



Review article

A Bibliometric Analysis of Molecular Marker Studies on *Linum usitatissimum* from 1998 to 2025

Gülru Yücel ^{a,*}, Oğün Demir ^b, Şahane Funda Arslanoğlu ^c & Behiye Banu Bilgen ^d

^a Ondokuz Mayıs University, Faculty of Agriculture, Department of Agricultural Biotechnology, Samsun, Türkiye

^b Nezahat Gökyiğit Botanic Garden, Department of Biodiversity and Information, İstanbul, Türkiye

^c Ondokuz Mayıs University, Faculty of Agriculture, Department of Field Crop, Samsun, Türkiye

^d Tekirdağ Namık Kemal University, Faculty of Agriculture, Department of Agricultural Biotechnology, Tekirdağ, Türkiye

Abstract

Linum usitatissimum is an economically important species that is a dicotyledonous, self-pollinated, and annual herbaceous plant. *L. usitatissimum* provides both oil and fiber, which have a wide range of uses. The genetic variation existing within the genome is important to preserve the genetic resources and establishment of an effective breeding programmes successfully. Several molecular markers have been employed to analyse genetic characterization within the different genotypes of the species or among other plant species, including *L. usitatissimum* as well. Various molecular markers e.g., SSR, SCOT, RAPD, IRAP, REMAP, ISSR, and iPBS were used to understand the genetic diversity and genotyping of flax varieties, and to characterize relationships in *L. usitatissimum*. In the presented study, bibliometric analysis was performed to evaluate the published articles related to molecular marker studies in *L. usitatissimum* from 1998 to 2025 based on the WOS database. Searching the Web of Science Core Collection (WOS) by "*Linum usitatissimum*" and "molecular markers" criterias were analyzed, and the parameters include category areas, subject, country of publication, and country collaborations. According to the research results, a total of 91 published data were identified through research analysis from 1998 to 2025. Plant science, agronomy, and genetics/heredity were the top three categories. Canada and China have been the top contributors to research on molecular markers in *L. usitatissimum* based on WOS data. This bibliometric study evaluates the molecular marker analyses from different perspectives based on bibliometric analyses, which may be helpful to researchers working on this field and give an idea for possible projects. As a result, this study is the first bibliometric approach that aims to guide future studies by revealing molecular marker studies on flax genotypes between 1998 and 2025.

Keywords: *L. usitatissimum*, Molecular Marker, Bibliometric analyses.

Received: 02 October 2025 * **Accepted:** 14 December 2025 * **DOI:** <https://doi.org/10.29329/ijiaar.2025.1375.1>

* Corresponding author:

Gülru Yücel is an assistant professor in the Department of Agricultural Biotechnology at Ondokuz Mayıs University in Samsun, Türkiye. Her research interests include Plant Biotechnology, Plant Cytogenetic and Plant Genetic. She lives and works in Samsun, Türkiye.
Email: gulru.yucel@omu.edu.tr

INTRODUCTION

The *Linum* genus is member of the Lineaceae family. The genus comprises approximately 180 annual and perennial species. The member of the genus distributed throughout the subtropical and temperate areas of the world (McDill et. al., 2009). It has been mentioned that since endemism rate and the important number of the species found Anatolia may suggested one of the gene center for the genus *Linum* (Yılmaz et al., 2003; Ulcay, 2023).

Linum usitatissimum is known as the only economically important species of the genus *Linum* (Tadesse et al., 2009). It is mentioned as an ancient crop (Wang et al., 2012) which is an annual and self-pollinated cultivated species (Nag et al., 2015) with $2n = 30$ chromosome number (Rachinskya et al., 2011). *L. usitatissimum* is commonly cultivated as an oil and fiber source (Wang et al., 2012). Its stem produces the high quality fibers which have an important strength and durability (Singh et al., 2011). The fibers are used as a raw material source for various purposes, e.g., curtain, yarn, insulating material, and textile (Yılmaz & Uzun 2019). The seeds include oil that is rich in omega-3, lignans, and digestible proteins (Singh et al., 2011; Arslanoğlu & Aytaç 2020). Flax has been utilized widely following the cotton (Aytaç et al., 2020). However, the cultivation area of flax has been decreased after 1964 with the accelerated use of the cotton and synthetic fiber resources (Hazneci & Arslanoğlu 2021). Although cotton is Turkey's most produced fiber plant, cotton-producing regions are limited by different factors such as climate factors (Aytaç et al., 2020), which make the flax production crucial as an excellent alternative fiber souce (Hazneci & Arslanoğlu 2021). Since the common use of flax, it has been mentioned which makes it significantly important to develop the new varieties with desired characters e.g., resistant varieties and higher productivity. To obtain new varieties with desired characters comprehensive information about its genetic characteristics are necessary (Rachinskya et al., 2011).

Recently, there have been a number of reports from different perspectives to know more about the genome of *L. usitatissimum* and provide beneficial information to use in breeding studies (Wang et al., 2012; Yurkevich et al., 2017). Based on literature, one of the research fields about the *L. usitatissimum* is molecular marker analysis (Fu et al., 2005; Uysal et al., 2010; Smýkal, et al., 2011; Rachinskya et al., 2011; Habibollahi et al., 2018; Koçak et al., 2023, Cuiping & Liu 2024).

The plant breeding programmes were supported significantly with the improvement of the molecular marker technology since 1980. In the last three decades, the interest in obtaining knowledge about the sequences of plant genomes as well as the physiological and molecular roles of plant genes, has increased, which has a significantly important effect on molecular genetics and its efficiency in plant breeding programmes (Nadeem et al., 2012).

Genetic diversity is known as the variation in genes among species or between individuals of the same species (Begna and Teressa 2024) and is used for classical and molecular breeding in plant breeding programs (Begna & Teressa 2024; Aşkar 2025). Determining genetic diversity is an important for sustainability, and genetic characterization is also essential in breeding studies, such as identifying genotypes resistant to biotic and abiotic stress factors. Genetic diversity is one of the most fundamental resources in the development of genetic breeding programs (Sütcü et al., 2022). Identifying species with high genetic diversity and conducting genetic characterization studies are invaluable in breeding studies to achieve the desired goals. Molecular markers are known as one of the effective techniques for determining genetic diversity (Begna & Teressa 2024; Aşkar 2025).

