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ARAŞTIRMA MAKALESİ **RESEARCH ARTICLE**

Bibliometric analysis of quantitative genetics research in animal science in the last decade

Son on yılda hayvan bilimlerinde kantitatif genetik araştırmalarının bibliyometrik analizi

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ABSTRACT

This study aimed to analyse the articles published with Clarivate Analytics' Web of Science (WoS) in quantitative genetics in animal science with the bibliometric method, which can be used in all disciplines. The research data consists of a total of 1281 studies published between 2012-2021, title-based from WoS. A bibliometric approach was applied to the data with a comprehensive overview of thematic focus, citation analysis, country productivity, country collaboration, conceptual structure, historically direct citation network using the "bibliometrix" function in R software. Studies were categorized using K-means clustering and multiple concordance analysis (MCA). Clusters were created on the thematic map with KeyWord Plus. The results were as follows: the Journal of Dairy science was the most active journal. The most cited countries and hence the most productive countries were Brazil and the USA. The most preferred keyword in publications was "selection". Two separate clusters were formed in the conceptual structure map, generally on "milk production" and "genetic parameters". With the KeyWord Plus analysis, the most preferred keyword in the publications was "selection". Researchers can gain a general sense of what's going on in the field based on the findings, and also the findings may even motivate researchers to collaborate in the field. It is thought that this study can present useful contributions to researchers by clearly presenting trend research hotspots and the future direction of the field with a comprehensive overview.

ÖZET

Bu çalışma, Clarivate Analytics'in Web of Science (WoS) ile hayvan biliminde kantitatif genetik alanında yayımlanan makaleleri, tüm disiplinlerde kullanımı giderek artan bibliyometrik yöntemle analiz etmeyi amaçlamaktadır. Araştırma verileri, WoS'tan başlık bazında, 2012-2021 yılları arasında yayınlanmış toplam 1281 çalışmadan oluşmaktadır. Verilere, R yazılımındaki "bibliometrix" işlevi kullanılarak tematik odak, alıntı analizi, ülke üretkenliği, ülke işbirliği, kavramsal yapı, tarihsel olarak doğrudan alıntı ağının kapsamlı bir genel bakışıyla bibliyometrik bir yaklaşım uygulanmıştır. K-means kümeleme ile çoklu uyum analizi (MCA) kantitatif genetikte yapılan çalışmalar kategorileştirilmiştir. KeyWord Plus ile tematik harita üzerinde kümeler oluşturulmuştur. Sonuçlar şu şekildedir: "Journal of Dairy Science" en aktif dergi olmuştur. En çok alıntı yapılan ülkeler ve dolayısıyla en üretken ülkeler Brezilya ve ABD'dir. MCA ile kavramsal yapı haritasında iki ayrı küme oluşmuş olup, genel olarak "süt üretimi" ve "genetik parametreler" üzerinedir. KeyWord Plus analizi ile yayınlarda en çok tercih edilen anahtar kelime "seleksiyon" olmuştur. Araştırmacılar bulgulara dayanarak alanda neler olup bittiğine dair genel bir fikir edinebilir ve hatta bulgular araştırmacıları söz konusu alanda iş birliği yapmaya bile motive ettirebilir. Bu çalışmanın, trend araştırma noktalarını ve alanın gelecekteki yönünü kapsamlı bir genel bakış ile net bir şekilde sunarak araştırmacılara yararlı katkılar sağlanması amaçlanmıştır.

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INTRODUCTION

It is getting increasingly difficult to keep track of everything published due to the rapid increase in the number of scholarly publications. Therefore, synthesizing past research findings plays an increasingly important role in effectively using the existing knowledge base and advancing a research line (Aria & Cuccurullo, 2017). In particular, academic institutions increasingly rely on and use citation analysis to make hiring, promotion, tenure and funding decisions (Franceschet, 2010). At the same time, scientific literature represents scientific activity and so, publishing scientific publications is the primary goal of the scientific community (Lundberg, 2006). For this reason, by analyzing the number of published papers and their citation frequency, bibliometrics is used to assess scientific interests, productivity, and impact. The term "bibliometrics", also known as "scientometrics", is derived from the Greek terms "biblion" and "metricus" meaning "book" and "measurement", respectively (Abubakar et al., 2021). In recent years, bibliometrics has become a standard tool for scientific policy and research methodologies.

Bibliometric analysis provides a structured analysis of a large dataset despite the overwhelming abundance of new knowledge, conceptual breakthroughs, and data. It also benefits researchers by giving the "big picture" of current research by extracting trends across time, discovering the themes under study, altering the borders of fields, and identifying the most productive scientists and organizations (Crane, 1973; Aria & Cuccurullo, 2017). The term "bibliometrics" also refers to a branch of the library and information science that investigates the growth of literature on a certain subject, the number of individual scholars, the quantity and quality of literature supplied by groups of researchers, and the relationship between institutions (Abubakar et al., 2021). The benefit of bibliometric analysis is that it may be used to develop helpful quantitative indicators of collaboration and interdisciplinary research measurements. Hence, bibliometric analysis is used in all disciplines because of the useful advantages mentioned above. Aside from these benefits, there are some drawbacks. The linear link between citation count and scientific quality is its main drawback (Ismail et al., 2012). The reason for this disadvantage is that citations from articles to articles and even from countries to countries are indicative of intellectual connections between authors and organizations that know each other (Manuelian et al., 2020). In addition, bibliometric analysis is complicated because it involves numerous phases and many different analysis and mapping software tools, which are normally only available under commercial licenses (Guler et al., 2016). In addition to disadvantages mentioned above, bibliometrics is also quite difficult for scientists who do not have general programming skills. There are many softwares for the bibliometric analysis. However, many of these do not fully assist researchers in the flow of their proposed work (Aria & Cuccurullo, 2017). Nevertheless, generally preferred software programs are CitNetExplorer, VOSviewer, SciMAT, BibExcel, Science of Science (Sci2) Tool, CiteSpace, and VantagePoint (www.thevantagepoint.com) (Chen, 2006; Persson et al., 2009; Sci2 Team, 2009; Cobo et al., 2011, 2012; Van Eck & Waltman 2010, 2014). In addition to these softwares, there is an open-source Rstudio software that provides specific analysis functions. In the Rstudio environment, the bibliometrix R-package contains a number of tools in bibliometrics and scientometry for quantitative studies. Quantitative genetics, also known as complex trait genetics, is the study of such characteristics (e.g. growth traits) and is based on a model in which multiple genes impact the trait and non-genetic factors may also play a role (Yardibi et al., 2021). These characteristics, which demonstrate a continuous distribution, have an economic value and are always the subject of research in animal breeding studies. In recent years, bibliometric analyzes have been carried out on different subjects in various branches of science. Although there was a general study in which bibliometric analysis was applied in animal science before (Hill, 2010), no study was found in the literature to examine the papers in the field of quantitative genetic theory, which is the basis for animal breeding with bibliometric analysis.

