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A comprehensive bibliometric evaluation of research articles concerning CRISPR/Cas technology applied to forest and fruit trees

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Abstract: The application of CRISPR/Cas genome editing has swiftly grown beyond just model plants and annual crops to also cover woody perennials, which face obstacles such as extended juvenile stages, significant heterozygosity, and resistance to *in vitro* regeneration that hinder standard breeding approaches. This study offers a bibliometric overview that focuses on CRISPR/Cas research specifically related to forest and fruit trees. Between the years 2013 and 2025, 1,098 records were collected from the Web of Science Core Collection, after which screening by title and abstract was conducted, resulting in 464 publications deemed relevant, including 376 original articles and 88 reviews. The study analysed publication patterns, investigated taxa, contributing countries, journals, and editing techniques, alongside mapping keyword co-occurrence through VOSviewer. Annual output increased from 2 papers in 2014 to 107 in 2025, with fruit trees and grapevine (47%) and forest trees (38%) as the main groups. Research was concentrated on a few genera, led by *Populus* (145 publications), *Citrus* (79), *Vitis* (75) and *Malus* (53). China and the USA contributed to 47% and 28% of the publications, respectively. Cas9 remained the dominant editing system, while base editing, Cas12a and transgene-free approaches, including RNP- and protoplast-based delivery, became more frequent after 2020. Keyword analysis revealed four thematic clusters, related to wood formation in poplar, disease resistance in citrus, *in vitro* regeneration and transgene-free editing in fruit species, and breeding for flowering and fruit traits. The results show a rapidly growing but taxonomically narrow research field, in which efficient regeneration and delivery systems remain key requirements for extending genome editing to a wider range of woody species.

• Introduction

CRISPR/Cas systems have become the most widely used tools for targeted genome modification in plants; the toolbox now includes Cas12a, base editors and the delivery of preassembled ribonucleoproteins (RNPs).

Forest and fruit trees have long juvenile phases, high heterozygosity and often clonal propagation, so a breeding cycle may take decades. Genome editing can change an elite clone directly, but depends on efficient transformation, *in vitro* regeneration and removal of the editing cassette. The first edits were reported in sweet orange (2014), poplar (2015), apple and grapevine (2016).

Aim: Analyse CRISPR/Cas research on forest and fruit trees indexed in the Web of Science Core Collection (2013–2025): publication output, taxa, countries, journals, most cited papers, editing systems, delivery methods and thematic structure.

• Material and method

- **Data source:** Web of Science Core Collection, retrieved on 15 October 2026; articles and reviews published in 2013–2025
- **Search:** genome-editing terms (CRISPR, Cas9, Cas12, base and prime editing, etc.) AND woody-plant terms (forest and fruit trees, conifers and 23 genera, e.g. *Populus, Pinus, Malus, Citrus, Vitis*)
- **Screening:** 1,098 records screened by title, abstract and keywords (AI-assisted, verified by the authors on 110 records with 100% agreement); 464 publications included
- **Data extracted:** year, type, journal, countries, citations, taxa, editing system, delivery method, transgene-free outcome; three periods (2014–2019, 2020–2022, 2023–2025)
- **Science mapping:** VOSviewer 1.6.21, author keywords with ≥ 4 occurrences (25 keywords), resolution 0.7

• Results and discussions

Publication output. The 464 publications comprised 376 original articles (81.0%) and 88 reviews (19.0%). Output rose from 2 papers in 2014 to 107 in 2025; 86.6% appeared from 2020 onwards (compound annual growth ≈ 32% in 2016–2025). Fruit trees and grapevine accounted for 47.0%, forest trees for 37.5% and tropical or industrial crops for 4.3%.

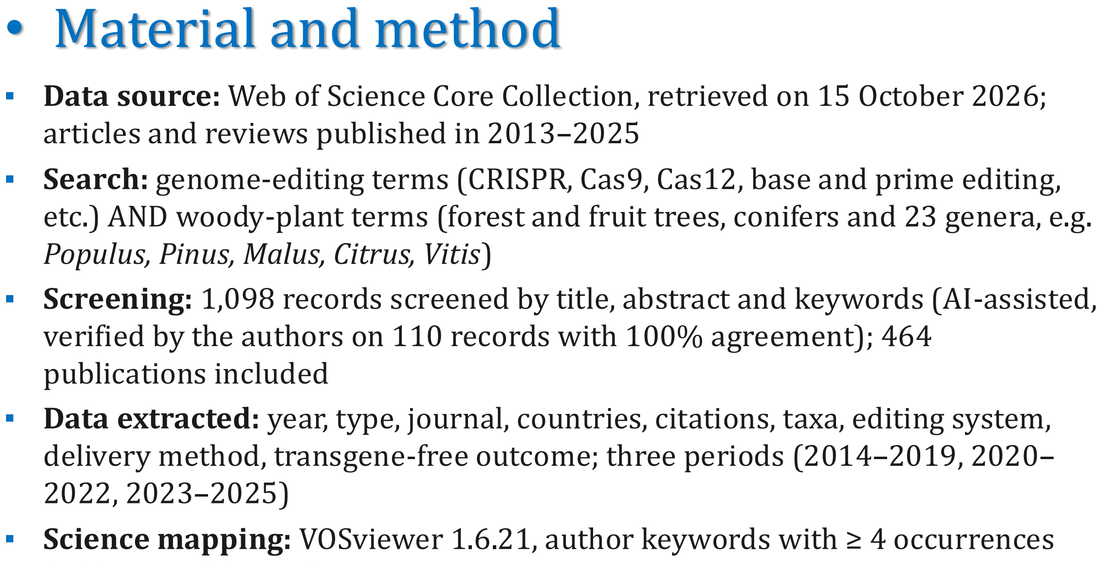


Figure 1. Annual number of included publications by woody plant group (2014–2025)