Molecular markers are DNA fragments that are associated with any gene region in the genome. Molecular marker techniques are based on the principle of detecting polymorphic gene regions in the DNA, which are formed from the deletions, insertions, point mutations, or errors during repeated DNA replication (Yorgancılar et al., 2015). Several types of DNA molecular markers have been developed and successfully applied for many years. DNA based molecular markers are divided into two main groups based on detection method: hybridization-based markers (e.g., restriction fragment length polymorphism-RFLP) and polymerase chain reaction (PCR)-based markers, (such as AFLP, CAPS, RAPD, SCAR, SRAP, and SSR) (Sarwat et al., 2011; Nair and Pnadey, 2021; Bilgen and Kaya, 2023). The suggestion/selection of parental lines for breeding programmes (Yaldız et al., 2018; Ali et al., 2020), gene mapping and selection (Nair & Pnadey, 2021), revealing of the genetic diversity (Yaldız et al., 2018; Aşkar, 2025), mapping and phylogeny analysis (Stägel et al., 2008), determining pollen contamination in seed orchards (Bilgen and Kaya, 2014) are some of the significant contributions of the molecular marker studies in plants. Molecular markers may have advantages such as easy to use, high reproducibility, and less quantity of DNA, however they may also have disadvantages such as being less polymorphic, expensive, and requiring high quality DNA content in some cases (Nadeem et al., 2018).

Recently, bibliometric analyses have become popular across different scientific fields to support the understanding of research topics and their patterns and trends (Bilgen & Kaya, 2023; Wani et al., 2023; Yardibi et al., 2023; Cerimi et al., 2025). Bibliometric analysis is a method to investigate and analyze a large amount of scientific data (Donthu et al., 2021). It has been reported that different contributions of the bibliometric analyses such as quantitatively and visually analyzing (Shawahna and Nairat 2021), provide a valuable source to represent available literature in a particular field (Yardibi et al., 2021), and shed light on the emerging trends (Donthu et al., 2021). Therefore, this presented bibliometric research aims; (1) to give important implications and insights for future studies about flax genotypes, (2) to analyze the literature about molecular markers studies *L. usitatissimum*, and (3) to provide a general evaluation of the related current studies, and highlight this field in *L. usitatissimum*.

MATERIALS and METHOD

The bibliometric analyses performed to evaluate the scientific literature on the molecular marker studies in *L. usitatissimum* which is a unique economically important species of the genus. To obtain comprehensive coverage, the research was conducted with using keywords by "molecular markers" and "*L. usitatissimum*". The search was performed using Web of Science (WOS) to obtain highly relevant publications. Data including authors, journal title, year of publication, abstract, keywords, DOI, and Web of Science categories were included in the records that were exported in BibTeX format. The data collection was performed on August 8, 2025. The retrieved related data includes published articles from 1998 to 2025. For this, a total of 91 related publications were downloaded for *L. usitatissimum*. The retrieved related data was consisted of article, review, book chapter, and proceeding papers. Duplicate entries were not included in the analysis. Python (version 3.12) was used to process all bibliographic data. The following libraries were used: matplotlib (Hunter, 2007) and seaborn (Waskom, 2021) for visualization; wordcloud (Mueller, 2020) for keyword cloud generation; geopandas (Jordahl et al., 2020) and shapely (Gillies et al., 2025) for spatial mapping; pandas (McKinney, 2010) for data handling and cleaning; and networkx (Hagberg et al., 2008) for collaboration network analysis. The flow chart of the material and method process is given in Figure 1.

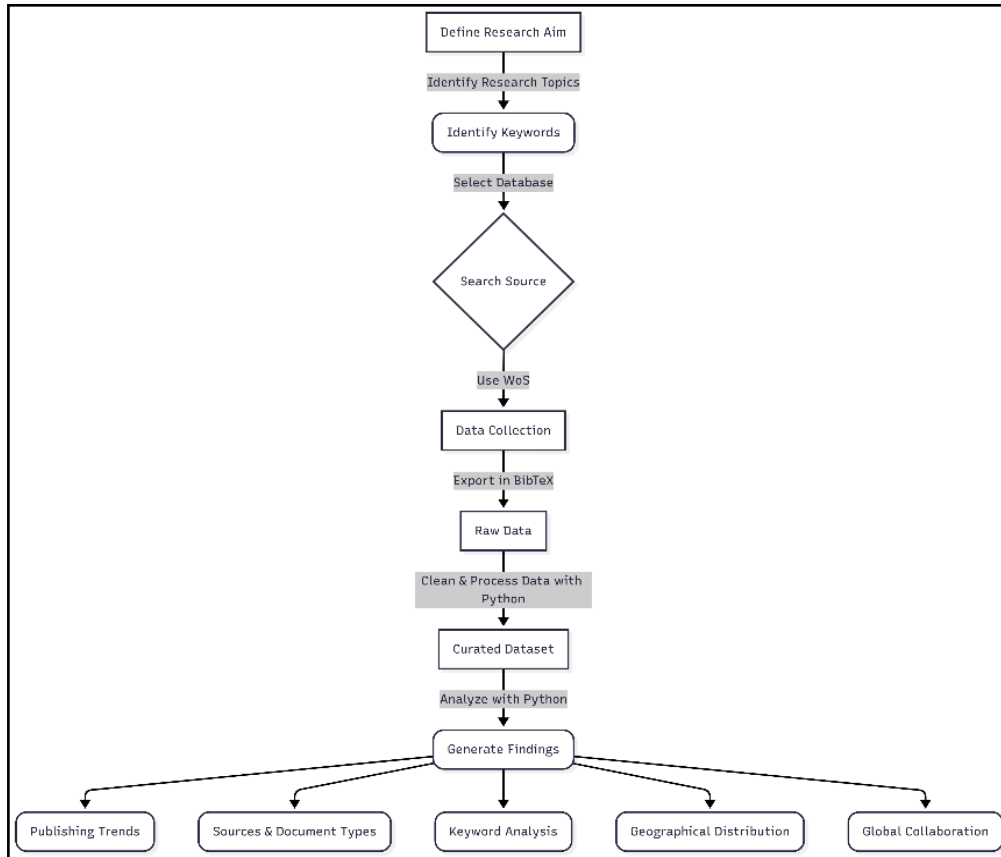


Figure 1. The flow chart of the material and method procees.