The major goal of this study was to analyze the structure, current status, and future directions of quantitative genetic research in the animal science literature by appliying a bibliometric approach. Using mathematical and statistical methods, this study aimed to provide a quantitative and qualitative analysis of the relevant literature, which can provide an overview of quantitative genetics and help to grasp research boundaries for future developments. For this aim, this work used bibliometric analysis to evaluate quantitative genetics research in animal sciences over the last ten years with Rstudio software.

MATERIALS and METHODS

Data

Using the CAB Abstracts thesaurus database, close and relevant terms related to the word "quantitative genetics" were included to adequately characterize the records.

Keywords used with the help of CAB Abstracts thesaurus database were: "quantitative genetics" OR "quantitative traits" OR "estimated genetic parameters" OR "animal breeding" OR "breeding value" OR "predicted breeding value" OR "breeding value estimation" OR "genotype-by-environment interactions" OR "phenotypic variation" OR "genetic parameters" OR "genetic variance" OR "heritability" OR "genetic covariance" OR "genetic variation" OR "genetic trend" OR "genetic correlation" OR "genetic covariance" OR "inbreeding depression" OR "inbreeding" OR "animal models" OR "threshold models" OR "multitrait model" OR "genotype environment interaction" OR "Best Linear Unbiased Prediction" OR "Best Linear Unbiased Estimation" OR "mixed model method" OR "sire evaluation" OR "genetic trend" OR "direct and maternal effect" OR "sire effect" OR "maternal effect".

In order to perform the analysis, the records were taken from the Web of Science Core Collection (WoS) on 2 July 2021. WoS was chosen as the database because of the wide coverage of the cited journals. "Science Citation Index Expanded (SCI/ EXPANDED)" was chosen also as the citation index type and "article" was selected as the document type. At the same time, studies in all languages and with the web of science category "Agriculture Dairy Animal Science" were selected. The search began in May 2021 and ended on December 2, 2021 and the time period between 2012 and 2021 was used for the analysis. The data of the study was updated once a month in order to include new articles added to WoS database. As a result, the study was carried out with 1281 records based on the titles of the articles.

Statistical analysis

Since Rstudio is a publicly available language and environment for data analysis and visualization, the study was conducted using the latest version (1.442) of this program (RStudio Team, 2020) on Windows 10. It is also used for a wide range of statistical tools, such as conceptual structure using Factorial Analysis, which is well known approach in text mining, microarray analysis, time series, linear and nonlinear models, classification, clustering, and so on (Gagolewski, 2011; Derviş, 2019).

The "bibliometrix" function was used in the research to perform descriptive analysis of the bibliographic data frames, network creation for bibliographic coupling, co-citation, collaboration, and co-occurrence analyses, conceptual structure mapping, and network mapping.

At least one cited source must appear in the bibliographies or reference lists in two related articles for them to be considered as bibliographically combined (Kessler, 1963). In such a case, it is evaluated as a bibliographic coupling. The following formula can be used to generate a bibliographic coupling network:

$$B_{cocit} = A \times A' \quad \textbf{Eq.(1)}$$

where *A* is a Reference Matrix for Documents x Cited. The number of bibliographic couplings between documents *i* and *j* is shown by element b_{ij}. *Bcoup* is a non-negative matrix and symmetric:

$$B_{coup} = B'_{coup} \quad \textbf{Eq.(2)}$$

The number of references that two articles, *i* and *j*, have in common, as indicated by the element b_{ij} of the matrix Bcoup, determines the power of the bibliographic coupling. When two articles are cited in the same third article, it is called "co-citation". The general formula for determining a co-citation network is:

$B_{coup} = A' \times A$ **Eq.(3)**

where *A* is a Document × Cited reference matrix. Matrix B_{cocit} is symmetric, just like matrix B_{coup}. The number of co-citations between papers *i* and *j* is indicated by element b_{ij}. The number of documents in the data frame where *a* reference is cited is represented by B_{cocit}'s main diagonal. That is, the number of local citations of the reference *i* is represented by the diagonal element b_{ii}. A scientific collaboration network consists of nodes that represent authors and links that represent co-authorships. Glänzel and Schubert (2004) describe it as "one of the most well-documented types of scientific collaboration." The general formula for calculating an author cooperation network is:

$B_{coll} = A' \times A$ **Eq.(4)**

where *A* is a Document × Author matrix. The b_{ij} element represents the number of partnerships between authors *i* and *j*. The number of documents authored or co-authored by researcher i is represented by the diagonal element b_{ii}.

