holistic, interdisciplinary frameworks underpinned by robust international consortia. This work introduces novel analytical perspectives to refine breeding protocols and enhance practical implementation.

Keywords: bibliometric analysis in animal science; climate-resilient breeding; genomic selection application; heat stress mitigation; interdisciplinary breeding strategy; knowledge graph analysis

INTRODUCTION

The Fleckvieh cattle, a prominent dual-purpose breed for combined milk and meat production, exhibit robust climatic adaptability alongside superior milk fat and protein profiles, cementing their status as a strategic genetic resource in sustainable beef systems (Cziszter et al. 2017). Therefore, in-depth exploration of the genetic characteristics and production performance of Fleckvieh cattle

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is of great significance for improving the overall efficiency of animal husbandry. Breeding, as an efficient genetic improvement strategy, has been widely adopted in the improvement of the Fleckvieh breed. By introducing new genetic variations, it is possible to not only enhance the production performance of Fleckvieh cattle, improve their adaptability and disease resistance, but also expand their gene pool, effectively alleviating the problem of genetic decline caused by inbreeding.

With the rapid development of information science, a knowledge graph analysis has become an important tool for revealing the research frontiers and trends in the field of animal husbandry (Cui et al. 2023; Jiang et al. 2023; Ghassemi Nejad et al. 2023). The CiteSpace knowledge graph analysis software can visualise key information in scientific literature, such as co-occurrence of keywords, author collaboration networks, and co-citation of references. This helps researchers identify research hotspots, discover potential research trends, and explore the connections between different research fields. This study aims to use CiteSpace for a knowledge graph analysis to systematically review the research progress in Fleckvieh breeding, identify research hotspots and frontier issues, and provide guidance for future research directions. This is of great theoretical and practical significance for guiding breeding practices and optimising breeding strategies.

MATERIAL AND METHODS

Literature sources and search strategy

Using computer-based searches, we retrieved literature from the Web of Science (WoS) database from January 1994 to November 2024. The search condition was:

> TS (Topic) = [(Fleckvieh OR German Simmental) AND (growth performance OR reproductive performance OR milk production OR meat production)].

Non-article documents (e.g., conference proceedings, news reports, social data, patents, and books) were excluded from the search results. Full records with cited references were exported in TXT format for analysis.

Research methods

Bibliometric analysis was conducted using the CiteSpace v6.4.R1 Advanced software to analyse:

(*i*) Publication volume trends;
(*ii*) Scientific collaboration networks;
(*iii*) Reference co-citation patterns;
(*iv*) Keyword co-occurrence and clustering.

Compared to earlier versions, CiteSpace 6.4.R1 Advanced enhances node information processing capacity, enabling comprehensive visualisation of complex literature relationships and developmental trajectories.This facilitates hotspot tracking and frontier identification.

In the Networks drawn by CiteSpace 6.4.R1 Advanced software, N represents the number of nodes in the network, and E represents the number of connections. The software uses the value of betweenness centrality to represent the importance of nodes. Nodes with betweenness centrality exceeding 0.1 are generally referred to as key nodes and are highlighted with coloured circles. The size of the coloured circle indicates the frequency of keyword occurrence, and the colour of the circle represents the time of keyword occurrence (Frigeri et al. 2023).

RESULTS

Analysis of annual publication volume

This study retrieved 655 English-language articles, with 650 retained after initial screening. Following de-duplication via CiteSpace, a final dataset of 649 articles was obtained.

As shown in Figure 1, publication outputs in Fleckvieh breeding research exhibited marked fluctuations over the past three decades. From 1994 to 2003, a low but gradually increasing number of outputs reflected the emergent phase of the field. The years 2004–2006 were characterised by fluctuating growth, followed by accelerated growth during 2007–2010. The peak activity period (2011–2016) saw notable spikes in 2012 and 2015. Outputs stabilised at 25 articles annually from 2017–2020, before entering a declining phase after 2021. A minor resurgence occurred in 2022, succeeded by continued declines through 2023–2024.

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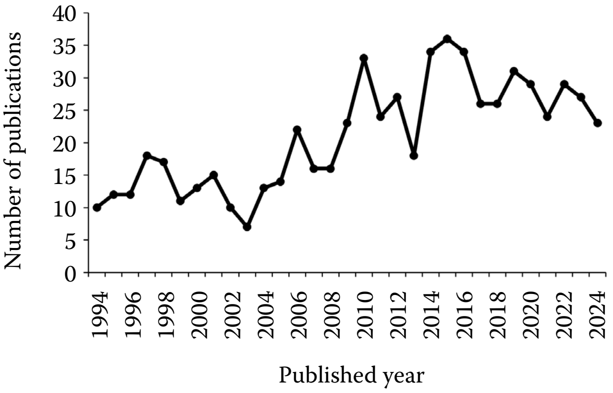


Figure 1. Related literature publication of Fleckvieh hybrid breeding research

The analysis of the annual publication volume in the field of Fleckvieh breeding shows that the trend of publication volume first increases, then it stabilises, and finally it decreases slightly. This trend is related to the maturity of the research field, the investment in research funding, policy support, and the level of attention from the scientific community. Overall, the publication volume in Fleckvieh breeding research has shown significant fluctuations in different years, which are closely related to the cyclical nature of research projects, the publication cycle of research results, and the changing research hotspots in the academic community.

Analysis of annual publication volume

This study retrieved 655 English-language articles, with 650 retained after screening. Deduplication via CiteSpace yielded a final dataset of 649 articles.

The g-index mechanism (k = 25) was applied to analyse country/institutional/author collaboration patterns in Fleckvieh breeding research.

As shown in Figure 2, with N = 290 and E = 536, it indicates that there are 290 core institutions and units involved in the research of Fleckvieh breeding. Combined with Table 1 and Table 2, it is found that among the top 5 institutions in terms of the publication volume, one is located in Austria, two in Germany, and two in the Czech Republic. These institutions are the University of Natural Resources and Life Sciences, Vienna (68 publications), University of Munich (63 publications), Technical University of Munich (62 publications), Czech Institute of Animal Science (53 publications), and Mendel University in Brno (44 publications). In terms of the centrality, the top 5 institutions are Technical University of Munich (0.15), University of Munich (0.11), University of Natural Resources and Life Sciences, Vienna (0.09), Aarhus University (0.09), and Czech Institute of Animal Science (0.07).