RESULTS and DISCUSSION

In this research, bibliometric analysis was performed to evaluate the published data about molecular marker analysis in *L. usitatissimum*. All of the data spanning the period from 1998 to 2025 was retrieved from the WOS database.

Searching the Web of Science Core Collection (WOS) by "molecular markers" and "*L. usitatissimum*" criteria revealed that 91 published studies. (Figure 2). Among these, 93.4% (n=85) were classified as research articles, with the remaining contributions including 3 reviews, 2 book chapters, and 1 conference paper on molecular marker studies in *L. usitatissimum* (Figure 2).

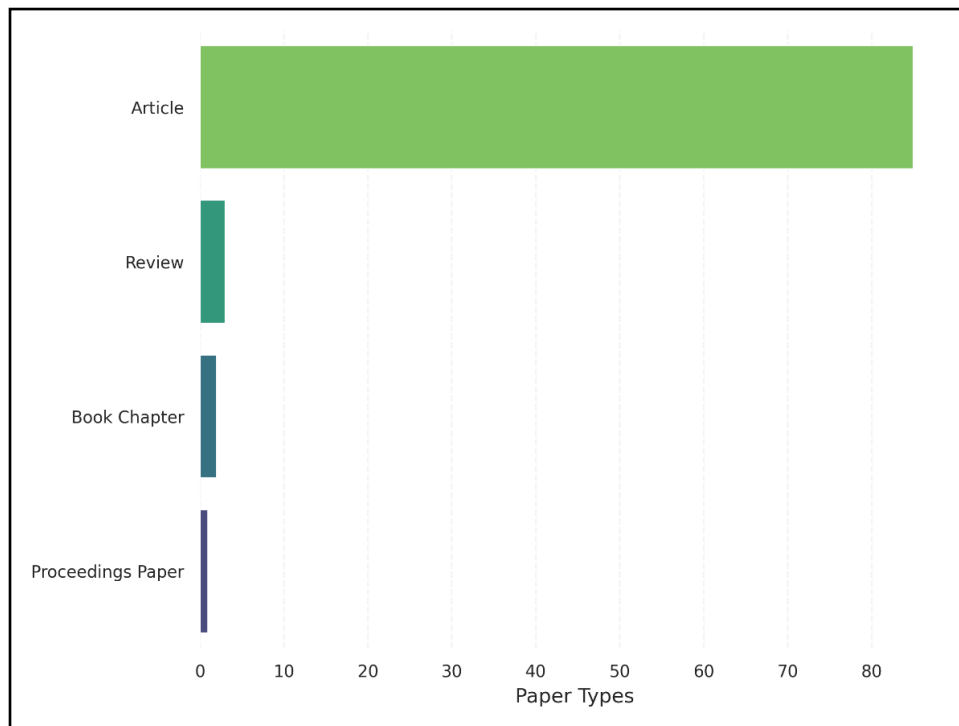


Figure 2. Published paper type on molecular marker analysis in *L. usitatissimum*.

The number of published papers per year from 1998 to 2025 on molecular marker analysis in *L. usitatissimum* is shown in Figure 3. The publication activity was very low from 1998 to 2011. From 2011, publication activity has generally increased compared to the previous years however, the highest publication activity came out in 2018 and 2023 with 12 and 10 records, respectively.

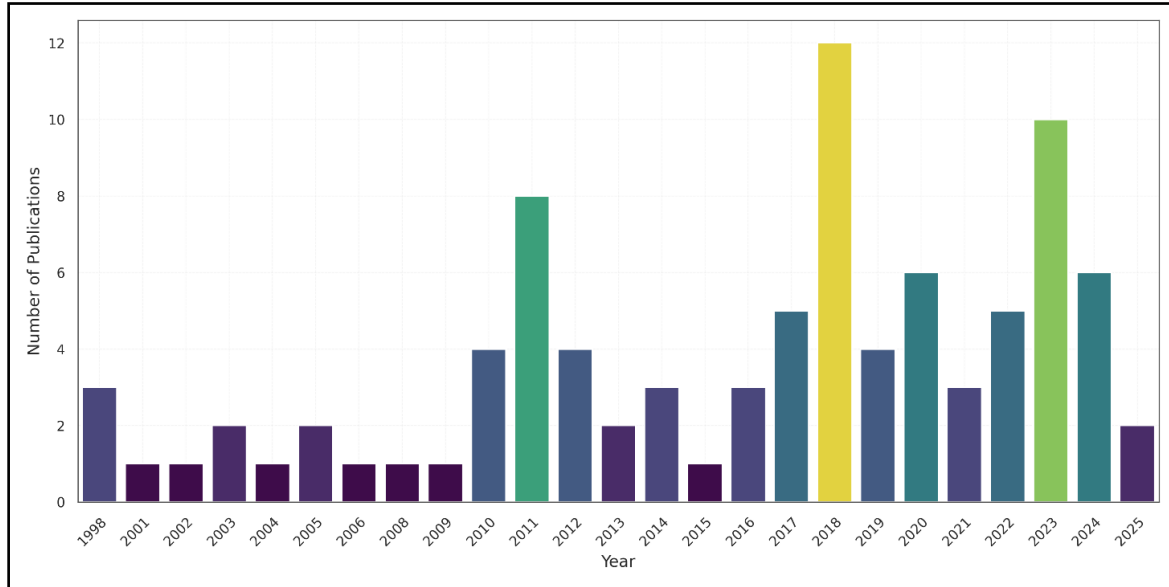


Figure 3. The number of published papers per year from 1998 to 2025 on molecular marker analysis in *L. usitatissimum*.

