

REVIEW

Open Access



Development of molecular resources for the genetic improvement of noug (*Guizotia abyssinica* (L.f) Cass): a mini review

Motbaynor Terefe* and Dejene Girma

Abstract

Noug (*Guizotia abyssinica* (L.f) Cass) is an important edible oil-producing crop. Ethiopia is the center of origin and diversity for noug and thousands of noug accessions are being maintained at the Gene Bank in Ethiopian Biodiversity Institute (EBI). The crop is grown mainly for edible oil and the by-product named as noug-cake is widely used as animal feed. However, the production and productivity of noug is too low compared to other oilseed crops mainly due to the self-incompatible nature of the crop species, shattering, lodging, indeterminate growth habit, pests, and diseases. The development and application of molecular resources and tools have played a great role in the improvement of oilseed crops worldwide. Although conventional breeding has been used to develop commercial noug varieties, the application of modern genomic tools to enhance the use of noug germplasm resources is very limited. In this work, we have reviewed the scientific literature available on the development and application of molecular resources on oil-producing crops and specifically reveal research gaps on noug genetic improvement and highlight broadly applicable and affordable short-term strategic interventions.

Keywords: Noug, Diversity, Genomic tools, Genetic improvements, Molecular resources

Introduction

Oilseed crops are predominantly grown worldwide for the production of edible oil being used as an important source of fatty acids and nutrients (Yadav et al. 2012). Additionally, oilseed crops are used for biofuel production, livestock feed, pharmaceuticals, soap production, hair oils, textiles, and paints (Rahman and Jiménez 2016; York and Garden 2016). The total worldwide oilseed production for the year 2019/20 was 574.62 million metric tons from 279.2 million hectares, only from major oilseed crops (USDA 2019). In Ethiopia, about 7,850,196.94 quintals from 747, 803.78 hectares were obtained for the year 2018/19 (CSA 2019). The leading oil crop-producing countries are Brazil, USA, Argentina, China, and

India (USDA 2019). Some of the oilseed crops produced worldwide are; soybean (*Glycine max* L.), sunflower (*Helianthus annuus* L.), cottonseed (*Gossypium hirsutum* L.), coconut (*Cocos nucifera*), peanut (*Arachis hypogaea* L.), groundnut (*Arachis hypogaea*) safflower (*Carthamus tinctorius* L), rapeseed (*Brassica napus* L.), palm (*Elaeis guineensis* Jacq.), castor bean (*Ricinus communis* L.), mustard (*Brassica carinata*) (Farooq et al. 2016) and noug/Niger seed (*Guizotia abyssinica* (L.f) Cass). From these; noug is considered as one of the minor and under-utilized oilseed crops due mainly to limited research short of what the crop deserves for its improvements.

Noug (*Guizotia abyssinica*) is an edible oilseed crop indigenous to Ethiopia (Baagoe 1974) which has been cultivated for approximately 5000 years (Ramadan 2012). *Guizotia abyssinica* has a diploid genome constituting ($2n=2x=30$) chromosome number and belongs to the family composite/Asteraceae/ (Dagne 1995). Out

*Correspondence: motbaynor2008@gmail.com

National Agricultural Biotechnology Research Center, Ethiopian Institute of Agricultural Research, P.O.Box 249, Holeta, Ethiopia



© The Author(s) 2022. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

of the six species in the genus *Guizotia*; *Guizotia abyssinica* is the only cultivated one. Noug is a dicotyledonous herb with moderate to well branch and grows up to 2 m in height (Fig. 1A and B). The stems are soft, hairy, hollow with a diameter up to 2 cm, and branched. The leaves are opposite or alternate at the stem apices, with lanceolate to obovate leaf blades, 3–23 cm × 1–6 cm, variable in shape, with an entire or toothed margin, ciliate, and softly hairy on both surfaces. The root system is well developed, with a taproot with numerous lateral roots, especially in the top 5 cm. As well as the seeds are small achenes (fruits), 3–6 mm long × 1.5–4 mm wide and glossy black in color (Bulcha 2007). The hermaphroditic disk florets, usually 40–60 per capitulum are arranged in three whorls. Those at the edge opening first, followed progressively by the next in line to the center of the head (Alemaw and Wold 1995; Getinet and Sharma 1996).