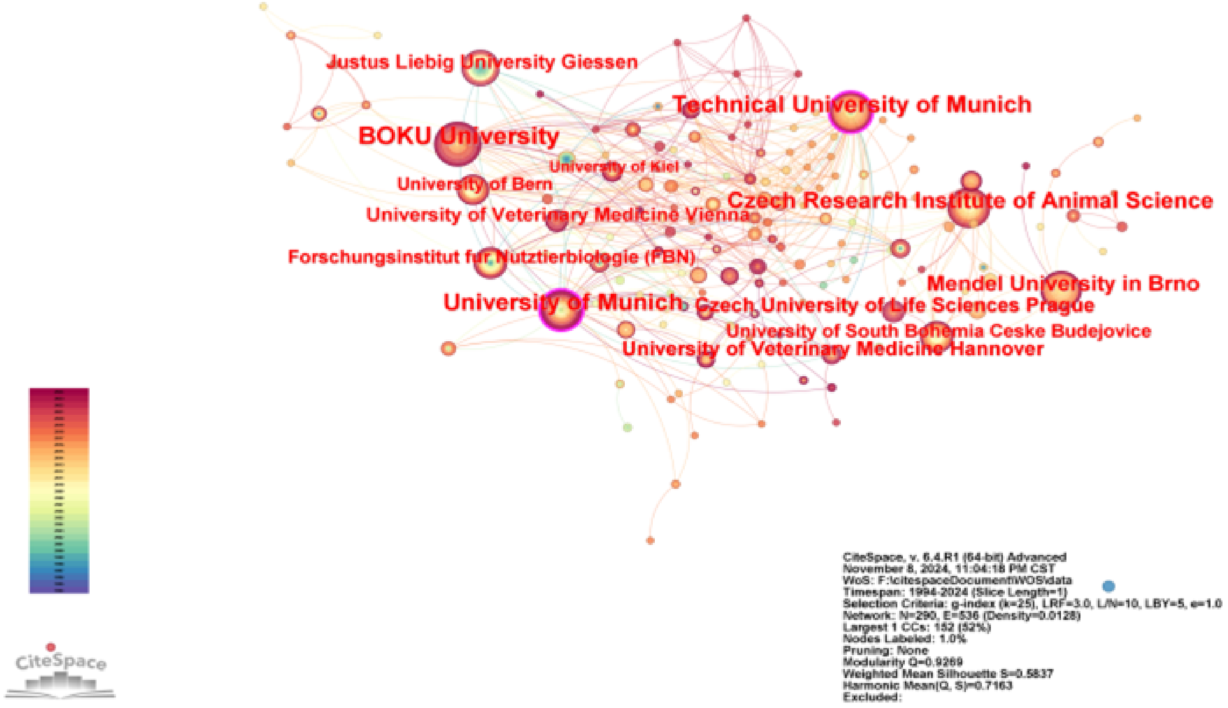


Figure 2. Cooperative mapping of research institutions studying Fleckvieh hybrid breeding

Table 1. The top 10 institutions, countries, and authors in terms of the publication volume

Rank	Institution	Number	Country	Number	Author	Number
1	BOKU University	68	Germany	278	Distl, O	22
2	University of Munich	63	Czech Republic	130	Pausch, H	17
3	Technical University of Munich	62	Austria	117	Egger-Danner, C	16
4	Czech Research Institute of Animal Science	53	Switzerland	64	Fries, R	16
5	Mendel University in Brno	44	Brazil	18	Emmerling, R	15
6	University of Veterinary Medicine Hannover	30	Hungary	17	Fuerst-Waltl, B	15
7	Czech University of Life Sciences Prague	29	USA	16	Fuerst, C	14
8	University of Veterinary Medicine Vienna	28	Croatia	12	Schwarzenbacher, H	14
9	Justus Liebig University Giessen	25	Poland	11	Chladek, G	13
10	Forschungsinstitut fur Nutztierbiologie (FBN)	22	Italy	10	Steinwidder, A	12

Table 2. The top 10 institutions, countries, and authors in terms of the centrality

Rank	Institution	Centrality	Country	Centrality	Author	Centrality
1	Technical University of Munich	–	Germany	0.1	Steinwidder, A	0.11
2	University of Munich	0.11	China	0.1	Gredler, B	0.11
3	BOKU University	0.09	Austria	0.07	Baumung, R	0.1
4	Aarhus University	0.09	Czech Republic	0.07	Emmerling, R	0.09
5	Czech Research Institute of Animal Science	0.07	Belgium	0.05	Fuerst-Waltl, B	0.09
6	University of South Bohemia Ceske Budejovice	0.07	Brazil	0.04	Averdunk, G	0.05
7	Mendel University in Brno	0.06	USA	0.1	Distl, O	0.04
8	Forschungsinstitut für Nutztierbiologie (FBN)	0.06	Switzerland	0.1	Curik, I	0.04
9	United States Department of Agriculture (USDA)	0.06	Egypt	0.07	Seefried, F	0.04
10	National Research Institute for Agriculture, Food and Environment (INRAE)	0.05	Spain	0.07	Augustini, C	0.03

In the present study the CiteSpace software was used to analyse the distribution and collaboration networks of countries, institutions, and authors in the field of Fleckvieh breeding research. The g-index mechanism (k = 25) revealed international collaboration patterns (N = 52 countries, E = 167 connections) as shown in Figure 3.

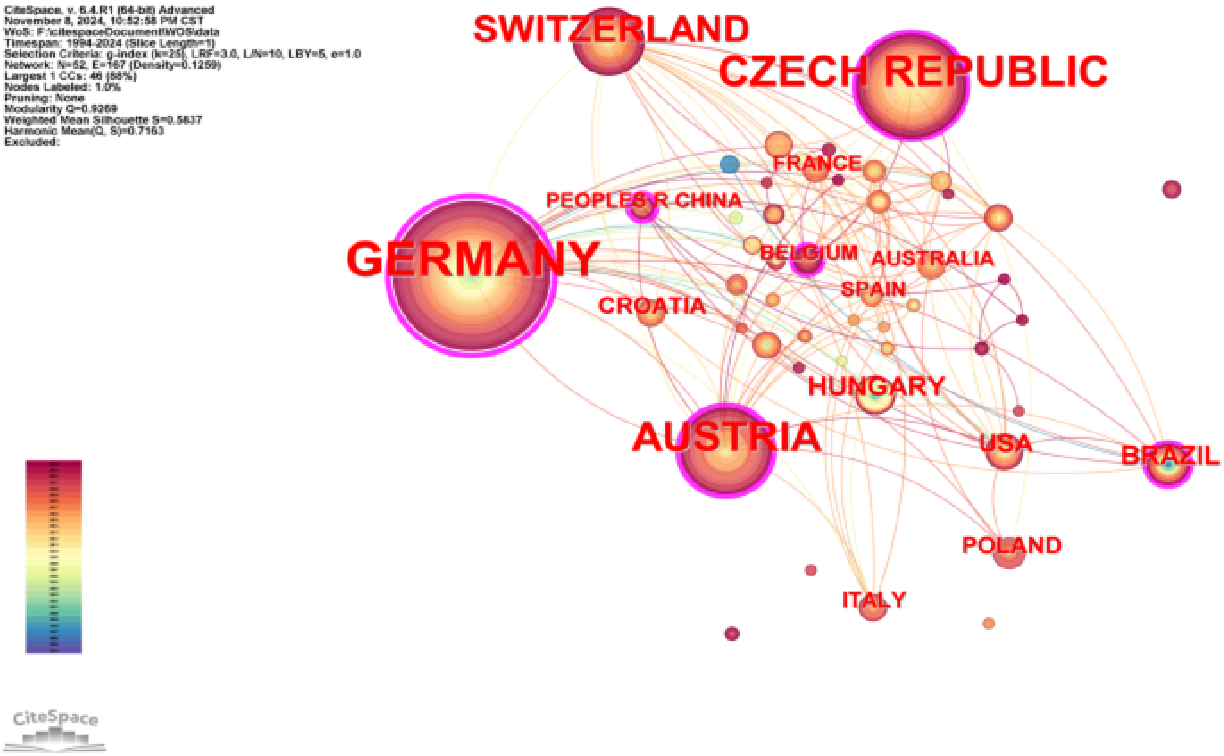
As shown in Table 1 and Table 2, the top 5 countries in terms of the publication volume are Germany (278 publications), Czech Republic (130 publications), Austria (117 publications), Switzerland (64 publications), and Brazil (18 publications). In terms of the centrality, the top 5 countries are Germany (0.1), China (0.1), Austria (0.07), Czech Republic (0.07), and Belgium (0.05).

The author network (N = 714, E = 1 421; Figure 4) demonstrated: the top 5 authors in terms of the publication volume are Distl, O (22 publications), Pausch, H (17 publications), Egger-Danner, C (16 publications), Fries, R (16 publications), and Emmerling, R (15 publications), as well as Fuerst-Waltl, B (15 publications). The top 5 authors in terms of the centrality are Steinwidder, A (0.11), Gredler, B (0.11), Baumung, R (0.1), Emmerling, R (0.09), and Fuerst-Waltl, B (0.09). Notably, the centrality of the top 10 authors is above 0.01.