It has been observed that the published articles belong to 17 different WOS categories. Figure 4 presents the number of articles in 17 WOS categories. The number of articles in the top 10 WOS categories are as follows; Plant Sciences with 47 records, Agronomy with 27 records, Genetic\&Heredity with 25 records, Biotechnology\&Applied Microbiology with 12 records, Biochemistry\&Molecular Biology with 11 records, Horticulture with 10 records, Chemistry\&Multidisciplinary with 5 records, Multidisciplinary Sciences with 4 records, Biology with 3 records, and Biochemical Research Methods with 3 records (Figure 4). The analysis of subject focus reveals that, according to WOS (Web of Science) categories, the predominant area of publications is plant sciences, accounting for 51.6% with 47 records. This is followed by agronomy at 29.6% with 27 records and genetics & heredity at 27.4% with 25 records. This distribution highlighted the importance of molecular marker analyses in different fields of science to enlighten the genome of *L. usitatissimum*.

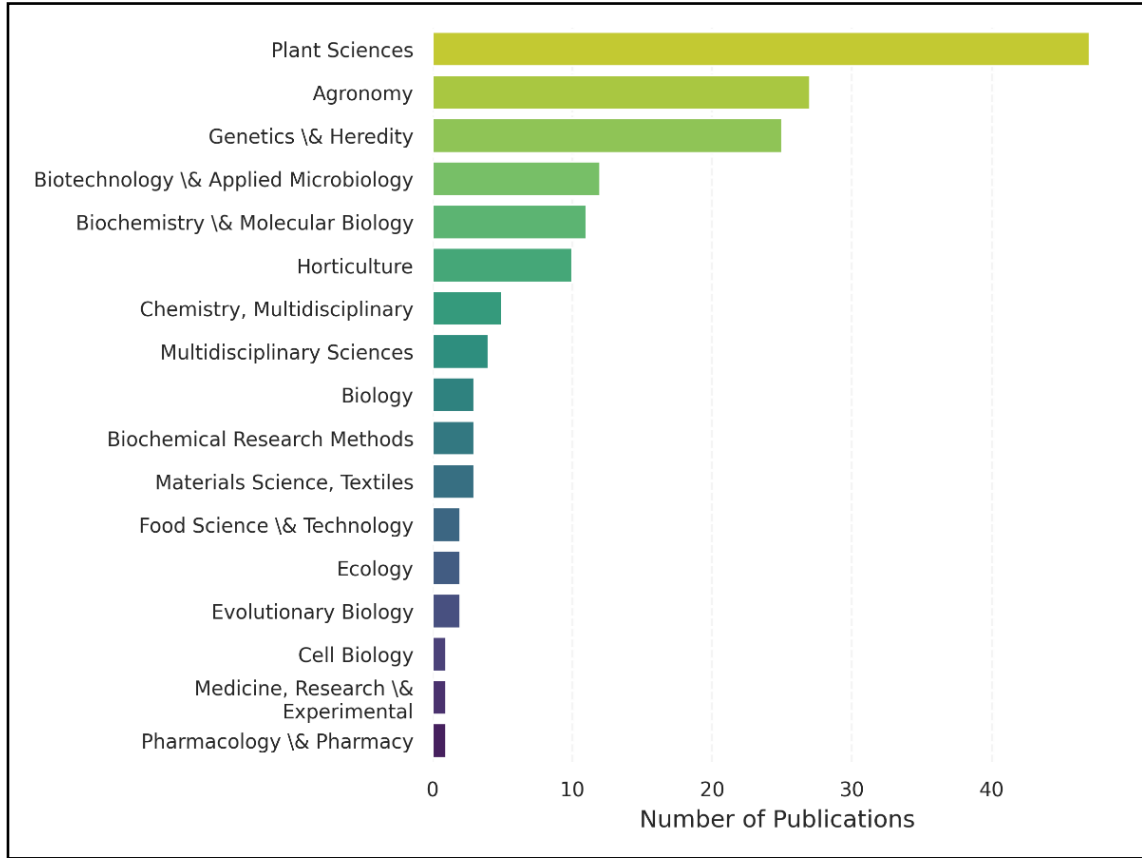


Figure 4. Web of Science Categories of 91 published articles on molecular marker analysis in *L. usitatissimum* during 1998-2025.

Based on the search results of WOS Publication Titles, 51 journals were reported, and the top 10 journal list including the published paper which was collected following the "*Linum usitatissimum*" and "molecular marker" criteria is shown in Table 1. Genetic Resources and Crop Evolution, Frontiers in Plant Science, and International Journal of Molecular Sciences take the first three ranks among the collected journals by WOS. The journals with the highest number of articles included Genetic Resources and Crop Evolution (n = 10), followed by Frontiers in Plant Science (n = 7) and the International Journal of Molecular Sciences (n = 5).

Table 1. Search results of the top ten WOS Publication Titles of published articles

Wos publication titles	Number of Articles
Genetic resources and crop evolution	10
Frontiers in plant science	7
International journal of molecular sciences	5
Molecular breeding	5
Bmc plant biology	4
Bmc genomics	4
Journal of natural fibers	3
Theoretical and applied genetics	3
Cytology and genetics	3
Russian journal of genetics	2

In terms of retrieved data from 1998 to 2025, countries published data related to molecular marker analyses in *L. usitatissimum* were shown in Figure 5. A total of 27 countries reported; however first 20 countries that have more publications compared to the others were listed in Table 2. Among these countries, Canada was the country which has the highest published data with 30 records. Following the Canada, China, India, and Chile were the countries also contributed the most to molecular marker analysis in *L. usitatissimum* during 1998-2025, respectively (Table 2). However, the contribution from Türkiye amounted to just 2 publications which may indicate that molecular marker analysis is limited and must accelerate to support breeding studies.