The last network creation analysis is co-word analysis. The goal of a co-word analysis is to map and cluster terms collected from keywords, titles, or abstracts in a bibliographic collection using a word co-occurrence network to construct the conceptual structure of a framework. In other words, the conceptual structure is displayed by co-word networks of scientific field. It accomplishes this through the use of correspondence analysis (CA), multiple correspondence analysis (MCA), or Metric Multidimensional Scaling (MDS). Using the following formula, a co-word network can be created:

$B_{coc} = A' \times A$ **Eq.(5)**

where *A* is a Document × Word matrix. The element bij specifies how many times the words *i* and *j* appear together. The number of documents containing the word *i* is represented by the diagonal element b_{ii}.

The Bibliometrix R-package allows the conceptual structure to be used in two approaches: the network approach and the factorial approach. The conceptual structure function based on factorial approach uses three methods: Multiple Correspondence Analysis (MCA), Correspondence Analysis (CA) and Multidimensional Scaling (MDS). MCA is a graphical and numerical analysis of multivariate categorical data using an exploratory multivariate technique (Greenacre & Blasius, 2006). This technique uses a two-dimensional graphic to illustrate the conceptual structure. Close to the mean points (categories) are plotted closer to the origin of the MCA plot. Points that are distant from the mean, however, are plotted farther away. The other approach of conceptual structure of the bibliometrix is network approach. This also provides Co-occurrence network, thematic evaluation and thematic maps. The co-occurrence network based on KeyWords Plus establishes a link between the keywords. According to Aria et al. (2021), each keyword represents a network node or vertex and the edge linking two nodes is proportional to the number of times two keywords appear in the same keyword list. In other words, the co-occurrence network allows for a graphical representation of possible keyword associations (Tijssen & Van Raan, 1994). It is feasible to find highly interconnected groupings of terms that represent themes and subjects in this network. Various algorithms exist to define these terms. Even if there are many algorithms for term definition, the Louvain community detection algorithm was preferred in this study since Lancichinetti & Fortunato (2009) claimed that it gave the best results when tested versus various benchmarks on Community Detection methods (Blondel et al., 2008). At the same time, normalization with association and automatic layout with 20 nodes is selected as default options to achieve the KeyWord Plus co-occurrence network. The other option of network approach of conceptual structure is thematic map. A thematic map obtained by network approach is a Cartesian visualization of term clusters generated by cluster analysis of a co-occurrence network. Along the two axes, a thematic map is generated based on Callon's centrality and density rank values (Callon et al., 1991). The X-axis depicts the centrality of a network cluster from which it can be understood that it is a measure of the importance of a theme in the evolution of the field of research. On the other hand, the Y-axis represents density which can be interpreted as a measure of the theme's evolution (Cahlik, 2000; Cobo et al., 2015).

Another bibliometric analysis method is the "co-citation analysis" which is the most popular bibliometric analysis method (Ding et al., 2001). Contemporary research is characterized by scientific collaboration. Hence, authors can also be evaluated in bibliometric studies based on their proclivity to collaborate with one another. Co-citation analysis can reveal details about how scientific research is organized intellectually. It contains cited sources, cited references, and the author of the co-citation. According to Leung et al. (2017), the size of the bubble represents the number of normalized citations received by articles, while the thickness of the lines denotes the power of co-citation links. The authors implied that the co-citation relationship between the two articles is determined by their proximity and connectedness. And the color of the bubble indicates which cluster the article belongs to.

Another bibliographic network is the country cooperation network. The Star Algorithm was chosen for the network layout and the association strength measure was used in the current study for the normalization association strength for the country collaboration network (Aria & Cuccurullo, 2017).

As Garfield (2004) points out, bibliometrix also provides historiographic analysis. Direct citations make up the historiography network. It creates a chronological order of conceptual links. The chronologically most relevant citation network is named as "Historiography".

One of the different choices of bibliometrics is the "Trend Topics". It can show density research topics and future research directions like the thematic map. In the Trend Topic, the dimension of the nodes indicates the publication number of topics and the time when the topics have been popular.

RESULTS and DISCUSSIONS

Fundamental information regarding data frame

According to the results of this study, in the last 10 years, 4087 authors have published 1281 articles (Table 1). The number of single-authored articles in the resulting studies is quite low (Aria et al., 2021). This result clearly shows the positive effect of working in coordination in research on animal breeding on academic publication.

Table 1. Main bibliometric profile of quantitative genetics research in animal science

Çizelge 1. Hayvan biliminde kantitatif genetik araştırmalarının ana bibliyometrik profili

Description	**Results**
Sources (Journals, Books, etc.)	56
Documents	1281
Average years from publication	4.62
Average citations per documents	8.014
Average citations per year per document	1.288
References	25400
Articles	1249
Article; book chapter	3
Article; early Access	6
Article; proceedings paper	23
Keywords Plus (ID)	2287
Author's Keywords (DE)	2235
Authors	4087

Table 1 (continued). Main bibliometric profile of quantitative genetics research in animal science
Çizelge 1 (devamı). Hayvan biliminde kantitatif genetik araştırmalarının ana bibliyometrik profili

Description	**Results**
Author Appearances	6921
Authors of single-authored documents	22
Authors of multi-authored documents	4065
Single-authored documents	27
Documents per Author	0.313
Authors per Document	3.19
Co-Authors per Documents	5.4
Collaboration Index (CI)	3.24

The frequency distribution of the keywords associated with the article by Thomson Reuters' ISI Web of Knowledge databases (ID) was 2287 and the frequency distribution of the authors' keywords (DE) was 2235. While choosing keywords for their own article, the authors were inspired by the keywords in the publications published in the ISI Web of Knowledge database.

The average number of authors per co-authored paper is called the Collaboration Index (CI) (Elango & Rajendran, 2012; Koseoglu, 2016). In the present study, the CI was found to be 3.24 indicating that the research team falls somewhere between 3 and 4 in the subject of quantitative genetics in animal breeding.