These are some of the physiological distinguishing characteristics from the closest species.

Noug grows best on poorly drained, heavy clay soil, and is not dependent on highly valued agricultural inputs (Alemaw and Wold 1995; Geleta and Ortiz 2013; Tadele 2018). It's optimally grown in Ethiopia in the temperature range of 15–23 °C and 1600–2200 m asl with an annual rainfall of around 500–1000 mm (Getinet and Sharma 1996) but also there are indications that it can be grown as low as 1200 m asl and above 2700 m asl (Geleta and Ortiz 2013). Major growing areas in Ethiopia are Gonder, Shewa, Wollo, Gojjam, Wollega, Jimma, Tigray, and Illubabur (Getinet and Sharma 1996). It's extensively produced in Ethiopia and India and also on a small scale in several other countries. India ranks first in the area, production, and export of noug in the world followed by Ethiopia (Rai et al. 2016). In Ethiopia; it is the second



Fig. 1 Field cultivation status (A), Flowering stage (B), Harvested seed (C), and Packaged pure edible oil (5L) (D) of Noug/Niger seed. Source: (<https://www.landwirtschaftskammer.de/fotos/zoom/r/ramtillkraut.jpg>; <https://www.springhausagro.com/niger?pgid=k76pue4k-c1d1968d-2640-410b-abf5-07bb829e7b9f>; <https://twobrothersindiashop.com/blogs/farmers-kitaab/niger-seeds-khurasni-ram-til-long-forgo-ten-oil-seed-with-applications-in-tribal-medicine>; <https://cnetcommerce.com/dukem-pure-niger-seed-oil-5l>)

oilseed crop next to sesame (*Sesamum indicum* L.) in terms of production; from 257,950.4 hectares obtained about 2,963,227.47 quintals which contributes about 2.03% of the national grain total production (CSA 2019). It is cultivated, consumed, and sold by several smallholders with high-value socio-economic importance (Geleta et al. 2002). The Ethiopian Biodiversity Institute (EBI) conserved germplasm collections from different agro-ecological regions in the country. The country is the major source of noug germplasms.

Noug is mainly used as human food. It contributes up to 50% of the Ethiopian oilseed crop (MoA 2016) and 3% of Indian national production (Getinet and Sharma 1996). However; both Ethiopia and India are heavily reliant on oil imports for their domestic use. The noug oil is used to protect against cardiovascular disorders and to treat burns (Adarsh et al. 2014), and also for other cultural and medicinal values in Ethiopia and as the main birds feed in the USA (Geleta et al. 2002). The seed is warmed in a kettle over an open fire, crushed with a pestle in a mortar, and then mixed with crushed pulse seeds to prepare a stew in Ethiopia and 'Chibto' and 'litlit' are also the preferred food for young boys (Getinet and Sharma, 1996). The pressed cake left after oil extraction is used for livestock feed as a good source of protein, carbohydrate, and fiber (Kandel and Porter 2002).

The noug seed contains 17–30% protein, 34–39% carbohydrate, and 9–13% fiber (Ramadan 2009). The oil content of the Ethiopian noug seed ranges between 27–56% (Geleta et al. 2011) and its predominant fatty acid composition vary with linoleic acid (C18:2) 54–85%, oleic acid (C18:1) 3.3–31.1%, palmitic acid (C16:0) 7.8–10%, and stearic acid (C18:0) 5–8% (Dagne and Jonsson 1997). The noug seed also contains essential minerals and nutrients for food (Tsehay et al. 2021).