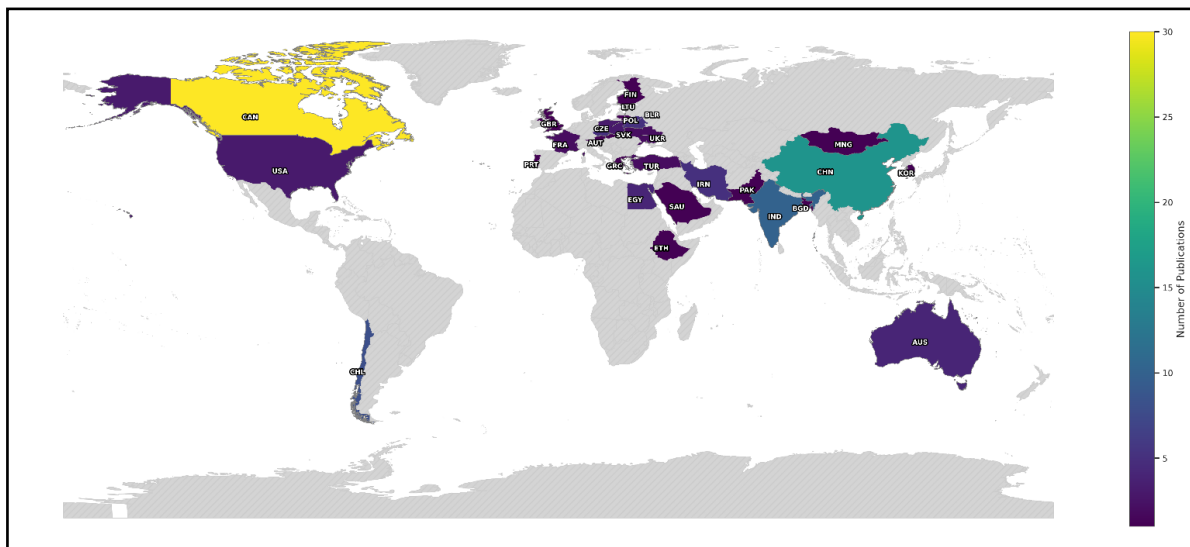


Figure 5. Main contributors to the research on molecular marker analysis in *L. usitatissimum* in term of countries.

One of the important characteristics for bibliometric studies is keyword analysis which is useful tool to present an outlook of the research trend in the field under study. The Figure 7 represents the word cloud created using the most important keywords associated with molecular marker studies in *L. usitatissimum*. Retrieved data reported 200 data and indicated flax, linum, usitatissimum, genetic, marker, diversity, SSR, polymorphism, and linseed had the highest frequency, respectively (Figure 7). In the analysis, the most frequently used term was "flax" (f=1.0), followed by "linum" (f=0.79), "usitatissimum" (f=0.71), and "genetic" (f=0.61). The most frequently occurring marker term was SSR (f=0.25).

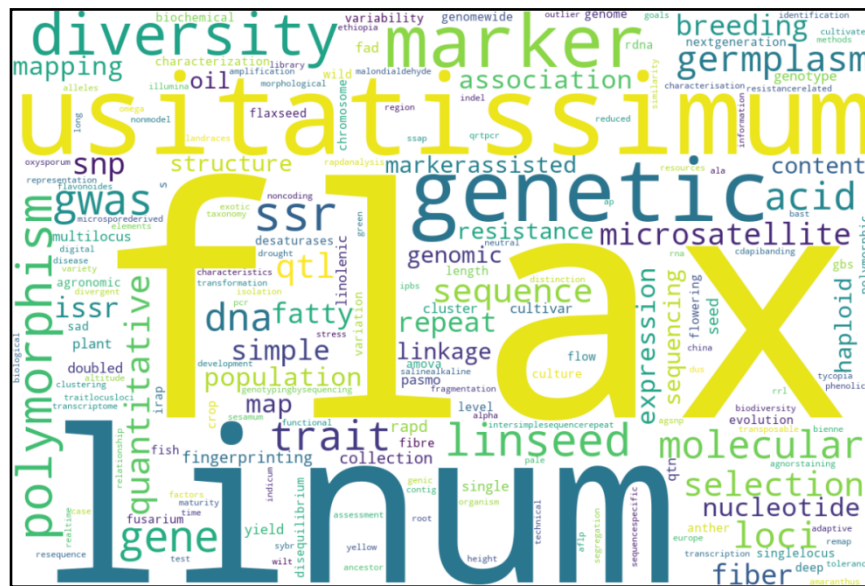


Figure 7. The word cloud of keywords

This conducted bibliometric analysis provides a general view of molecular marker analysis on the species *L. usitatissimum*. Analysis of genetic diversity and characterization of flax gene pool and are crucial information for the breeding programs (Habibollahi et al., 2018b), which is why they make performing molecular marker analysis or related analysis crucial in various plants. As we can see from the obtained data, different types of molecular marker analysis e.g., AFLP (Wakjira et al., 2005), SSR, ISSR (Uysal et al., 2010; Cuiping & Liu 2024), RAPD (Fu et al., 2005), IRAP (Smýkal et al., 2011), REMAP (Abbasi Holasou et al., 2016) and iPBS (Koçak et al., 2023), allowed the understanding of the genetic diversity and genotyping of flax varieties, characterization of relationships among the individuals of *L. usitatissimum*. RAPD markers are used to detect genetic diversity to obtain useful findings which is an important to understand flax domestication and exploring novel gene source for flax improvement (Fu et al., 2005), genetic diversity assessment among flax genotypes based on AFLP indicated AFLP is an effective method to discriminate accessions (Wakjira et al., 2005). SSR markers and some morphological characters were evaluated for the identification of cultivars (Cuiping & Liu

2024), and ISSR and iPBS markers were used to analyse genetic diversity and population structure in flax genotypes (Koçak et al., 2023).

It has been mentioned that there are bibliometric studies on flax (Majumdar et al., 2022; Nwankwo et al., 2023; Gao et al., 2023) however, they mostly focused on related the application of natural fibers in concrete (Gao et al., 2023), which may make it necessary to conduct bibliometric analyses also with different topics related to *L. usitatissimum*. Bibliometric analyses based on WOS with flax-related research (from 2000 to 2022) were performed on flax research history, hotspots, and emerging trends, which could support to put forward ideas and suggestions for the development of the flax industry. Five important research areas were presented (1) flax genetics, (2) fiber quality, (3) flaxseed products, (4) biocomposite with flax fiber, (5) cellulose and its application. Canada was reported one of the important countries in flax studies with published articles (Gao et al., 2023) and these results showed similarity with the presented study which showed Canada had important number of the published data and collaboration as well. As we can see from the reported bibliometric analyses, genetics of flax has been reported in five important research areas, which is why molecular markers and related studies with analyze them may suggest a crucial field in the genome studies of *L. usitatissimum*.