Considering the trend in the last 10 years, the number of articles published in 2021 (n=86) decreased by 41.10% compared to 2012 (n=146). In this decline, it can be thought that the COVID-19 pandemic had a negative effect on the performance of the authors. When looking at the first top 10 sources, it was seen that most of the articles were published in the Journal of Dairy Science with 162 articles. This is followed by the Journal of Animal Science (107), Journal of Animal Breeding and Genetics (94), Livestock Science (91), Genetics Selection Evolution (88) and Animal (72).

Another issue in the results of the bibliometric analysis is the bibliometric indicators. Academic or source performance can be measured using a variety of bibliometric indicators (publication count, citation count, h-index, m-quotient, hc-index, e-index, g-index, and i-10 [i-n] index). These indicators provide preliminary information about the productivity and the quality of the research (Khanna, 2014). From these indicators, WoS can calculate h-index, m-index (m-quotient) and g-index. The source impacts are summarized in Table 2 using the h-index, m-index, and g-index indicators. According to the h-index, m-index, g-index, TC, and NP, the "Journal of Dairy Science" has a very prestigious significance in quantitative genetic research in animal breeding. The journal "Genetics Selection Evolution" with h-index of 19 and g-index of 30 ranked 2nd with the number of publications of 76. However, the journal "Genetics Selection Evolution" was ranked fifth in the most relevant sources category. At the same time, in terms of the h-index, m-index and g-index, the "Livestock Science" journal is rated fourth in the most relevant journals category while it is placed fifth in terms of h-index, m-index (m-quotient), and g-index. Figure 1 presents descriptive statistics that show fundamental information regarding the data frame.

In the second experiment, the phosphites and Fosetyl-Al treatments prevented the development of bacterial speck disease on tomatoes from 22.8% to 90.3% (Figure 2). While the disease severity rate in the positive control was 43.0%, the disease severities in treated plants were 33.19% in copper phosphite, 30.9% in calcium phosphite, 15.4% in potassium phosphite, 10.4% in zinc/manganese phosphite, 9.3% in magnesium phosphite, and 4.2% in Fosetyl-Al applications. Compared to all phosphites, Fosetyl-Al showed the most significant reduction in disease development with a rate of 90.3% efficacy. In addition, magnesium phosphite reduced the disease severity at 78.35%, zinc/manganese phosphite at 75.8% and potassium phosphite at 63.2% rates.

Table 2. Top 10 prolific source impact according to bibliometric indicators

Çizelge 2. Bibliyometrik göstergelere göre en üretken 10 kaynak etkisi

Source	**h index**	**g index**	**m index**	**TC**	**NP**
Journal of Dairy Science	25	37	2.500	2252	143
Genetics Selection Evolution	19	30	1.900	1195	76
Journal of Animal Science	18	24	1.800	1112	102
Journal of Animal Breeding and Genetics	15	20	1.500	717	85
Small Ruminant Research	13	17	1.300	545	59
Livestock Science	13	20	1.300	627	76
Poultry Science	12	18	1.200	377	27
Animal	12	25	1.200	828	65
Animal Genetics	11	18	1.100	369	25
Asian-Australasian Journal of Animal Sciences	9	12	0.900	211	37

h index (h): The number h of papers with at least h citations is the highest (Hirsch, 2005)

g index (g): The greatest number of papers (g) that garnered at least g2 citations (Egghe, 2006)

m quotient (m): The academic age divided by the h index (Hirsch, 2005)

TC: times cited

NP: Number of papers

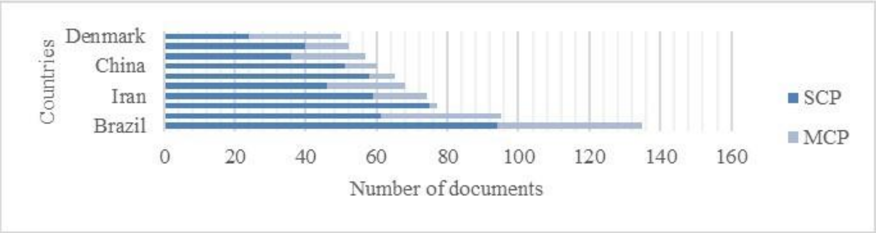

Figure 1. Number of documents published between 2012 and 2021. SCP (represented by the dark-colored bars) and MCP (represented by the light-colored bars) are the indexes of the intra-country and inter-country collaboration, respectively.

Şekil 1. 2012 ile 2021 yılları arasında yayınlanan belge sayısı. SCP (koyu renkli çubuklarla temsil edilmektedir) ve MCP (açık renkli çubuklarla temsil edilmektedir) sırasıyla ülke içi ve ülkeler arası işbirliğinin endeksleridir.

For the citation analysis, Web of Science uses ";" as the default separator, typically as a field separator character. The number of times an author in this collection has been cited by other authors in the collection is measured in local citations (Aria & Cuccurullo, 2017). It was found that Douglas Falconer's book (Falconer, 1996) was the most cited reference in the scientific publications (n=143) between 2012-2021, according to the results of the citation analysis using bibliometrix.

The conceptual Structure-function in Bibliometrix was used to do multiple correspondence analysis (MCA), which was aforementioned above, to generate a conceptual structure of the field. For categorical variables, MCA is a combination of multivariate and graphical approaches (Greenacre & Blasius, 2006). Using the k-means clustering, data is divided into meaningful or usable groups (or clusters) in MCA analysis. In this method, which includes both vertical and horizontal dimensions and is used to evaluate the conceptual structure map, the interpretation of the category points is guided by the centroid principle. The category coordinates are the weighted average of the coordinates clustered around that category according to this principle. The further away the variables grouped from the category, the more they break from the categories; conversely, the further away from the variables cluster from the categories, the less the separation and the more the variables relate to the categories. The results are evaluated using the relative placements of the points and their distribution along the dimensions. Because the distribution of words is more similar, they are more closely represented (Figure 2). In this figure, the two separate clusters of quantitative genetics in animal science categories as well as the accompanying variables are shown. Represented by the blue cluster in animal science, strong quantitative genetics are highly distinguished by its associated traits (lactation, body condition score, somatic cell score, fertility, dairy cattle, milk yield and production traits). The second red cluster in animal science exhibits very strong and improved quantitative genetics that is clearly differentiated by its related variables (weaning weight, age, holstein, coefficient, size and birth weight).