Co-citation analysis of references

In academic research, co-citation analysis serves as a significant methodological approach. This technique examines how two or more references are cited together in subsequent publications, revealing conceptual relationships between papers and their influence within scholarly discourse. Co-citation frequency and centrality constitute key metrics for assessing a reference impact, reflecting their academic prominence and network roles.

Through systematic organisation of co-citation frequencies and centrality scores from retrieved references, this study constructed a co-citation



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Timespan: 1994-2024 (Slice Length=1)
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Network: N=52, E=167 (Density=0.1259)
Largest 1 CCs: 46 (88%)
Nodes Labeled: 1.0%
Pruning: None
Modularity Q=0.9269
Weighted Mean Silhouette S=0.5837
Harmonic Mean(Q, S)=0.7163
Excluded:
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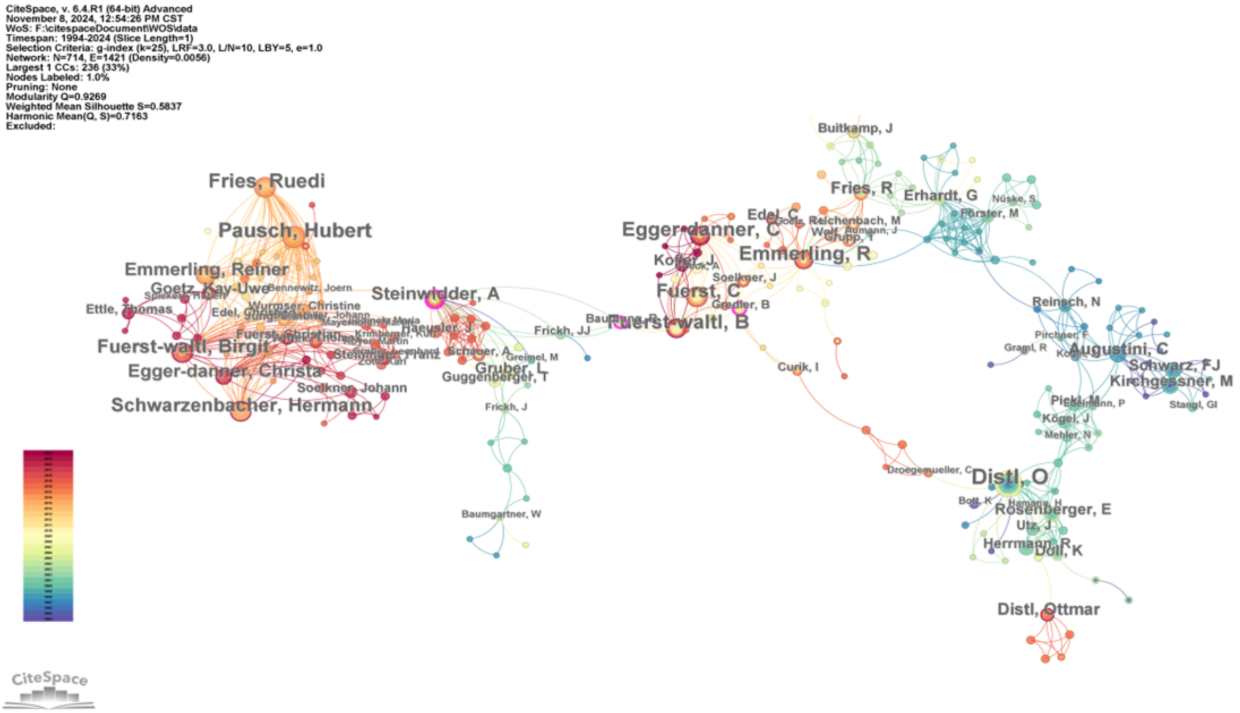
Figure 3. National cooperative atlas of Fleckvieh hybrid breeding research



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WoS: F:\citespaceDocument\WOS\data
Timespan: 1994-2024 (Slice Length=1)
Selection Criteria: g-index (k=25), LRF=3.0, L/N=10, LBY=5, e=1.0
Network: N=714, E=1421 (Density=0.0056)
Largest 1 CCs: 236 (33%)
Nodes Labeled: 1.0%
Pruning: None
Modularity Q=0.9269
Weighted Mean Silhouette S=0.5837
Harmonic Mean(Q, S)=0.7163
Excluded:
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Figure 4. The author cooperative atlas of Fleckvieh hybrid breeding research

network. This enabled the identification of key academic nodes and research hotspots. Detailed results are presented in Table 3 and Table 4.

The study employed the g-index mechanism (k = 25) to curate publications and construct a co-citation network (N = 947 nodes, E = 2 346 links)

Table 3. Co-citation frequency of reference literature

Rank	Number	Author	Published year	Reference	Journal
1	16	Daetwyler, HD et al.	2014	Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle	*Nature Genetics*
2	14	Jansen, S et al.	2013	Assessment of the genomic variation in a cattle population by re-sequencing of key animals at low to medium coverage	*BMC Genomics*
3	13	Pausch, H et al.	2013	Imputation of high-density genotypes in the Fleckvieh cattle population	*Genetics Selection Evolution*
4	10	Pausch, H et al.	2014	A nonsense mutation in tmem95 encoding a nondescript transmembrane protein causes idiopathic male subfertility in cattle	*PLOS Genetics*
5	9	Pausch, H et al.	2011	Genome-wide association study identifies two major loci affecting calving ease and growth-related traits in cattle	*Genetics*

Table 4. Top 5 central references

Rank	Centrality	Author	Published year	Reference	Journal
1	0.02	Jansen, S	2013	Assessment of the genomic variation in a cattle population by re-sequencing of key animals at low to medium coverage	*BMC Genomics*
2	0.01	Daetwyler, HD	2014	Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle	*Nature Genetics*
3	0.01	Jung, S	2014	A nonsense mutation in PLD4 is associated with a zinc deficiency-like syndrome in Fleckvieh cattle	*BMC Genomics*
4	0.01	Pausch, H	2011	Genome-wide association study identifies two major loci affecting calving ease and growth-related traits in cattle	*Genetics*
5	0.01	Ledinek, M	2019	Analysis of lactating cows in commercial Austrian dairy farms: diet composition, and influence of genotype, parity and stage of lactation on nutrient intake, body weight and body condition score	*Italian Journal of Animal Science*

as shown in Figure 5. According to Tables 3 and 4, the top 5 most co-cited references were authored by "Daetwyler, HD et al.", "Jansen, S et al.", and "Pausch, H et al." Specifically, the reference ranked first had 16 citations, the second had 14 citations, and the third, fourth, and fifth references (all first-authored by Pausch, H) collectively had 32 citations.

In terms of the centrality, the top 5 references were authored by Jansen, S (0.02), Daetwyler, HD (0.01), Jung, S (0.01), Pausch, H (0.01), and Ledinek, M (0.01).