Despite its multiuse, the national average productivity is very low, which is only 1.1ton/ha (CSA 2019; Fig. 2). This might be due to individual or combined factor/s contribution of; the plants' indeterminate growth habit, shattering lodging, and self-incompatibility (strict out-crossing nature) (Geleta et al. 2007), weeds, pests, diseases, and insects (Getinet and Sharma 1996). Until very recently noug has attracted little research attention and mainly remained as an underutilized oilseed crop (Dempewolf et al. 2015).

Breeding noug (research) in Ethiopia started in 1961 at Debrezeit experimental station, Debrezeit, and continued at Holeta Research Station, Holeta (Alemaw and Alemayehu, 1992). The overall breeding objective was to develop high-yielding and disease-resistance varieties that are adapted to vertisols, with synchronized flowering and maturity, semi-dwarf stature, and thin hull (Alemaw and Alemayehu, 1992). So far, only five improved varieties are under production (Table 1) which are released in different years (MoA 2016), much less than twenty-six (26) sesame improved varieties.

These varieties were developed using conventional breeding approaches mostly selection. With the

Table 1 Lists of improved varieties year of release, yield and oil contents

Varieties	Year of release	Yield (kg/ha)	Oil content (%)
Ginchi-1	2010	884	45.9
Shambu-1	2002	970	39
Kuyu	1994	1060	41
Fogera	1988	820	41
Esete-1	1988	830	39
Landraces	–	724	38

Source: Alemaw and Alemayehu (1992), Misteru 2008; Wirtu 2021)

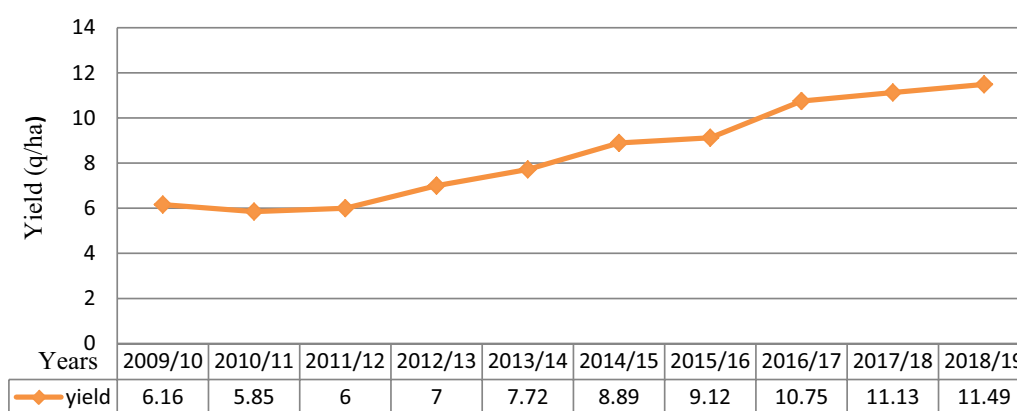


Fig. 2 Average yield increment of noug for the last 10 years in Ethiopia (qt/ha). Source: CSA (2019)

availability of molecular resources, however, the efforts of noug breeders can be complemented to enhance the efficiency of varietal development and increase genetic gain.

Ethiopia is the center of origin for noug and is expected to have highly diversified genetic resources that are essential to improve specific traits. However, the development, utilization, and conservation of genetic resources depend on the understanding of their genetic information. This paper reviews molecular resources adopted and developed for noug so far and highlights research gaps for future improvement and utilization of noug, special emphasis on tools for genetic improvement and application of different genetic marker systems for diversity study of noug is given.

Tools for the genetic improvement of oilseed crops

In oilseed crops, limited research focus has been vested as compared to cereal crops in the context of developing new varieties. Studies on the new cultivars' development in the oilseed crops primarily focus to increase yield, oil content or quality, and biotic and abiotic stress resistance. In the ensuing sections tools employed for the genetic improvement of major oilseed crops are given with special emphasis on noug.