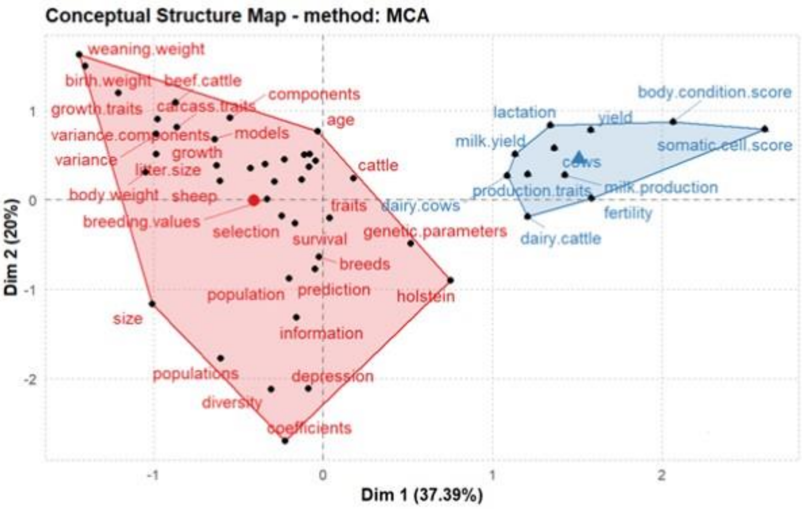

Figure 2. Conceptual structure map with Multiple Correspondence Analysis based on KeyWords Plus on genomic selection research

Şekil 2. Genomik seçilim araştırmasına dayalı KeyWords Plus'a dayalı Çoklu Uyum Analizi ile kavramsal yapı haritası

The keywords used by 4087 authors in their research were extracted from the documents. Figure 3 shows the authors' top 10 keywords without editing synonyms: "selection" (229 times), "traits" (201 times), "growth" (133 times), "dairy-cattle" (113 times), "cattle" (112 times), "performance" (109), "cows" (91 times), "parameters" (79 times), "yield" (78 times), "weight" (75 times). The fact that "selection" is one of the authors' top ten keywords corresponds to the fact that Brazil has the world's largest cattle population and that researchers in Brazil have published the most studies in the field of quantitative genetics (Figure 3).

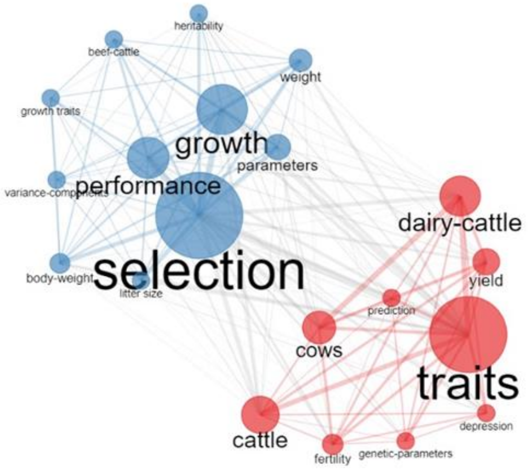

Figure 3. Co-occurrance network based on KeyWord Plus

Şekil 3. KeyWord Plus tabanlı eş oluşum ağı

According to their centrality and density rating, the KeyWords Plus analysis yielded four clusters, which were depicted on a thematic map (Figure 4). The X axis depicts the centrality (i.e., the degree of interaction between the network clusters in contrast to the other clusters) of a theme and provides information about its significance. The density (which indicates the internal strength of a cluster network and can be assumed to be an indicator of the theme's evolution) is represented by the Y axis (Figure 4). The first quadrant identifies motor themes, while the second recognizes specialty themes (i.e. the themes of limited importance for the field), the third defines emerging or declining topics and the fourth identifies basic and transversal themes (Aria et al., 2021). As seen in Figure 4, one cluster was positioned in the central and has a high centrality and density. The most often used terms were “dairy cattle”, “cattle” and “cows”. Only one well-developed theme was discovered in the first cluster, with the KeyWords Plus “selection”, “trait” and “growth” as the most frequently recurring terms. No clusters were formed in the second and forth quarter meaning that no clusters of limited importance for the field were formed. In the third quarter, one cluster was positioned as in the first. The third quarter's cluster has low centrality and density indicating that this was weakly developed and peripheral. The cluster in the third quarter comprised “depression”, “information” and “population” as the most frequent KeyWords plus.