Co-occurrence and cluster analysis of keywords

By analysing the cluster map of research hotspots in breeding, particularly as shown in Figure 6, it is evident that the top-ranked keyword is "Fleckvieh cattle" (#2), indicating that breeding of Fleckvieh cattle is a significant research direction in this field. This is tied to the genetic characteristics and production performance of Fleckvieh cattle as an important beef breed. The second-ranked keyword is "meat quality" (#0), which highlights that meat quality

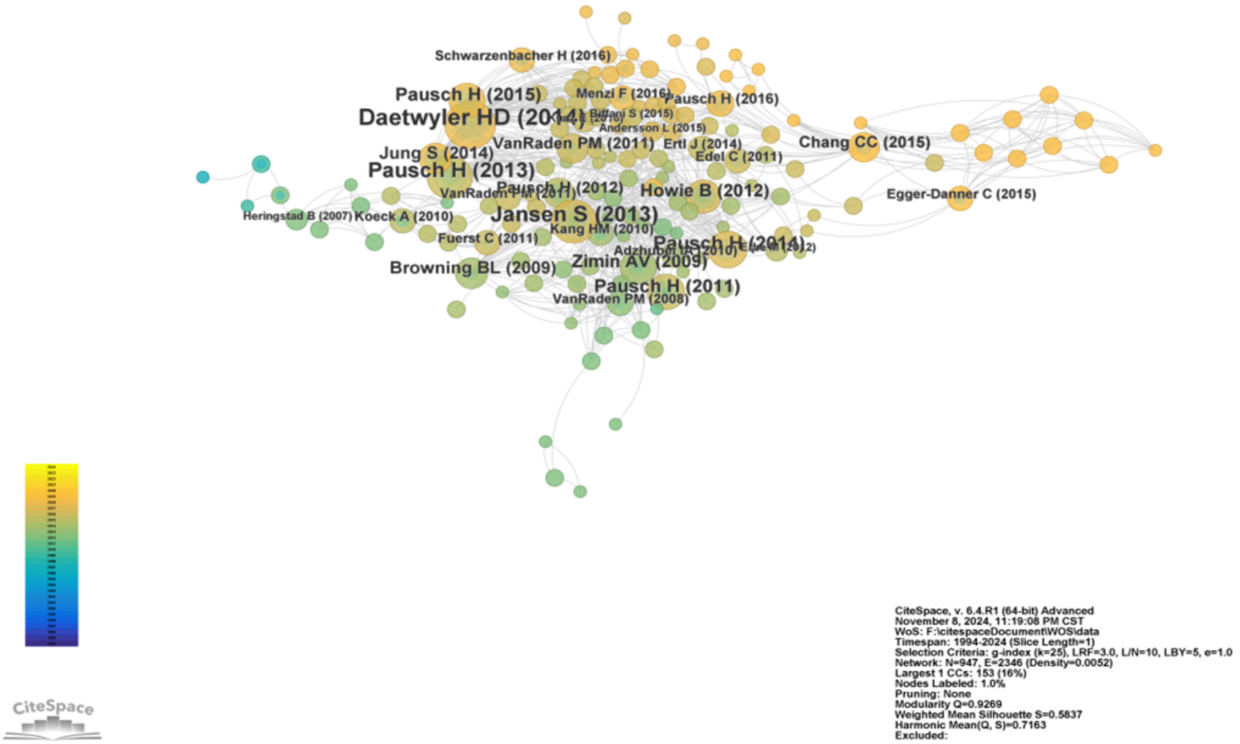

Figure 5. Frequency mapping of cited literature in Fleckvieh hybrid breeding studies

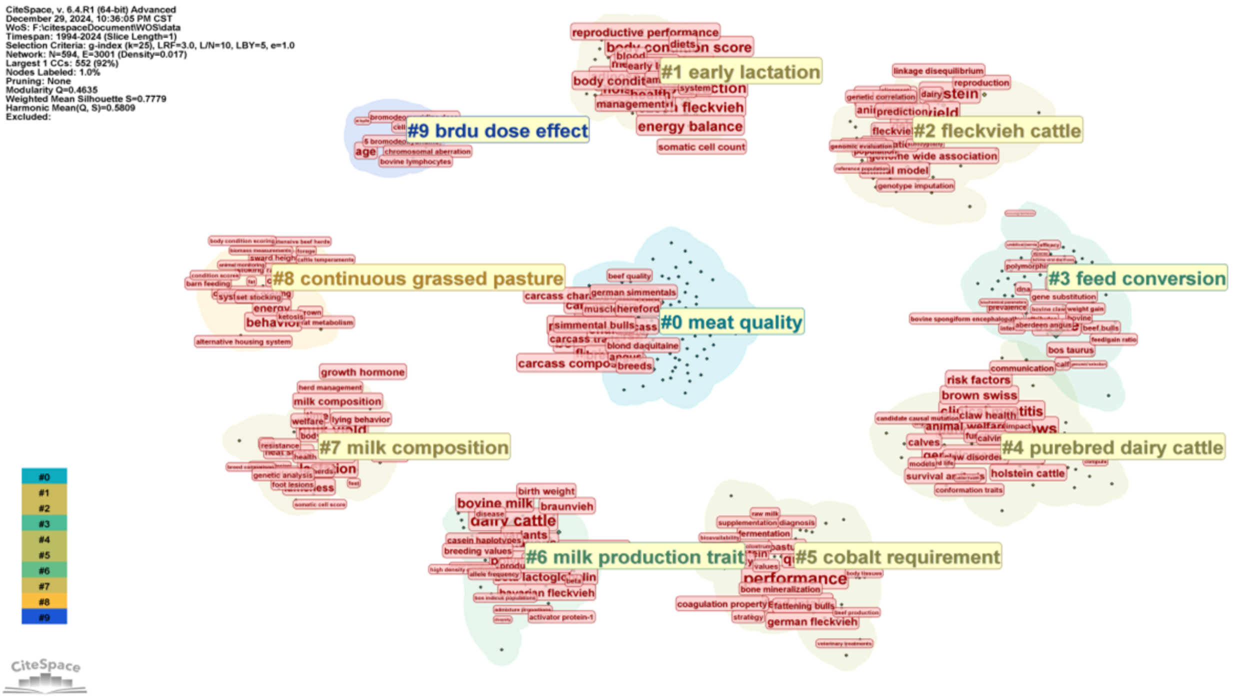

Figure 6. Keyword cluster map for the Fleckvieh breeding study

is a key research topic in this field. This is associated with the demand for high-quality meat from consumers and the competition in the meat market. The third-ranked keyword is "milk composition" (#7), reflecting the importance of milk composition analysis in this field, which is closely related to the nutritional value of dairy products and consumer health needs.

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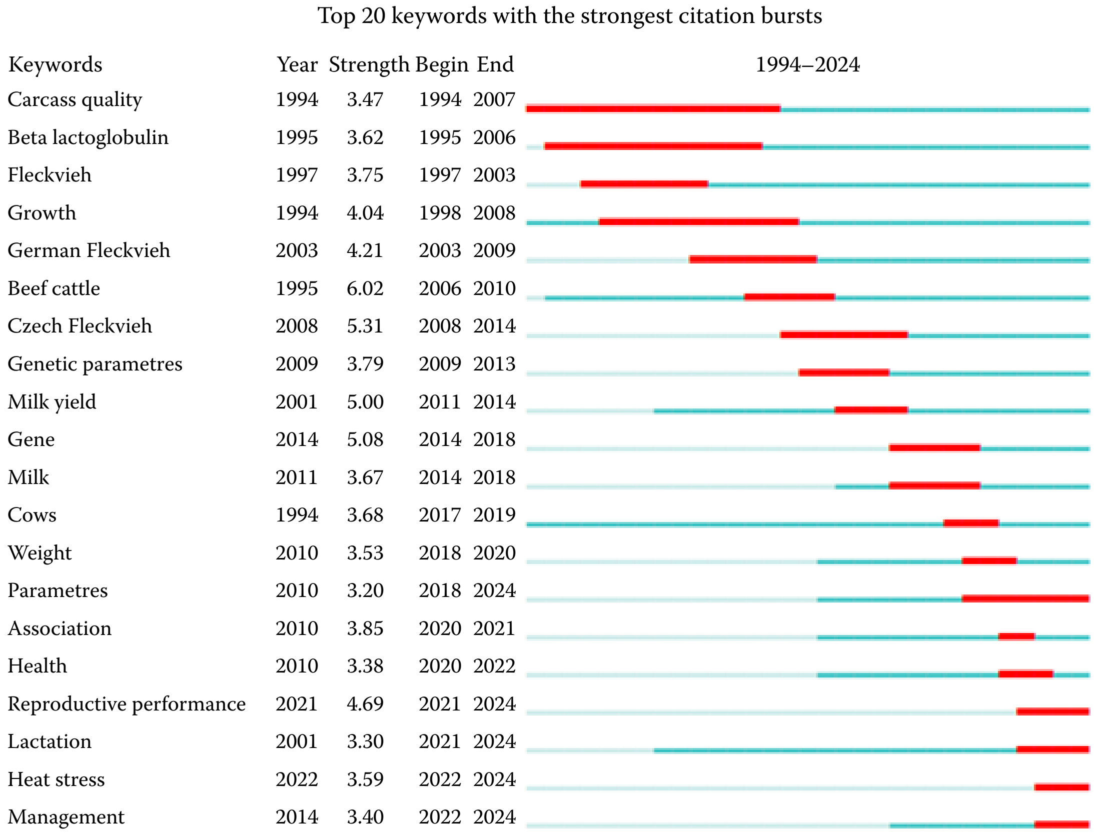
The core keywords in the study include “purebred dairy cattle” (#4), “cobalt requirement” (#8), and “continuous grazing” (#3). This indicates that research in this area pays more attention to dairy cattle genetics, nutritional requirements, and sustainable grazing practices.