Molecular markers for diversity analysis and marker-assisted breeding in oilseed crops

Reliable molecular markers have significantly speeded up modern plant breeding by enhancing genetic gains and reducing the breeding cycles. Different types of molecular marker systems are widely applied to oilseed crops for genotyping and breeding efforts. For instance, the genetic diversity of some major oilseed crops was studied and assisted the breeding efforts using RAPD in Caster

bean (Gajera et al. 2010), AFLP in Safflower (Zhang et al. 2006), RFLP in Sunflower (Gentzbittel et al. 1994), ISSR in groundnut (Mondal et al. 2009), SSR, and/or EST-SSR in Soybean (Liu et al. 2010) and SNPs in Cotton (Song et al. 2018). The progress in the exploitation of genetic diversity and utilization of the genetic gains on major oilseed crops shifted the interest also to minor-oilseed crops.

The molecular understanding of noug germplasms is imperative; this could be significant in the varietal identification and implementation of improved breeding and conservation programs. Attempts at genetic characterization of noug using a few molecular markers revealed considerable variation. For instance, using RAPD (Dagne and Jonsson 1997), AFLP (Geleta et al. 2008), ISSR (Hussain et al. 2015; Petros et al. 2007), SSR (Dempewolf et al. 2015; Abebaw and Solomon 2017; Aboye et al. 2020) markers (Table 2). However, they were limited in the high resolution genetic analysis, and they should be complemented with other high-throughput markers.

Markers play a great role in the identification and selection of QTLs that control economically important traits. Marker-assisted breeding (MAB) can be used to increase the efficiency of selecting parents and the effectiveness of backcross (Semagn et al. 2006). This technique has been successfully applied in different oilseed crops such as disease resistance hybrid selection in Sunflower (Sahin et al. 2018), marker-assisted selection for oleic acid controlling genes in groundnut, marker-assisted introgression of fatty acid desaturase mutant allele in peanut (Janila et al. 2016), and marker-assisted backcross selection for seed oleic acid content in peanut (Huang et al. 2019).

In noug, breeding was based on phenotype screening. Subsequently, few molecular markers were developed

Table 2 Utilization of molecular markers for diversity and phylogenetic analysis of noug (*Guizotia abyssinica*)

Marker	Populations	Year	Study aims	References
RAPD	70 populations of Ethiopian origin	2007	Genetic diversity study and its correlation with their respective altitude range	Geleta et al. (2007)
RAPD	18 cultivars from Indian origin	2008	Genetic diversity evaluation	Nagella et al. (2008)
AFLP	70 population from Ethiopia	2008	Genetic diversity analysis	(Geleta et al. 2008)
ISSR	35 accessions from Indian Origin	2015	Genetic diversity using ISSR and biochemical markers (oil content parameters)	Hussain et al. (2015)
ISSR	37 populations from Ethiopia	2007	Genetic diversity study	Petros et al. (2007)
SSR	29 noug and 4 from its wild progenitor obtained from Ethiopia	2015	Pattern of domestication, genetic diversity within noug and between its wild progenitor	Dempewolf et al. (2015)
SSR	65 accession from Ethiopian origin	2017	Genetic diversity assessment	Abewaw and Solomon (2017)
SSR	100 accessions from Ethiopian origin	2018	SSR based Genetic diversity estimation	Aboye et al. (2020)
SNP/KASP	24 accessions from Ethiopia	2020	Developing new SNP/KASP markers for population genetics analysis	Tsehay et al. (2020)
SNP/SSR	30 genotypes from Ethiopia	2022	RNA-Seq based transcriptome sequencing to generate novel genomic resources and assess their microsatellite frequencies	Gebeyehu et al. (2022)

and applied for genetic diversity study in noug (Table 2), but there is a need for linkage and QTL mapping of traits of interest and marker-assisted selection and/or breeding. To use MAS/MAB, markers closely linked to genes/QTLs controlling target agronomic traits should be identified (Janila et al. 2016). A wide range of traits might be targeted by the breeders for genetic improvement of noug i.e. abiotic stress tolerance, disease resistance, and yield and quality types which might be controlled by one or more genes. In the future, marker-assisted selection and introgression of desirable traits using tightly linked molecular markers may be a breakthrough to boost the production and productivity of noug.