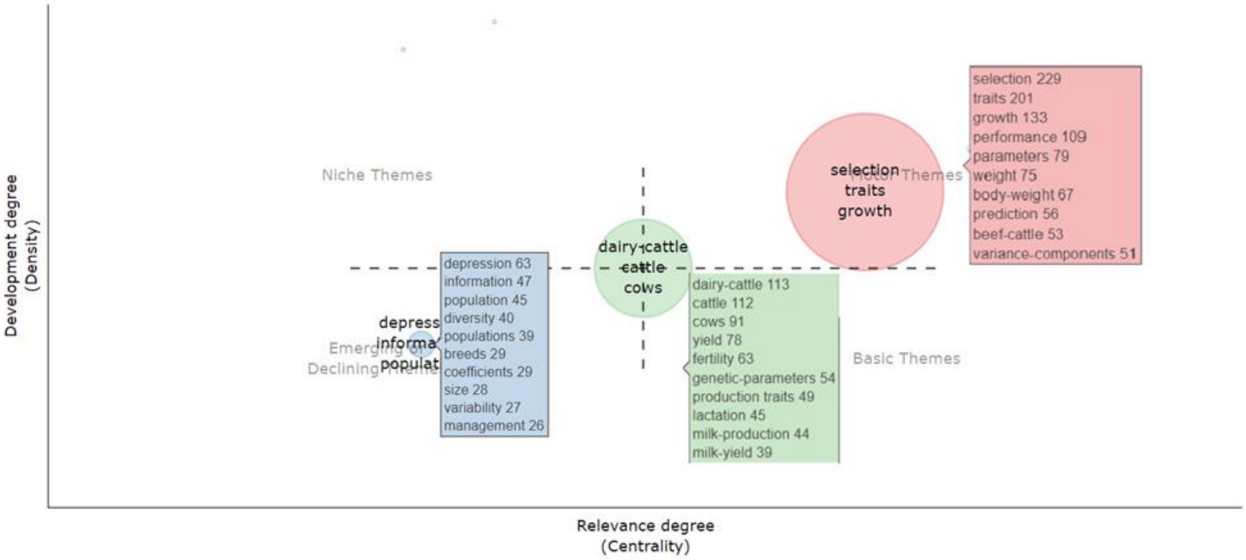

Figure 4. Clusters obtained by the KeyWords Plus analysis on a thematic map

Şekil 4. Tematik harita üzerinde KeyWords Plus analizi ile elde edilen kümeler

Figures 5 demonstrate more bibliographic network examples that consider cooperation. Clusters make up the network structure with each color representing a component. The co-citation network reveals the most cited people. D.S. Falconer’s book “Quantitative Genetics” is the most cited while K. Meyer, who developed the tool for the mixed-pattern analyzes and P.M. VanRaden, who has published multiple methods for calculating genomic prediction, are highlighted in different colors in the common citation network. Figure 5 (b) shows the international collaborations for the selected studies. The country of the author of each article was taken from the link to identify collaborations. The USA and Brazil (was shown in Figure 3) had the most cooperation (largest nodes), which was expected given that those countries released more multiple country documents (was shown in Figure 1) than other countries.

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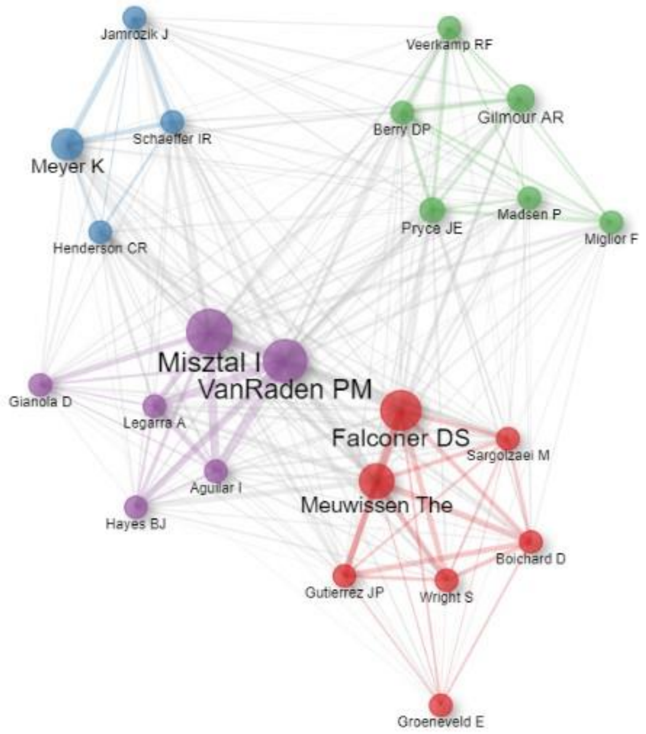

(a)

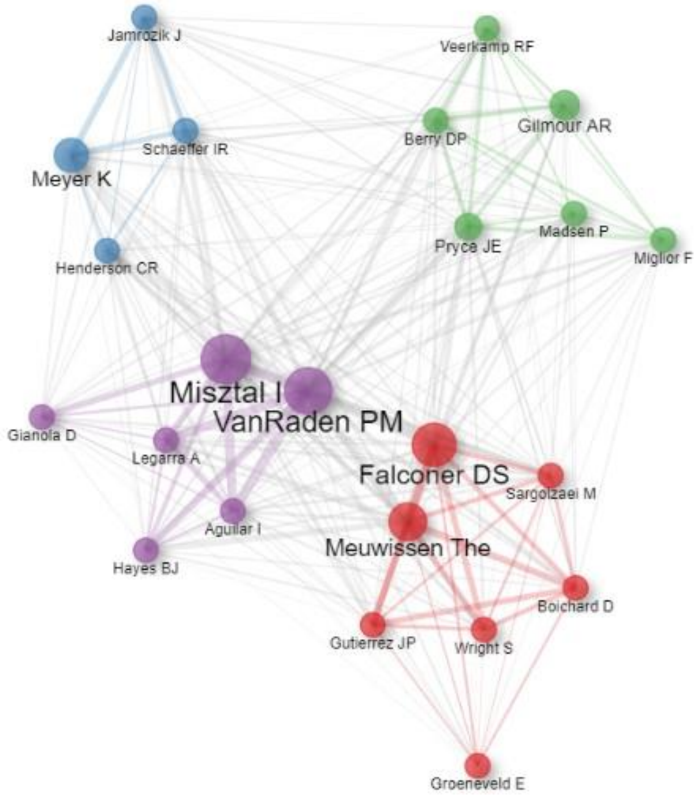

Figure 5. Visualized co-citation network (a) and Country collaboration network (Star layout) (b) in the quantitative genetic research