The depth and diversity of research on these core keywords are greater for several reasons. Research on dairy cattle genetics helps improve the production efficiency and health of dairy cows. Nutritional requirement studies are crucial for ensuring the health of dairy cows and the quality of dairy products. Research on sustainable grazing practices contributes to the sustainable development of animal husbandry.

For research on “Fleckvieh cattle”, the reasons may include improving the production efficiency of beef cattle, enhancing meat quality, and meeting the market demand for high-quality meat products. Research on “meat quality” may be related to improving the market competitiveness of meat products, meeting the consumer demand for high-quality meat, and increasing the economic benefits of animal husbandry. Research on “milk composition” may be associated with developing healthier dairy products, meeting the consumer demand for nutrition and health, and enhancing the sustainability of dairy farming. The depth of these cluster studies is reflected in the in-depth exploration of specific genetic characteristics of cattle breeds, meat quality evaluation methods, and milk composition analysis. The diversity of research is demonstrated by the wide range of fields covered from genetics and nutrition to sustainable agricultural practices. These fields of research are interwoven and collectively drive progress in the field of animal husbandry. Through this analysis, we can see the focus and trends of research in the field of animal husbandry, as well as how these studies are combined with market demand, animal health, and sustainable development goals.

Analysis of research frontiers

The CiteSpace analysis of keyword bursts identified the 20 most prominent emergent terms (Figure 7). Notably, multiple terms exhibited concentrated burst activity between 2010 and 2024.



Top 20 keywords with the strongest citation bursts

Keywords	Year	Strength	Begin	End
Carcass quality	1994	3.47	1994	2007
Beta lactoglobulin	1995	3.62	1995	2006
Fleckvieh	1997	3.75	1997	2003
Growth	1994	4.04	1998	2008
German Fleckvieh	2003	4.21	2003	2009
Beef cattle	1995	6.02	2006	2010
Czech Fleckvieh	2008	5.31	2008	2014
Genetic parametres	2009	3.79	2009	2013
Milk yield	2001	5.00	2011	2014
Gene	2014	5.08	2014	2018
Milk	2011	3.67	2014	2018
Cows	1994	3.68	2017	2019
Weight	2010	3.53	2018	2020
Parametres	2010	3.20	2018	2024
Association	2010	3.85	2020	2021
Health	2010	3.38	2020	2022
Reproductive performance	2021	4.69	2021	2024
Lactation	2001	3.30	2021	2024
Heat stress	2022	3.59	2022	2024
Management	2014	3.40	2022	2024

Figure 7. Ranking map of burst keywords in Fleckvieh breeding research (1994–2024)

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The term beef cattle demonstrated the highest burst intensity (strength = 6.02) during its active period from 1995 to 2010. Recent surges (the last 3–5 years) featured reproductive performance (2021–2024; strength = 4.69), lactation (2021–2024; strength = 3.30), and heat stress (2022–2024; strength = 3.59) as dominant terms.

This temporal pattern reveals evolving research priorities in Fleckvieh breeding studies. The sustained prominence of beef cattle during the late 20th century likely corresponds to the development of foundational breeding programmes. Contemporary shifts towards reproductive performance and heat stress management align with emerging challenges posed by climate change and sustainability imperatives in modern livestock production. The focus on lactation parameters further underscores growing emphasis on dairy-beef dual-purpose optimisation within breeding strategies.

DISCUSSION

Discussion on scientific collaboration networks

Analysis of international collaboration networks. The breeding of Fleckvieh cattle originated in southern Germany, Austria, and in the Czech Republic. The genetic evaluation of German Simmental (Fleckvieh) cattle is jointly conducted by three relatively independent institutions in Germany and Austria. Analysis of the global distribution of research activity in Fleckvieh breeding reveals a highly imbalanced pattern. Among the top 10 countries by publication volume, eight are European, one is North American, and one is South American. European countries dominate the research landscape, accounting for 82% of total publications. Germany notably demonstrates the highest publication volume and centrality, indicating close international collaboration, high research quality, and predominant academic influence.

As the birthplace of Fleckvieh cattle, Germany maintains a long-standing breeding tradition supported by well-established systems. The breed emerged from crosses between Swiss Simmental and German Red Holstein cattle, with subsequent genetic contributions from other lineages. Located in Central Europe, Germany benefits from abundant agricultural resources and favourable climatic conditions, providing an optimal environment for Fleckvieh breeding programmes. In 2024, German scholars published 13 papers, including four studies on genetics and breeding addressing genetic disorders (Reinartz et al. 2023; Solzer et al. 2024), evaluation methodologies (Pimentel et al. 2024), and resilience traits (Keßler et al. 2024), three papers on nutrition and management covering feed efficiency biomarkers (Haak et al. 2024), milk composition, and virtual fencing applications (Hamidi et al. 2024), four health-related investigations examining post-slaughter behaviour (Lucking et al. 2024), hoof pathology management (Kofler et al. 2024), gastrointestinal diseases (Huber et al. 2024), and pathogen genomics (Barta et al. 2024); alongside contributions to food safety protocols (Bischof et al. 2024), and physiological markers in calves (Landinger et al. 2024).

Among the top 10 countries in publication volume, four are developing countries, reflecting widespread interest and investment in this field across different economic levels. The research capabilities of developing countries are gradually strengthening, forming a certain competitive posture with developed countries. Brazil, the only developing country and non-European country in the top five in terms of the publication volume, benefits from its vast grassland areas and abundant natural resources, including water (Fereira et al. 2024). This is also related to the country's development strategy of "agriculture-based nation building" (Sparovek et al. 2010). However, in 2024, the research topics published by developing countries were relatively limited. After screening with $k = 25$, the papers focused on three main areas: dairy cow nutrition and calf health development (Kappes et al. 2024), reproductive management and pregnancy loss (Abdalla et al. 2024), and the application of antioxidants in animal reproduction (Gongora-Bardales et al. 2024). This suggests that developing countries have fewer studies on animal welfare, food safety, and disease prevention, areas that may require further strengthening.