Overall, further understanding of the existing variation using more molecular marker tools will help the available genetic resources for further improvement and conservation.

Linkage and QTL mapping

Linkage and quantitative trait loci (QTL) mapping help to identify the relative location of various genetic markers present in the chromosome of crops (Singh et al. 2015) and to identify regions of the genome contributing to variation in desirable traits. High-density genetic maps are particularly important for genome assembly and precise mapping of interest agronomic traits (genes) for marker-assisted selection (Song et al. 2018). This approach has been applied in oilseed crops like identification of QTL markers contributing to plant growth, oil yield, and fatty acid composition in *Jatropha* (King et al. 2015), SSR based genetic mapping and identification of QTLs in Sesame (Wang et al. 2017), high-density genetic map construction, and identification of QTLs controlling oleic acid and linoleic acid in peanut using SSR and specific length amplified fragment sequencing (SLAF-seq) markers (Hu et al. 2018) and mapping of quantitative trait loci for yield-related traits in peanut using high-resolution SNPs markers (Liang et al. 2018).

Noug is a complete out-crossing crop that makes it difficult to develop inbred lines that are the basis for linkage and QTL map construction. Attempts on the development of self-compatible lines were made by Geleta and Bryngelsson (2010) through reciprocal cross-pollination. As a result, completely self-compatible genotypes have been developed for the first time with various associated advantages. Interestingly, two of the compatible lines (C19-1 and K13-1) were utilized for transcriptome sequencing (Tsehay et al. 2020). Additionally, self-compatible genotypes were developed through crossbreeding and selfing and were used for RNA-seq based sequencing (Gebeyehu et al. 2022). Once self-compatible genotypes are identified, it is simple to generate pure-lines maintaining traits for generations. However, there was

no further report on pure-line development attempts for linkage and QTL mapping or other genomic studies in noug. This implies the need for generation of pure-lines, QTL mapping, and the identification of important agronomic traits. One possible explanation for the crop's limited studies on QTL mapping and molecular mechanisms of noug could be lack of research vigilance.

Genome-wide association studies and genomic selection

Genome-wide association studies (GWAS) and genomic selections (GS) are powerful tools to understand the regulatory loci and the genetic architecture of complex traits of interest in plants at the whole genome level (Kushwaha et al. 2017; Werner et al. 2018). The ultimate goal of GWAS also called association mapping or linkage disequilibrium (LD) mapping is to dissect the association of markers/QTLs and complex quantitative traits involved in phenotypic variation. Whereas GS refers, to the genome-wide based selection of traits-associated markers by capturing the genetic variance (de Koning 2016). With the development of high-resolution SSR and SNPs markers, a large number of GWAS and GS studies have been reported in oilseed crops such as in Safflower (Ambreen et al. 2018), soybean (Zhang et al. 2016), Sesame (Li et al. 2014) and Cotton (Gapare et al. 2017).

A GWAS and GS study in noug is scarce and, both GWAS and GS will help to clearly understand the genetic basis of complex traits that are productive for noug.

In general, noug offers very plausible genomic tools and techniques to increase its production and productivity, which is now very low as compared to other oilseed crops. The pioneering tools were developed and applied in noug with the primary aim of determining the taxonomic classification, genetic diversity, and its relationship with wild relatives (Tables 2, 3).