Woody taxa. Research was concentrated on four genera, addressed together in 70% of the publications (Table 1). Conifers appeared in only 18 publications (3.9%), *Eucalyptus* in 8 and *Quercus* in one. This reflects the availability of reference genomes and efficient transformation systems, such as the poplar clones.

Table 1. Most studied woody taxa (share of the 464 publications)

Genus / taxon	Group	Publications	% of total
Populus (poplar, aspen)	Forest	145	31.3
Citrus	Fruit / grapevine	79	17.0
Vitis (grapevine)	Fruit / grapevine	75	16.2
Malus (apple)	Fruit / grapevine	53	11.4
Actinidia (kiwifruit)	Fruit / grapevine	26	5.6
Other conifers	Forest	12	2.6

Countries, journals and citations. Authors came from 46 countries, led by China (218 publications; 47.0%) and the USA (130; 28.0%), followed by Italy (41), France (22), India and Spain (21 each). China's share grew from 37% (2014–2019) to 53% (2023–2025), while that of the USA fell from 37% to 24%. The 139 journals were led by *Frontiers in Plant Science* (46); the 16,989 citations (mean 36.6) favoured early papers, e.g. DNA-free editing of grapevine and apple protoplasts (510).

Editing systems and delivery. Cas9 was reported in 290 of the 376 original articles (77.1%), but its share fell from 85% to 72%. Cas12a (20 articles) and base editing (19) appeared only after 2019; prime editing remained marginal (4). Transgene-free or DNA-free outcomes were reported in 48 articles (12.8%), rising to 16% in 2023–2025, through RNPs delivered into protoplasts or excision of the editing cassette. Regeneration of whole plants from single cells remains the main bottleneck.

Thematic structure. Keyword co-occurrence revealed four clusters (Figure 2): wood formation and lignin in poplar (blue), citrus canker and *CsLOB1* (yellow), regeneration, protoplasts and transgene-free editing in fruit species (red), and breeding, early flowering and fruit quality (green).

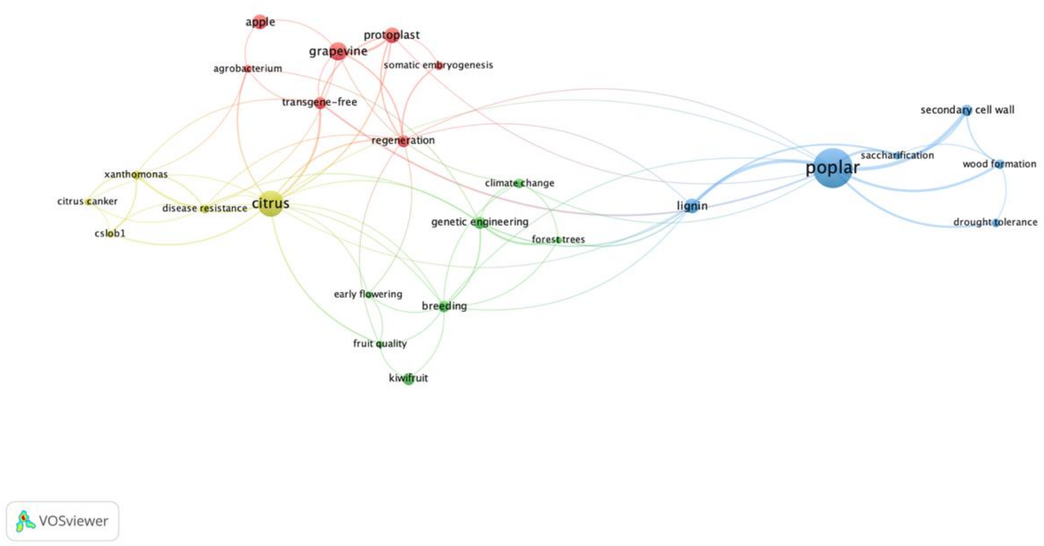


Figure 2. Keyword co-occurrence map (author keywords, minimum four occurrences, VOSviewer)

• Conclusions

- CRISPR/Cas research on forest and fruit trees grew from 2 publications in 2014 to 107 in 2025; 86.6% of the 464 publications appeared after 2019
- The field is taxonomically narrow: *Populus, Citrus, Vitis* and *Malus* were addressed in 70% of the publications, while conifers, most broadleaved forest trees and tropical tree crops remain poorly represented
- China (47%) and the USA (28%) dominate research output, with a growing share of China
- Cas9 remains dominant, but Cas12a, base editing and transgene-free approaches have become more frequent since 2020
- Efficient regeneration and delivery systems for more genotypes are the main requirement for extending genome editing to other woody species