Analysis of institutional and author collaboration networks. The top 10 institutions in terms of the publication volume in the field of Fleckvieh breeding are primarily located in Germany, Czech Republic, and Austria, which aligns with the findings from the international collaboration map. These countries exhibit high publication frequencies, indicating their active involvement and in-depth research in the field.

Institutions in Germany, like Technical University of Munich and University of Munich, stand out in both publication volume and centrality, highlighting Germany's leading role in this area. High centrality of these institutions indicates that their research on Fleckvieh cattle breeding, hybrid vigour utilisation, and dual-purpose performance has a significant influence and authority, guiding global research directions and practical applications.

Although the Czech Research Institute of Animal Science and Mendel University in Brno do not have the highest publication volumes, their strong centrality rankings reveal their important positions and influence in animal science research. These institutions focus on specific research areas such as animal genetics and reproductive biology, with their findings highly cited and valued in the field.

The density of the institutional collaboration map (density = 0.012 8) is an order of magnitude lower than that of the international collaboration map (density = 0.125 9), indicating that the level of collaboration among institutions is lower than that among countries. This suggests a need for stronger collaborative ties between institutions. The Bavarian Cattle Breeding Association (BVN) in Germany has played a crucial role in the breeding and promotion of Fleckvieh cattle, both domestically and internationally. For example, it has established bull stations in countries like Romania and Croatia to provide artificial insemination services. This transnational cooperation highlights the importance of close institutional collaboration and the necessity of sharing resources, technology, and experience to enhance breeding efficiency and quality.

Professors Steinwidder, A from Austria and Gredler, B from Switzerland are both highly productive and central authors. However, the most prolific author is Professor Distl, O from the Institute of Animal Breeding and Genetics at the University of Veterinary Medicine Hannover in Germany, whose centrality is relatively lower. This may be related to the duration of the author's research career but also it underscores the importance of balancing article quantity with collaboration among authors.

Discussion on co-citation analysis of references

Highly cited references form the foundation of a research field. The analysis reveals that the publication years of highly cited references are relatively concentrated between 2011 and 2014 (Idamokoro 2023). The most cited reference is the article "Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle" by Daetwyler, HD et al., published in *Nature Genetics* in 2014 (Daetwyler et al. 2014). This indicates its significant impact in the field. The reference with the highest centrality is "Assessment of the genomic variation in a cattle population by re-sequencing of key animals at low to medium coverage" by Jansen, S et al., published in *BMC Genomics* in 2013, suggesting that this paper is the most authoritative in the field (Jansen et al. 2013).

Additionally, the analysis shows that the top 10 journals in terms of the publication frequency include *Nature Genetics* and *BMC Genomics*, which are the most frequently cited. This highlights the authority of these two journals in the field of cattle reproduction and breeding.

Discussion on research hotspots

Keywords serve as distilled representations of the core theme of a study. Through the cluster analysis of keyword co-occurrence patterns, 12 distinct research hotspots have been delineated within this domain (Table 5). These clusters, derived from semantic linkages in the keyword network, map the conceptual architecture of the current scholarly inquiry.

They include: meat quality, early lactation, Fleckvieh cattle, feed conversion, purebred dairy cattle, cobalt requirement, milk production trait, milk composition, continuous grazing, bromodeoxyuridine (BrdU) dose effect, beef trait, and restricted milk feeding. The following analysis focuses on the top four cluster themes in terms of the keyword frequency: meat quality, early lactation protein, formation of the Fleckvieh breed and genetic mutations, and feed conversion rate.

Meat quality. The key research terms for this theme are beef cattle, growth, meat quality, beef, and bull. Analysis of the relevant literature shows that research on meat quality has gone through five main stages:

(*i*) Hormone Regulation Mechanism Research Stage (1994): The initial studies focused on the changes in plasma concentrations of key hormones during cattle growth, such as growth hor-

Table 5. Major research themes in Fleckvieh breeding based on a keyword analysis

Rank	Label (silhouette value)	Main keywords	Number
0	meat quality (0.779)	beef cattle	33
		growth	25
		meat quality	20
		beef	14
		bulls	11
1	early lactation (0.666)	dairy cows	71
		milk production	36
		Czech Fleckvieh	24
		fertility	22
		energy balance	21
2	Fleckvieh cattle (0.796)	holstein	32
		yield	31
		selection	20
		gene	11
		accuracy	9
3	feed conversion (0.788)	cattle	130
		Bos taurus	5
		calf	5
		prevalence	2
		attributes	2
4	purebred dairy cattle (0.8)	cows	33
		clinical mastitis	20
		parameters	18
		milk	17
		genetic parameters	13
5	cobalt requirement (0.688)	performance	62
		quality	20
		protein	9
		feed intake	8
		German Fleckvieh	8
6	milk production trait (0.873)	dairy cattle	76
		bovine milk	15
		associations	13
		polymorphism	10
		variants	9
7	milk composition (0.788)	traits	35
		milk yield	35
		lactation	17
		heat stress	6
		lameness	6
8	continuous grassed pasture (0.939)	behaviour	14
		energy	6
		components	4
		continuous grazing	3
		systems	2
9	bromodeoxyuridine (BrdU) dose effect (0.977)	age	7
		bromodeoxyuridine dose	1
		cells	1
		artificial insemination (AI) bulls	1
		5 bromodeoxyuridine	1
10	beef trait (0.995)	beef traits	2
		artificial insemination (AI)	1
		field test	1
		dual purpose cattle	1
11	restricted milk (0.991)	organic farming	2
		automatic milking	2
		ad libitum milk	1
		artificially rearing	1

mone (GH), insulin-like growth factor-1 (IGF-1), insulin, and glucagon. These hormones were found to exhibit different trends under different genders and nutritional levels. This stage of research laid the foundation for understanding the regulatory mechanisms of growth hormones in relation to cattle growth performance, revealed the important role of hormones in cattle growth and development, and provided important biological background knowledge for subsequent studies.

(*ii*) Breed Improvement and Nutritional Supplementation Research Stage (1998): As the exploration of factors affecting cattle growth performance deepened, research began to focus on the impact of breed differences and nutritional supplementation on meat quality. On the one hand, by comparing the carcass characteristics of different crossbred cattle, such as carcass weight, dressing percentage, and fat content, significant differences were found between breeds. This provided important references for breed improvement and guided breeding efforts towards higher meat quality. On the other hand, the impact of vitamin E on beef cattle growth performance and meat quality was explored.

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Although it was found that high doses of vitamin E had no significant effect on beef cattle growth performance and meat quality, this study provided a scientific basis for nutritional supplementation in beef cattle, clarified the role and dosage limits of vitamin E in beef cattle nutrition, and avoided resource waste caused by blind supplementation (Schwarz et al. 1998; Voriskova et al. 1998).

(*iii*) Breeding Value Assessment and Meat Quality Research Stage (2010): In the 21st century, research began to focus on the impact of breeding values of beef sires on the high-value carcass parts of their offspring. The correlation between breeding values and specific meat quality parts was found to be weak, indicating that breeding should not rely solely on breeding values but also other factors should be considered such as nutrition and environment to comprehensively improve meat quality. This stage of research promoted the refinement of breeding work and encouraged researchers to pay more attention to the comprehensive consideration of multiple factors during breeding (Bouska et al. 2008).

(*iv*) Meat Quality Improvement and Health-Oriented Research Stage (2013): With increasing attention to healthy diets, research began to focus on the health attributes of meat quality. Analysis of the chemical composition and fatty acid profile of the *longissimus dorsi* muscle in Simmental cattle revealed that the fatty acid composition was not beneficial to human health due to higher levels of saturated fatty acids and a lower ratio of polyunsaturated to saturated fatty acids. This finding led researchers to investigate the impact of genetic parameters on fatty acid composition, providing a new direction for improving the meat quality through genetic improvement to develop beef cattle breeds that meet the demands for a healthy diet (Stokovic et al. 2013).