Another bibliometric analysis were carried out based on flax disease to enlighten researchers and put forward an idea to get a high and healthy harvest based on Scopus data. In the mentioned research, 243 articles were retrieved. The obtained results indicated that an important part of the data (52%) was in the category of agricultural and biological science, biochemistry and genetics. Canada, were in list of the countries with higher publications compared to other countries. Furthermore, it has been suggested that international exchanges and cooperation require improvement (Karimova et al., 2023). This bibliometric study (Karimova et al., 2023), indicated similar points with presented study such as Canada had the highest publication number in terms of molecular marker, also agronomy and biology were also in the top ten categories. In another research, bibliometric analysis for natural fibers were performed as well (Majumbar et al., 2022).

CONCLUSION

This conducted bibliometric analysis provides a comprehensive evaluation of the research landscape regarding the molecular marker in *L. usitatissimum*. By employing information in graphs and tables, the results were summarized clearly. According to bibliometric analysis, the number of molecular marker studies has started to increase, which may show the increasing importance of the studied field for *L. usitatissimum*. Besides, the conducted bibliometric analysis revealed information such as the number of published data, categories, popularly used keywords, collaborations, which may contribute to the scientists involved in this research field and give an idea to focus future projects. Therefore, this study not only provides a detailed analysis of studies on molecular marker analysis in *L. usitatissimum*

during 27-year period (1998-2025), but also provides a significant scientific framework for future studies.

Author Contributions

In this study, Conceptualisation, GY, BBB and ŞFA; Data Collection, OD; Interpreted data; GY, BBB, ŞFA and OD, Writing original draft preparation, GY and BBB, Writing, review, and editing, GY, BBB, OD, and ŞFA. All authors have read and agreed to the published version of the manuscript.

Funding

This study was not funded by any institution or organization.

Responsible Artificial Intelligence Statement

No artificial intelligence support was received in any part of this study.

Conflicts of Interest

The authors declare that there are no conflicts of interest related to the publication of this study.

Ethics Approval

In all processes of this study, the principles of Pen Academic Publishing Research Ethics Policy were followed.

This study does not require ethics committee approval as it does not involve any direct application on human or animal subjects.

REFERENCES

- Abbasi Holasou, H., Abdollahi Mandoulakani, B., Jafari, M., & Bernousi I. (2016). Use of IRAP and REMAP markers to interpret the population structure of *Linum usitatissimum* from Iran. *Biologia*, **71**, 305–315 (2016). <https://doi.org/10.1515/biolog-2016-0042>
- Ali, F., Nadeem, M. A., Barut, M., Habyarimana, E., Chaudhary, H. J., Khalil, I. H., Alsaleh, A., Hatipoğlu, R., Karaköy, T., Kurt, C., Aasim, M., Sameeullah, M., Ludidi, N., Yang, S. H., Chung, G., & Baloch, F. S. (2020). Genetic diversity, population structure and marker-trait association for 100-seed weight in international safflower panel using SilicoDART marker information. *Plants*, **9**(5), 652. <https://doi.org/10.3390/plants9050652>
- Arslanoglu, S.F. and S. Aytac, The Important of Flax (*Linum usitatissimum* L) In Terms of Health. *International Journal of Life Sciences and Biotechnology*, 2020. **3**(1): p. 95-107. <https://doi.org/10.38001/ijlsb.690295>
- Aşkar, D. (2025). Genetic Characterization Of Bread Wheat M4 Populations Generated By Gamma Irridation And Investigation Of Brown Rust Resistance Genes. Master Thesis, Tekirdağ Namık Kemal University.

- Aytac, S., Başbağ, S., Arslanoglu, F., Ekinci, R., & Ayan, A.K. (2020). Lif Bitkileri Üretiminde Mevcut Durum ve Gelecek. Ziraat Mühendisleri IX. Teknik Kongresi, Bildiriler Kitabı Cilt 1. In *Proceedings of the TMMOB Ziraat Mühendisleri Odası*, Ankara, Turkey, 13–17 October 2020; pp. 463–491, ISBN 9786050113211.
- Baştürk, M.H. (2024). The Effects On Fiber Yield And Quality Of Flax Fiber (*Linum usitatissimum* var. *usitatissimum*) of Nitrogene Fertilizer Doses. Master Thesis, Ondokuz Mayıs University.
- Begna, T. & Teressa, T. (2024). Genetic Variability and Its Benefits in Crop Improvement: A review. *Middle East Journal of Agriculture Research*, 13(1), 128-136. DOI: 10.36632/mejar/2024.13.1.6.
- Bilgen, B.B. & Kaya, N. (2023). Microsatellite Markers: The Efficient Method for the Determination of Pollen Contamination in Conifer Seed Orchards. *International Journal of Innovative Approaches in Agricultural Research*. 7(3), 356-370. <https://doi.org/10.29329/ijiaar.2023.602.10>
- Bilgen, B.B. & Kaya, N. (2014). Chloroplast DNA variation and pollen contamination in a *Pinus brutia* Ten. clonal seed orchard: implication for progeny performance in plantations. *Turkish Journal of Agriculture and Forestry*, 38:540-549.
- Cerimi, K., Pöther, D.C., & Klar, S. (2025). A bibliometric analysis of fungal volatile organic compounds. *Fungal Biology and Biotechnol.*, 12, 12. <https://doi.org/10.1186/s40694-025-00203-x>.
- Cuiping, C., & Liu, Y. (2024). Genetic diversity and distinctness of flax (*Linum usitatissimum* L.) based on morphological and simple sequence repeat (SSR) markers. *Genet Resour Crop Evol* **71**, 4763–4777 (2024). <https://doi.org/10.1007/s10722-024-01933-4>
- Donthu N., Kumar S., Mukherjee D., Pandey N., & Lim W.M. (2021). How to conduct a bibliometric analysis: An overview and guidelines. *Journal of Business Research*, 133: 285-296. <https://doi.org/10.1016/j.jbusres.2021.04.070>
- Fu, Y.B. (2005). Geographic patterns of RAPD variation in cultivated flax. *Crop Sci.* 45, 1084–1091. doi: 10.2135/cropsci2004.0345
- Gao S., Chen S., Huang R., Guo Y., Qiu C., Long S., Wu Z., Wang., Qiu H., Zhao X., & Wang Y. (2023) Bibliometric Analysis of Research History, Hotspots, and Emerging Trends on Flax with CiteSpace (2000-2022), *Journal of Natural Fibers*, 20:1, 2194700, <https://doi.org/10.1080/15440478.2023.2194700>
- Gillies, S., van der Wel, C., Van den Bossche, J., Taves, M. W., Arnott, J., Ward, B. C., et al. (2025). Shapely (Version 2.1.1) [Computer software]. Zenodo. <https://doi.org/10.5281/zenodo.5597138>
- Habibollahi, H., Noormohammadi, Z., & Sheidai, Farahani F. (2018). Genetic Structure of Cultivated Flax (*Linum Usitatissimum* L.) Based On Retrotransposon-Based Markers. *Genetika*, 47(3): 1111-1122. <https://doi.org/10.2298/GENSR1503111H>
- Habibollahi, H., Noormohammadi, Z., Sheidai, M., Farahani H., Talebi SM., & Torabizadeh E., (2018b). Assessments of genetic diversity in Iranian flax populations using retrotransposon microsatellite amplification polymorphisms (REMAP) markers. *Nucleus* **61**, 55–60. <https://doi.org/10.1007/s13237-017-0218-3>.
- Hagberg, A. A., Schult, D. A., & Swart, P. J. (2008). Exploring network structure, dynamics, and function using NetworkX. In G. Varoquaux, T. Vaught, & J. Millman (Eds.), *Proceedings of the 7th Python in Science Conference* (pp. 11–15).