Induced mutagenesis and genetic transformation of oilseed crops

Induced mutation, in which mutation occurs as a result of chemical (ethyl methane sulfate (EMS), physical (X-rays, gamma rays, UV and ion beam), or biological (site-directed mutation or genome editing) mutagenic agents to create variability (Oladosu et al. 2016). Mutation breeding in crops relies on altering traits of interest using diverse mutagens (Tadele 2016). This mutation breeding program has been the base for the release of different new crop varieties globally. For example in oilseed crops, non-shattering Sesame capsules using gamma-ray and EMS (Wongyai et al. 2001), increased oil quality of soybean using site-directed mutagenesis (Haun et al. 2014) and EMS-based mutation of desaturase gene (FADH2-2) which resulted in high oleic acid content in

Table 3 Molecular tools and resources developed in noug (*Guizotia abyssinica*)

Molecular tools and resources	Years	References
Complete sequences of the internal spacer of the 18 s–26 s ribosomal DNA	2007	Bekele et al. (2007)
Whole chloroplast genome sequence and marker development	2010	Dempewolf et al. (2010)
Sequence data from different chloroplast regions	2010	Geleta et al. (2010)
Transcriptome sequencing and SNP/KASP markers	2020	Tsehay et al. (2020)
RNA-Seq based transcriptome sequencing	2022	Gebeyehu et al. (2022)

rapeseed (Won et al. 2018). Mutation breeding along with transgenic breeding becomes a pillar for modern breeding programs (Oladosu et al. 2016). Genetic transformation has been described as the fundamental tool for the genetic improvement of crops including major oilseed crops. For instance, herbicide-resistance (roundup ready) in Soybean (Padgett et al. 1995), disease resistance transgenic castor (Sood and Chauhan 2018), and oil quality in sunflower (Cveji, 2020).

After a multidisciplinary research approach has been started on noug in 1979, induced mutation research was initiated using gamma rays targeting for dwarfing genes (Alemaw and Alemayehu 1992) and showed promising results at F1 generation. However, it fails to transfer to the next generations. Since then, no more progress was made to implement induced-mutation breeding on noug. In another hand, the first report on the genetic transformation of noug was only protocol development for *Agrobacterium*-mediated genetic transformation in India (Yadava et al. 2012). However, it was not clearly defined and reproducible. Establishing a reproducible transformation protocol is a priority task to implement genetic transformation on noug.

Conclusion and future prospectives

Molecular resources have played a vital role in the genetic improvement of oilseed crops. Noug, which is a multi-purposed oilseed crop should benefit from these. Interestingly, despite being domesticated since the BCs and having a long history of cultivation, it is still referred to as a semi-domesticated crop for a variety of reasons (Dempewolf et al. 2015). This is critical for acquiring important genes from wild types and adapting to a new area in resisting harsh environments. The crop has genetic resources due to phenotype plasticity and molecular polymorphism, particularly in primary origin areas, which will be used for genetic improvements.

As demand for its oil consumption and industrial applications increases over time, its yield, oil content, and quality should be improved. However, the crop is facing different production and breeding constraints. The advancement

of molecular biology tools, as well as the presence of high genetic variation, reinforces the opportunity to improve the crop with the available resources. Remarks for general genetic improvement of noug to make it more competitive includes (i) further molecular characterization of noug landraces with more efficient molecular markers for breeding and conservation; (ii) utilization of techniques and means to consolidate noug improvement intents such as induced mutagenesis breeding for specific traits and QTL mapping of desirable traits (iii) Developing and applying highly advanced molecular tools and resources for further crop exploration, like as genome sequencing, genotyping by sequencing (GBS), transcriptome analysis for important gene function prediction, gene editing or manipulation, and genetic transformation, especially on proteins essential for fatty acid synthesis.

The utmost utilization of its genetic resources and giving research attention will have a great role in fulfilling the demand for edible oil worldwide and contribute to ensuring food security.

Acknowledgements

The authors would like to thank Dr. Genet Birmeta for the editing of the draft.

Author contributions

MT wrote the draft and revision of the manuscript; DG conceived the idea and edited the draft. Both the authors read and approved the final manuscript.

Funding

The authors did not receive any funding.

Availability of data and materials

Not applicable.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no any conflict of interest.