(*v*) Trace Elements and Growth Nutrition Research Stage (2023): The latest research further explored the role of trace elements in the growth of Fleckvieh cattle, such as iron, zinc, copper, and manganese. By measuring the concentration changes of these trace elements in cattle at different growth stages, data support was provided for adjusting trace element supplementation. This stage of research helps to optimise the nutritional formula for beef cattle, ensuring that they receive adequate trace elements during growth, thereby promoting healthy growth and laying a good nutritional foundation for improving the meat quality (Stokovic et al. 2013; Honig et al. 2023; Polgar et al. 2023).

Overall, research on meat quality in Fleckvieh cattle has evolved from the initial exploration of hormone regulation mechanisms to multiple aspects including breed improvement, nutritional supplementation, breeding value assessment, improvement of meat health attributes, and trace element nutrition, forming a multi-level and multi-dimensional research system. These studies are interconnected and progressive, continuously deepening the understanding of the factors affecting the growth performance and meat quality of Fleckvieh cattle. They provide strong theoretical support and practical guidance for the development of the beef cattle industry, promoting the field towards higher quality and healthier directions.

Early lactation protein. The key research terms for this theme are dairy cows, milk production, Czech Fleckvieh, fertility, and energy balance. Analysis of the relevant literature shows that research on early lactation protein has gone through five main stages:

(*i*) Early Research Stage (2008): The initial studies focused on the relationship between body condition score (BCS) changes around calving and lactation characteristics in dairy cows. It was found that cows with higher BCS before calving experienced the greatest BCS decline after calving, with BCS loss lasting up to 3 months. Additionally, the breeding value of the sire's net daily gain had a negative impact on the daughter's milk yield. When RBV NG ≤ 89, the daughter's fat-protein corrected milk yield could decrease by up to 279.12 kg. This stage of research laid the foundation for understanding the energy balance and BCS changes in early lactation, revealing the dynamic changes of energy and nutrients in cows during early lactation and their impact on lactation performance (Bouska et al. 2008).

(*ii*) Metabolism and Disease Association Research Stage (2012–2020): As research deepened, attention turned to the relationship between the metabolic status and diseases in early lactation. A 2012 study found that postpartum weight changes were closely related to reproductive performance, especially in Holstein cows, where weight changes could serve as an indicator of reproductive issues (Rehak et al. 2012). A 2020 study explored the relationship between lameness events and infrared-predicted biomarkers in milk, finding a certain link between lameness and metabolic disorders, with metabolic problems having a greater long-term impact on hoof and leg health in the early stages of lactation (Month 1 and Month 3). These studies further revealed the complex metabolic processes in cows during early lactation and their impact on health, providing new ideas for the prevention and control of related diseases (Mineur et al. 2020).

(*iii*) Comprehensive Assessment and Genetic Improvement Stage (2019–2021): In recent years, research has begun to consider multiple aspects of dairy cows, including production efficiency, health, and reproductive performance. A 2019 study pointed out that high-efficiency cows mobilise more body fat reserves for milk production during early lactation, leading to a longer duration of negative energy balance, and high-yielding groups require a higher concentrate ratio in the later stages of lactation to restore the body condition (Ledinek et al. 2019). A 2021 study assessed the impact of lameness on the reproductive performance of Fleckvieh cows, finding that lameness significantly extended the time from calving to breeding and from calving to conception. These studies indicate that in dairy cow breeding and management, efficiency needs to be more comprehensively defined, considering parameters such as BCS, health, and reproductive traits, to achieve sustainable improvement in dairy cow performance (Furst-Waltl et al. 2021).

Overall, research on early lactation protein in Fleckvieh cows has evolved from the initial study of the relationship between BCS changes and lactation characteristics to multiple aspects, including metabolism and disease association, comprehensive assessment, and genetic improvement, forming a multilevel and multidimensional research system.

These studies are interconnected and progressive, continuously deepening the understanding of physiological changes and their influencing factors during early lactation in dairy cows. They provide strong theoretical support and practical guidance for improving the production efficiency, health status, and reproductive performance of dairy cows, promoting the development of the dairy industry.

Genomic research on Fleckvieh cattle. The key research terms for this theme are Holstein, yield, selection gene, accuracy, and dairy cows. Analysis of the relevant literature shows that the research on meat quality has gone through three main stages:

(*i*) Early Research Stage (2014): The starting point of genomic research on Fleckvieh cattle was the gene localisation and functional study of specific genetic diseases. That year, a key study found a new recessive genetic disease in Fleckvieh cattle caused by a nonsense mutation (p.W215X) in the *PLD4* gene, which led to an impaired function of the encoded protein and thus affected the health of the cattle. This finding not only laid the foundation for understanding the genetic disease mechanisms in Fleckvieh cattle but also provided important genetic information for subsequent genomic research, pointing out the direction for future studies (Jung et al. 2014).

(*ii*) Genome-Wide Association Study Stage (2016–2018): With the rapid development of genomic technologies, research began to use methods such as genome-wide association studies (GWAS) to locate genes related to important traits like production performance and disease resistance in Fleckvieh cattle. In 2016, researchers developed a simple procedure to identify ancestral haplotypes shared among different cattle breeds, detecting common genomic regions associated with traits such as coat colour, milk protein, and fat content. This provided clues for understanding the genetic relationships between Fleckvieh and other cattle breeds. Subsequently, in 2018, through GWAS and meta-analysis, researchers identified multiple quantitative trait loci (QTL) related to milk yield, milk fat and protein content, fertility, and stature, and confirmed some known causal variants. These studies greatly enriched the genomic data resources of Fleckvieh cattle, providing important candidate genes and loci for subsequent gene function research and genetic improvement, and promoting the development of Fleckvieh cattle genomics to a higher level (Marete et al. 2018).

(*iii*) Genomic Prediction and Application Stage (2014–2017): Based on genome-wide association studies, research began to focus on how to apply genomic research findings to the breeding practice of Fleckvieh cattle. In 2014, a study compared the reliability of medium-density (50 K) and high-density (HD) marker sets in genomic prediction, finding that the HD marker set had significant advantages in improving prediction accuracy and reducing prediction inflation. This provided a basis for enhancing the accuracy of genomic prediction (Pausch et al. 2017). In 2017, researchers combined genotype data with whole-genome sequencing data to construct a large mapping population, further improving the accuracy of QTL localisation and providing possibilities for identifying causal mutations. These studies promoted the application of modern breeding technologies such as genomic selection in Fleckvieh cattle, helping to improve breeding efficiency and accuracy, and making the breeding work of Fleckvieh cattle more scientific and accurate (Ertl et al. 2014).

Overall, research on genomics related to Fleckvieh cattle has evolved from the initial genetic disease gene localisation in 2014, to genome-wide association studies from 2016 to 2018, and then to genomic prediction and application research from 2014 to 2017, forming a progressive and interconnected research system. These studies promote each other and provide mutual support, continuously deepening the understanding of the genomic structure and function of Fleckvieh cattle. They provide strong theoretical support and practical guidance for the genetic improvement and enhancement of the production performance of Fleckvieh cattle. The early genetic disease gene localisation studies laid the foundation for subsequent genome-wide association studies, which in turn provided a high number of candidate genes and loci for genomic prediction and application research. Genomic prediction and application research then transformed genomic research findings into actual breeding benefits, promoting the modernisation and accuracy development of Fleckvieh cattle breeding work. This has greatly enhanced the production performance and market competitiveness of Fleckvieh cattle, making an important contribution to the development of the field.