Şekil 5. Kantitatif genetik araştırmada görselleştirilmiş ortak alıntı ağı (a) ve Ülke işbirliği ağı (Yıldız düzeni) (b)

Historical direct citation network of the quantitative genetic research in animal science was shown in Figure 6. The network which was depicted in Figure 6 is a timeline based on the most relevant citations on the theme. Each flow of the same color denotes a direct citation and represents a concept and its evolution over time. Xiao et al. (2022) stated that the nodes in the flows in the network obtained by considering both local citations and general citations are core documents with higher citations. The citation stream with the most citations is in blue color, beginning with A.K. Sonesson's and D.M. Spurlock's research in 2012 (Sonesson et al., 2012; Spurlock et al., 2012) (Figure 6). This path provides a number of innovative approaches to the efforts in the area of animal breeding studies. In the years prior to 2012, researchers used pedigree relationships to control and monitor inbreeding as genomic relationships among election candidates were not used until 2012 (Sonesson et al., 2012). Hence, according to the citation analysis conducted in this present study (Figure 6), this article was seen as the most cited publication for that period. In another example getting several cites, Spurlock et al. (2012) provided a novel innovation in breeding in their study by discussing alternate definitions of efficiency in order to attain a more productive early lactation. As seen in Figure 6, the second-largest citation stream is in red, started in 2013. These red stream papers give information on inbreeding depression analyses utilizing SNP markers (Silió et al., 2013; Bjelland et al., 2013). There are only a few nodes in the other citation streams. Hence by the variety of colors on this map, it can be said that quantitative genetics in livestock has spanned a wide range of research areas and applications over the past ten years.

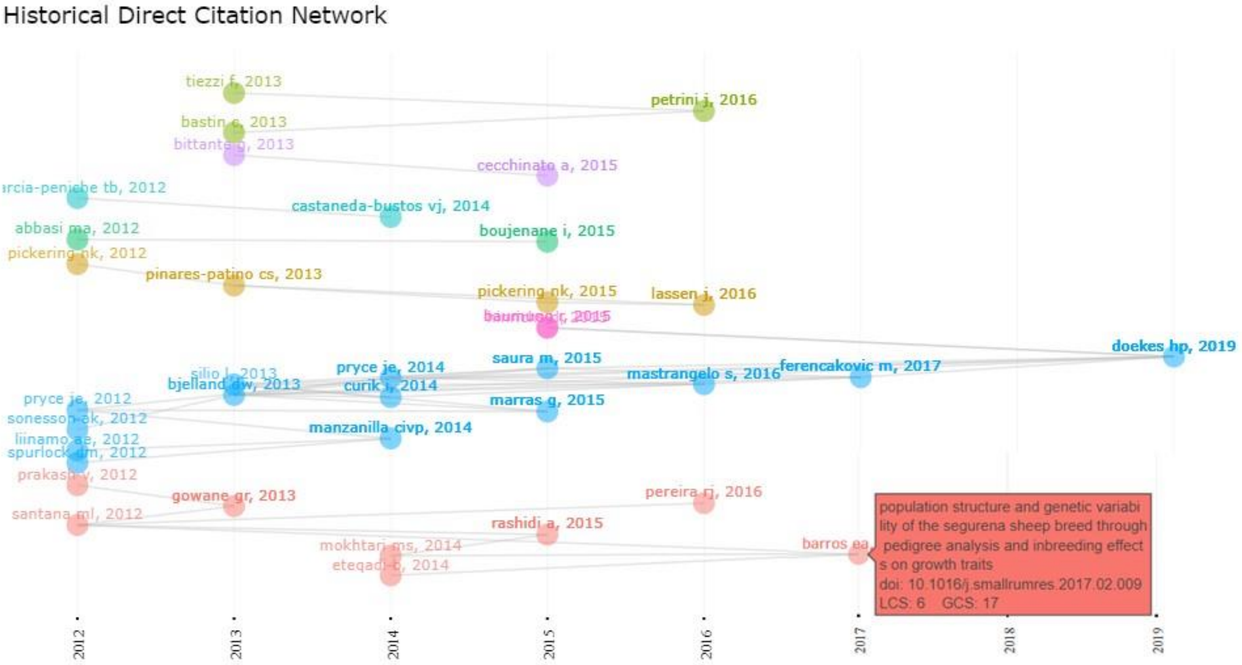

Figure 6. Historical direct citation network of the top cited papers of quantitative genetic research in animal science

Şekil 6. Hayvan biliminde kantitatif genetik araştırmaların en çok alıntı yapılan makalelerinin tarihsel doğrudan alıntı ağı

Figure 7 shows the evolution of trending topics in quantitative genetics over time based on the author's keywords. It is seen that the popularity of the topics such as "quantitative trait loci", "crossbred" and "(co)variance components" was higher between 2012 and 2014. Regarding the quantitative genetics, the "genetic trend" has been studied since 2012 but in 2014, it was studied more intensively. Rabbits' short gestation period and ability to give birth 6-7 times a year may have prompted intensive research in the field of quantitative genetics in 2013. In

2014, "persistency" became a trending topic and is still being studied. Between 2014 and 2017, especially in 2015, “litter size” and “random regression” themes were trend topics associated with quantitative genetics. On the other hand, there was a surge of interest in heritability in 2016 (Term frequency: 334). In 2017, however, "genetic correlation" is increasingly popular, despite the fact that it has been a hot topic since 2014. Again, according to Figure 7, the theme of "effective population size" in quantitative genetics was emphasized more in 2019. "Autozygosity" became a trend topic in 2020 and is currently the hottest trend topic while it was emerged as a new topic in 2015 (Figure 7).