- Hazneci E., & Arslanaoğlu Ş. F. (2021). Orta Karadeniz Bölgesinde Kırsal Alanlar İçin Keten Bir Şans Mı? Kârlılık Analizi ve Yapılabilirliği. *Tekirdağ Ziraat Fakültesi Dergisi*, 18 (3), 586-598. <https://doi.org/10.33462/jotaf.938556>
- Hunter, J. D. (2007). Matplotlib: A 2D graphics environment. *Computing in Science & Engineering*, 9(3), 90–95. <https://doi.org/10.1109/MCSE.2007.55>
- Jordahl, K., den Bossche, J. V., Fleischmann, M., Wasserman, J., McBride, J., Gerard, J., et al (2020). geopandas/geopandas: v0.8.1 (Version v0.8.1) [Computer software]. Zenodo. <https://doi.org/10.5281/zenodo.3946761>
- Karimova, S., Kholmuradov, E., Juliev, M., Boytoraeva, F., & Nuraliyev, H. (2023). A bibliometric analysis of global publications on flax (*Linum usitatissimum* L.) disease during 2001-2021. *Mustafa Kemal Üniversitesi Tarım Bilimleri Dergisi*, 28 (2), 413-426. <https://doi.org/10.1234256/mkutbd.1234256>
- Koçak, M. Z., Kaysim, M. G., Aydın, A., Erdinc, C., & Kulak, M. (2023). Genetic diversity of flax genotypes (*Linum usitatissimum* L.) by using agro-morphological properties and molecular markers. *Genetic Resources and Crop Evolution*, 70(8), 2279-2306. <https://doi.org/10.1007/s10722-023-01608-6>
- Nag S., Mitra J., Karmakar P.G. (2015). An Overview on Flax (*Linum usitatissimum* L.) and its Genetic Diversity. *International Journal of Agriculture, Environment and Biotechnology Citation: IJAEB*, 8(4): 805-817. DOI Number: 10.5958/2230-732X.2015.00089.3
- Majumdar K., Thakur B., Majumdar A. (2022) Natural Fiber Reinforced Concrete: Bibliometric and Network Analyses to Delineate the Current Status and Future Pathways, *Journal of Natural Fibers*, 19:17, 15963-15983, <https://doi.org/10.1080/15440478.2022.2140323>
- McDill, J., Repplinger, M., Simpson, B.B., & Kadereit, J.W. (2009). The Phylogeny of Linum and Linaceae Subfamily Linoideae, with Implications for Their Systematics, Biogeography, and Evolution of Heterostyly. *Systematic Botany*, 34(2), 386–405. <https://doi.org/10.1600/036364409788606244>
- McKinney, W. (2010). Data structures for statistical computing in Python. In S. van der Walt & J. Millman (Eds.), *Proceedings of the 9th Python in Science Conference* (pp. 51–56). <https://doi.org/10.25080/Majora-92bf1922-00a>
- Mueller, A. C. (2020). Wordcloud: A little word cloud generator in Python [Computer software]. GitHub. https://github.com/amueller/word_cloud
- Nadeem, M. A., Nawaz, M. A., Shahid, M. Q., Doğan, Y., Comertpay, G., Yıldız, M., Hatıoğlu R., Ahmad F., Alsaleh A., Labhane N., Özkan H, Chung G. & Baloch, F. S. (2017). DNA molecular markers in plant breeding: current status and recent advancements in genomic selection and genome editing. *Biotechnology & Biotechnological Equipment*, 32(2), 261–285. <https://doi.org/10.1080/13102818.2017.1400401>
- Nair, R.J., & Pandey, M.K. (2021). Role of Molecular Markers in Crop Breeding: A Review. *Agricultural Reviews*. DOI: 10.18805/ag.R-2322.
- Nwanko CO., Mahachi J., Olukani DO., Musonda I (2023). Natural fibres and biopolymers in FRP composites for strengthening concrete structures: A mixed review. *Construction and Building Materials*, 363, 129661. <https://doi.org/10.1016/j.conbuildmat.2022.129661>
- Rachinskaya, O.A., Lemesh, V.A., Muravenko, O.V., Yurkevich O.Yu., Guzenko E.V., Bol'sheva N.L., Bogdanova M.V., Samatadze T.E., Popov K.V., Malyshev S.V., Shostak N.G., Heller K., Hotyleva L.V., Zelenin A.V. (2011). Genetic polymorphism of flax *Linum usitatissimum* based on the use of