Received: 10 June 2022 Accepted: 23 July 2022

Published online: 02 August 2022

References

- Abebe M, Solomon A. Genetic diversity assessment of *Guizotia abyssinica* using EST derived simple sequence repeats (SSRs) markers. *Afr J Plant Sci*. 2017;11(4):79–85. <https://doi.org/10.5897/ajps.1512>.
- Aboye B, Gebrselassie W, Disasa T. Stimulating the genetic diversity of Ethiopian noug-*Guizotia abyssinica* L.f. cass. genotypes using SSR markers. 2020.
- Adarsh MN, Devi SP. A review of *Guizotia abyssinica*: a multipurpose plant with an economic prospective. *J Ind Pollut Control*. 2014;30(2):277–80.
- Alemaw G, Alemayehu N. Production and research on oilseeds in Ethiopia. First National Oilseeds Workshop, Addis Ababa (Ethiopia). 1992; 3–5 Dec 1991.
- Alemaw G, Wold A. An agronomic and seed-quality evaluation of noug (*Guizotia abyssinica* Cass.) germplasm in Ethiopia. *Plant Breed*. 1995;114(4):375–6.
- Ambreen H, Kumar S, Kumar A, Agarwal M, Jagannath A. Association mapping for important agronomic traits in safflower (*Carthamus tinctorius* L.) core collection using microsatellite markers. *Front Plant Sci*. 2018;9:1–15. <https://doi.org/10.3389/fpls.2018.00402>.
- Baagoe J. The genus *Guizotia* (Compositae). A taxonomic revision. 1974.
- Bekele E, Geleta M, Dagne K, Jones A, Barnes I, Bradman N, Thomas MG. Molecular phylogeny of genus *Guizotia* (Asteraceae) using DNA sequences derived from ITS. *Genet Resour Crop Evol*. 2007;54(7):1419–27. <https://doi.org/10.1007/s10722-006-9126-0>.
- Bulcha D. Record from PROTA4U. van der Vossen HA, Mkamilo, GS. (Editors). PROTA (Plant Resources of Tropical Africa / Ressources végétales de l'Afrique tropicale), Wageningen, Netherlands | Feedipedia. (2007).
- CSA (Central Statistical Agency). Sample survey area and production of major crops (private peasant holdings, meher season). 2019;1:1–58.
- Cvejić S, Radanović A, Dedić B, Jocković M, Jocić S, Miladinović D. Genetic and genomic tools in sunflower breeding for broomrape resistance. *Genes*. 2020;11(2):1–17. <https://doi.org/10.3390/genes11020152>.
- Dagne K. Karyotypes, C-banding and nucleolar numbers in *Guizotia* (Compositae). *Plant Syst Evol*. 1995;195(1):121–35.
- Dagne K, Jonsson A. Oil content and fatty acid composition of seeds of *Guizotia cass* (Compositae). *J Sci Food Agric*. 1997;73(3):274–8. [https://doi.org/10.1002/\(SICI\)1097-0010\(199703\)73:3%3C274::AID-JSFA725%3E3.0.CO;2-F](https://doi.org/10.1002/(SICI)1097-0010(199703)73:3%3C274::AID-JSFA725%3E3.0.CO;2-F).
- de Koning DJ, Meuwissen, et al. on genomic selection. *Genetics*. 2016;203(1):5–7. <https://doi.org/10.1534/genetics.116.189795>.
- Dempewolf H, Kane NC, Ostevik KL, Geleta M, Barker MS, Lai Z, Stewart ML, Bekele E, Engels JM, Cronk QC, Rieseberg LH. Establishing genomic tools and resources for *Guizotia abyssinica* (L.f.) Cass.-the development of a library of expressed sequence tags, microsatellite loci, and the sequencing of its chloroplast genome. *Mol Ecol Resour*. 2010;10(6):1048–58. <https://doi.org/10.1111/j.1755-0998.2010.02859.x>.
- Dempewolf H, Tesfaye M, Teshome A, Björkman AD, Andrew RL, Scascitelli M, Black S, Bekele E, Engels JM, Cronk QC, Rieseberg LH. Patterns of domestication in the Ethiopian oil-seed crop noug (*Guizotia abyssinica*). *Evol Appl*. 2015;8(5):464–75. <https://doi.org/10.1111/eva.12256>.