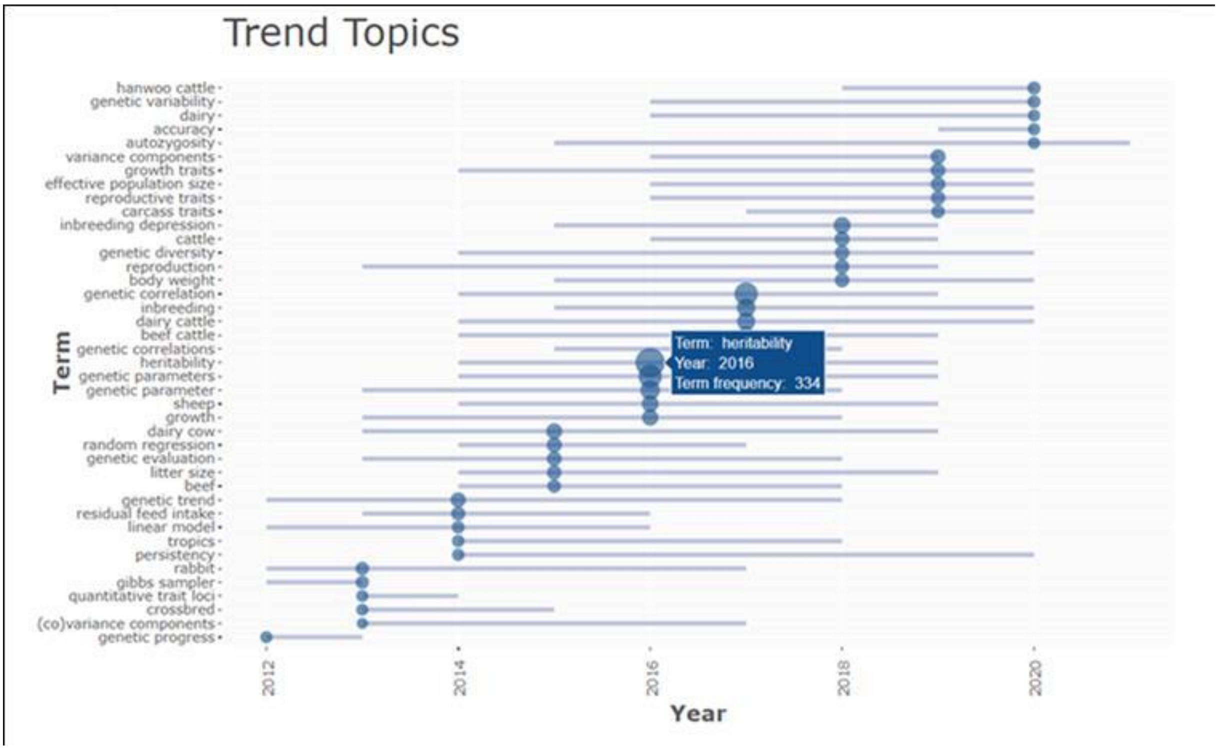

Figure 7. Trend Topics by the author’s keywords

Şekil 7. Yazarın anahtar kelimelerine göre Trend Konuları

The process of accumulating knowledge naturally becomes more complex as publications improve piecemeal over time and the number of publications continues to expand at an increasing rate. Determining the research trend of scientific fields is critical not only for research but also for policy making and implementation. In this light, scientific mapping is an important tool for academics in a wide range of subjects. The various software tools have been created for this aim. “Bibliometrix” is an open-source, versatile, and always-evolving tool written in the R programming language. Academic performance indicators provided by using Bibliometrics also offer visual convenience to researchers in terms of academic communication because academic and scientific success requires a lot of discussion and sharing of experiences. Luukkonen et al. (1992) reported that cooperation indicators are a tool for professional advancement and increased knowledge. According to Beaver and Rosen (1979), scientific collaboration is a reflection of science’s increasing professionalism. In this respect, it can be understood that Bibliometrix is a very valuable tool.

Together with its benefits, bibliometric analysis can be limited to the continuation of academic research because many more papers may have appeared in publications that have not yet to be indexed. In the current study, only the articles from Web of Science (WoS) were included and therefore, the research cannot cover the entire literature on the quantitative genetic research in animal science. It is important to note, however, that no scientific database is exhaustive, and each one, including Scopus and PubMed, has its own set of flaws and strengths (Falagas et al., 2008). With all of these restrictions in mind, it's clear that quantitative genetics research in animal science is on the rise, as evidenced by the present study's findings.

In conclusion, using data from WoS to learn more about the bibliometrics package in current research, the evolution of academic studies and trending issues of quantitative genetics in the animal sciences over the past decade were reviewed. The findings of the current study offer solutions to several important questions in quantitative genetics research. In addition, this study will benefit researchers working on themes that emphasize scientific trends and work with a bibliometric approach. Brazil and the United States, as noticed, were the forerunners in publishing quantitative genetic research papers. The WoS data platform claims that the most globally cited article was published by Meuwissen et al. (2016) in the last ten years. Douglas Falconer is a well-known scientist who has made significant contributions to quantitative genetics and mouse genetics throughout his career. Without a doubt, his textbook (Falconer, 1996) had the largest impact on quantitative genetics and bibliometrix has proven that it is still the most cited reference today. The "Journal of Dairy Science" has the best reputation for publishing quantitative genetic studies, according to the WoS database. Researchers can learn about current studies by subscribing to the journal in question. Also, according to the results obtained from the bibliometric analyses in this study, it was revealed that the theme of "autozygosity" in the quantitative field of animal science is still a new research topic. Therefore, this result, together with the trend topic, may show researchers a new research direction in the future.

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STATEMENT OF CONFLICT OF INTEREST

The author declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

STATEMENT OF ETHICS CONSENT

Ethical approval is not required as there are no studies with human or animal subjects in this article.

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