- molecular cytogenetic markers. *Russian Journal of Genetics*, 47(1), 56–65 (2011). <https://doi.org/10.1134/S1022795411010108>.
- Sarwat, M., Nabi, G., Das, S., & Srivastava, P.S. (2011). Molecular markers in medicinal plant biotechnology: past and present. *Critical Reviews in Biotechnology*, 2011, 1–19. DOI: 10.3109/07388551.2011.551872.
- Shawahna, R. & Nairat, Q. (2021). Research productivity in the field of physical exercise and epilepsy: A bibliometric analysis of the scholarly literature with qualitative synthesis. *Epilepsy & Behavior*, 121(Pt A):108058. <https://doi.org/10.1016/j.yebeh.2021.108058>
- Singh KK, Mridula, D., Rehal, J. & Barnwal P. (2011) Flaxseed: A Potential Source of Food, Feed and Fiber, *Critical Reviews in Food Science and Nutrition*, 51(3), 210-222, <https://doi.org/10.1080/10408390903537241>
- Smýkal, P., Bačová-Kerteszová, N., Kalendar, R., Corander, J., Schulman, A. H., & Pavelek, M. (2011). Genetic diversity of cultivated flax (*Linum usitatissimum* L.) germplasm assessed by retrotransposon-based markers. *Theoretical and Applied Genetics*, 122, 1385-1397. <https://doi.org/10.1007/s00122-011-1539-2>
- Sütcü, T., Bilgen, B.B., & Tuna, M. (2022). Analysis of Genetic Diversity Among Onobrychis Accessions with High Agronomic Performance by Simple Sequence Repeat (SSR) Markers. *Mol Biol Rep.*, 49,5659-5668. <https://doi.org/10.1007/s11033-022-07584-x>.
- Stägel, A., Portis E, Toppino, L., Rotino, G.L, & Lanteri S. (2008). Gene-based microsatellite development for mapping and phylogeny studies in eggplant. *BMC Genomics*, 9:357. <https://doi.org/10.1186/1471-2164-9-357>
- Tadesse T., Singh H. and Weyessa, B. (2009). Genetic Divergence in Linseed Germplasm. *J. Innov. Dev. Strategy*. 3(2):13-20.
- Ulcay, S. (2023). Histo-Anatomical Characteristics of Some Endemic Species of Linum (Linaceae). *Journal of the Institute of Science and Technology*, 13(2), 925-931. <https://doi.org/10.21597/jist.1214429>
- Uysal, H., Fu, Y. B., Kurt, O., Peterson, G. W., Diederichsen, A., & Kusters, P. (2010). Genetic diversity of cultivated flax (*Linum usitatissimum* L.) and its wild progenitor pale flax (*Linum bienne* Mill.) as revealed by ISSR markers. *Genetic Resources and Crop Evolution*, 57, 1109-1119. <https://doi.org/10.1007/s10722-010-9551-y>.
- Wakjira, A., Viljoen, C., & Labuschagne, M. (2005). Analysis of genetic diversity in linseed using AFLP markers. *Ethiopian J. Sci.*, 28(1), 41–50. <https://doi.org/10.4314/sinet.v28i1.18230>
- Wang, Z., Hobson, N., Galindo, L., Zhu, S., Shi, D., McDill, J., Yang L, Hawkins S, Neutelings G, Datla R, Lambert G, Galbraith DW, Grassa CJ, Geraldles A, Cronk QC, Cullis C, Dash PK, Kumar PA, Cloutier S, Sharpe AG, Wong GK, Wang J, Deyholos MK (2012). The genome of flax (*Linum usitatissimum*) assembled de novo from short shotgun sequence reads. *The Plant Journal*, 72(3), 461–473. <https://doi.org/10.1111/j.1365-313X.2012.05093.x>
- Wani, Z.A., Akhter, F., Ridwan, Q., Rawat, Y.S., Ahmad, Z., & Pant, S. (2023). A Bibliometric Analysis of Studies on Plant Endemism during the Period of 1991–2022. *Journal of Zoological and Botanical Gardens*. 2023; 4(4):692-710. <https://doi.org/10.3390/jzbg4040049>
- Waskom, M. L. (2021). seaborn: statistical data visualization. *Journal of Open Source Software*, 6(60), 3021. <https://doi.org/10.21105/joss.03021>

- Yardibi, F, Firat, M. Z, & Teke, E. Ç (2021). Trend topics in animal science: a bibliometric analysis using CiteSpace. *Turkish Journal of Veterinary & Animal Sciences* 45 (5): 833-840. <https://doi.org/10.3906/vet-2001-103>
- Yılmaz S., Uzun A (2019). Keten Tarımı. ISBN: 978-605-2207-25-3.
- Yılmaz Ö., Kaynak G., Vural M. (2003). A new taxon of *Linum* (Linaceae) from NW Anatolia, Turkey. *Ann. Bot. Fennici*, 40: 147–150.
- Yorgancılar M., Yakışır E., Tanur Erkoyuncu M (2015). Moleküler Markörlerin Bitki Islahında Kullanımı. *Journal of Bahri Dagdas Crop Research*, 4 (2),1-12.
- Yaldız, G., Camlica, M., Nadeem, M. A., Nawaz, M. A., & Baloch, F. S. (2018). Genetic diversity assessment in *Nicotiana tabacum* L. with iPBS-retrotransposons. *Turkish Journal of Agriculture and Forestry*, 42, 154-164. doi:10.3906/tar-1708-32
- Yurkevich, O.Y., Kirov, I.V., Bolsheva, N.L., Rachinskaya, O.A, Grushetskaya, Z.E., Zoschuk, S.A., Samatadze, T.E., Bogdanova, M.V., Lemesh, V.A., Amosova, A.V., & Muravenko O.V. (2017) Integration of Physical, Genetic, and Cytogenetic Mapping Data for Cellulose Synthase (CesA) Genes in Flax (*Linum usitatissimum* L.). *Frontiers in Plant Science*. 8:1467. <https://doi.org/10.3389/fpls.2017.01467>