Feed conversion rate. The key research terms for this theme are cows, clinical mastitis, parameters, milk, and genetic parameters. Analysis of the relevant literature shows that the research on feed conversion rate (FCR) in Fleckvieh cattle has gone through three main stages:

(*i*) Early Research Stage (1996–1997): The initial studies mainly focused on the relationship between the genetic background and production performance of Fleckvieh cattle. A 1996 study explored whether there was any association between the major histocompatibility complex (BoLA) class I alleles and carcass traits or reproductive performance in Fleckvieh cattle, finding that the BoLA-A region had no effect on the assessed traits (Arriens et al. 1996). In 1997, a study compared daily weight gain, carcass weight gain, dry matter and organic matter intake, and feed conversion rate between different genetic groups, including Fleckvieh cattle. It was found that there were no differences in feed conversion rate between the groups, but slaughter weight had an impact on daily weight gain and carcass weight gain (Jorge et al. 1997). These studies provided basic data for understanding the genetic characteristics and production performance of Fleckvieh cattle and laid the foundation for subsequent research on feed conversion rate.

(*ii*) Genomics and Feed Conversion Rate Research Stage (2001): In 2001, a study approached, from a genomic perspective, sequencing and comparing the T cell receptor alpha/delta joining gene region (TCRADJ) in cattle. It found certain sequence similarities among different species and detected multiple variant sites in Fleckvieh cattle (Fries et al. 2001). This study provided important genetic information for exploring the impact of genetic variations on production performance, such as feed conversion rate, and promoted the application of genomics in feed conversion rate research.

(*iii*) Disease and Production Performance Association Research Stage (2003–2020): As research delved deeper into the factors affecting production performance in Fleckvieh cattle, attention turned to the impact of diseases on feed conversion rate. A 2003 study assessed the impact of scabies on Fleckvieh cattle, finding that the feed conversion efficiency of infected groups was significantly lower than that of non-infected groups, but it improved after treatment (Rehbein et al. 2003). In 2020, a study investigated the prevalence of tick-borne diseases in cattle in a region of Algeria. Although the focus was on the diseases themselves, the epidemic had a potential negative impact on the overall health and production performance of cattle, including the feed conversion rate (Ziam et al. 2020). These studies revealed the adverse effects of diseases on production performance in Fleckvieh cattle and emphasized the importance of disease prevention and control in improving the feed conversion rate.

Overall, research on feed conversion rate in Fleckvieh cattle has evolved from the initial study of the relationship between genetic background and production performance to the association between diseases and production performance, and then to the integration of genomics and feed conversion rate research, forming a multilayered and multidimensional research system. These studies are interconnected and progressive, continuously deepening the understanding of factors affecting the feed conversion rate in Fleckvieh cattle. They provide strong theoretical support and practical guidance for improving production efficiency and breeding benefits in Fleckvieh cattle, promoting the development of the field.

Discussion on research frontiers and trends

The analysis of citation bursts across 20 keywords in Fleckvieh breeding research (1994–2024) reveals distinct phases of scholarly focus. Citation bursts denote periods of intensified academic attention to specific themes.

Early Research Stage (1994–2007): "Carcass quality" began to attract attention in 1994, with the burst lasting until 2007, suggesting that early research may have focused on the meat quality characteristics of Fleckvieh cattle. "Beta lactoglobulin" had a citation burst from 1995 to 2006, related to studies on milk composition. The term "Fleckvieh" itself experienced a citation burst from 1997 to 2003, reflecting an increase in research on the breed characteristics.

Mid-Stage Research (2003–2014): "Growth" and "Czech Fleckvieh" had citation bursts from 2003 to 2009, associated with studies on the growth performance and characteristics of specific breeds. "Genetic parameters" had a citation burst from 2009 to 2013, indicating a shift in focus towards the application of genetics in breeding. "Milk yield" and "milk" had citation bursts from 2011 to 2018, highlighting in-depth research on the milk production performance of Fleckvieh cattle.

Recent Research (2017–2024): "Reproductive performance" had a citation burst from 2021 to 2024, pointing to recent attention to the reproductive capabilities of Fleckvieh cattle. "Heat stress" and "management" had citation bursts from 2022 to 2024, reflecting research interest in how environmental factors and management practices affect the performance of Fleckvieh cattle. "Parameters" and "association" had citation bursts in 2018 and 2020, respectively, related to advancements in statistical methods and genetic association studies.

The discussion on research frontiers and trends shows that the focus has consistently been on "weight" and "health", with citation bursts in 2010 and 2020, indicating sustained attention to weight management and health issues in Fleckvieh cattle. Overall, the frontiers and trends in Fleckvieh breeding research have evolved from basic breed characteristics and growth performance to a more integrated study of genetics, reproductive performance, environmental adaptability, and management practices. This reflects the development of breeding science and the ongoing pursuit of improving the production efficiency and adaptability of Fleckvieh cattle. Over time, researchers have increasingly focused on how genetic improvement and optimised management can enhance the overall performance and adaptability of Fleckvieh cattle.

Based on the research frontiers and trends, the key areas of focus and frontiers in Fleckvieh breeding research over the next five years may include:

(*i*) Application of Genetics and Genomics: Given the citation bursts of "genetic parameters" and "association", future research is likely to further explore the application of genetics in breeding, including genomic selection, gene editing technologies, and in-depth studies on the genetic basis of specific traits.

(*ii*) Optimisation of Reproductive Performance: The citation burst of "reproductive performance" indicates that future research may focus on improving the reproductive efficiency and offspring quality of Fleckvieh cattle, potentially including advancements in reproductive technologies, optimisation of reproductive management, and studies on the genetic and environmental factors affecting reproductive disorders.

(*iii*) Environmental Adaptability and Heat Stress Management: The citation bursts of "heat stress" and "management" highlight attention to how environmental factors affect the performance of Fleckvieh cattle. Future research may concentrate on developing new management strategies and technologies to enhance the adaptability and production performance of cattle under different environmental conditions, especially in the context of climate change.

(*iv*) Continuous Study of Weight and Growth Performance: The citation bursts of "weight" and "growth" show sustained interest in the growth performance of Fleckvieh cattle. Future research may focus on optimising growth curves, improving feed conversion rates, and studying the genetic and environmental factors that affect growth.

(*v*) Lactation Performance and Management: The persistent citation burst of "lactation" suggests that future research will continue to focus on management and performance during lactation, including optimisation of milk yield, nutritional requirements during the lactation period, and genetic improvement of lactation performance.

(*vi*) Interdisciplinary Research: With the citation bursts of "management" and "association", future research is likely to place greater emphasis on interdisciplinary approaches, integrating knowledge from animal science, genetics, environmental science, and data science to achieve a comprehensive understanding and improvement of Fleckvieh cattle breeding.

CONCLUSIONS

This study employs the CiteSpace knowledge graph analysis to systematically map research trajectories in Fleckvieh breeding, yielding three principal findings:

(*i*) Research Priorities have transitioned from phenotypic trait analysis to integrative approaches combining genomics, environmental adaptation, and precision management. Six emergent frontiers are identified, emphasising genetic innovation and interdisciplinary synergy.

(*ii*) Geographical Leadership remains concentrated in Central Europe, with German, Czech, Austrian, and Swiss institutions – notably the Technical University of Munich and the University of Natural Resources and Life Sciences, Vienna – demonstrating the sustained academic influence through high publication output and collaborative centrality.

(*iii*) Methodological Contribution – knowledge graph visualisation proves instrumental in elucidating research patterns, offering strategic insights for breeding optimisation and cross- disciplinary collaboration.

In summary, Fleckvieh breeding research is advancing towards multidimensional, globally networked paradigms. This analytical approach provides novel conceptual tools to navigate evolving challenges in sustainable livestock production.

Conflict of interest

The authors declare no conflict of interest.

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