- Farooq M A, Ali B, Gill RA, Islam F, Cui P, Zhou W. Breeding oil crops for sustainable production: heavy metal tolerance. Breeding oilseed crops for sustainable production: opportunities and constraints. 2016;19–31. <https://doi.org/10.1016/B978-0-12-801309-0.00002-1>.
- Gajera BB, Kumar N, Singh AS, Punvar BS, Ravikiran R, Subhash N, Jadeja GC. Assessment of genetic diversity in castor (*Ricinus communis* L.) using RAPD and ISSR markers. *Ind Crops Prod*. 2010;32(3):491–8. <https://doi.org/10.1016/j.indcrop.2010.06.021>.
- Gapare W, Conaty W, Shiming QZ, Warwick L, Llewellyn D, Wilson I. Genome-wide association study of yield components and fibre quality traits in a cotton germplasm diversity panel. *Euphytica*. 2017. <https://doi.org/10.1007/s10681-017-1855-y>.
- Gebeeyehu A, Hammenhag C, Tesfaye K, Vetukuri RR. RNA-Seq provides novel genomic resources for noug (*Guizotia abyssinica*) and reveals microsatellite frequency and distribution in its transcriptome. *Front Plant Sci*. 2022;13:1–16. <https://doi.org/10.3389/fpls.2022.882136>.
- Geleta M, Bryngelsson T. Population genetics of self-incompatibility and developing self-compatible genotypes in niger (*Guizotia abyssinica*). *Euphytica*. 2010;176(3):417–30. <https://doi.org/10.1007/s10681-010-0184-1>.
- Geleta M, Ortiz R. The importance of *Guizotia abyssinica* (niger) for sustainable food security in Ethiopia. *Genet Resour Crop Evol*. 2013;60(5):1763–70. <https://doi.org/10.1007/s10722-013-9997-9>.
- Geleta M, Asfaw Z, Bekele E, Teshome A. Edible oil crops and their integration with the major cereals in North Shewa and South Welo, Central Highlands of Ethiopia: an ethnobotanical perspective. *Hereditas*. 2002;137(1):29–40. <https://doi.org/10.1034/j.1601-5223.2002.1370105.x>.
- Geleta M, Bryngelsson T, Bekele E, Dagne K. Genetic diversity of *Guizotia abyssinica* (L.f.) Cass. (Asteraceae) from Ethiopia as revealed by random amplified polymorphic DNA (RAPD). *Genet Resour Crop Evol*. 2007;54(3):601–14. <https://doi.org/10.1007/s10722-006-0018-0>.
- Geleta M, Bryngelsson T, Bekele E, Dagne K. Assessment of genetic diversity of *Guizotia abyssinica* (L.f.) Cass. (Asteraceae) from Ethiopia using amplified fragment length polymorphism. *Plant Genet Resour*. 2008;6(1):41–51. <https://doi.org/10.1017/S1479262108913903>.
- Geleta M, Bekele E, Dagne K, Bryngelsson T. Phylogenetics and taxonomic delimitation of the genus *Guizotia* (Asteraceae) based on sequences derived from various chloroplast DNA regions. *Plant Syst Evol*. 2010;289(1–2):77–89. <https://doi.org/10.1007/s00606-010-0334-x>.
- Geleta M, Stymne S, Bryngelsson T. Variation and inheritance of oil content and fatty acid composition in niger (*Guizotia abyssinica*). *J Food Compos Anal*. 2011;24(7):995–1003. <https://doi.org/10.1016/j.jfca.2010.12.010>.
- Gentzbitzel L, Zhang YX, Vear F, Griveau B, Nicolas P. RFLP studies of genetic relationships among inbred lines of the cultivated sunflower, *Helianthus annuus* L.: evidence for distinct restorer and maintainer germplasm pools. *Theor Appl Genet*. 1994;89(4):419–25. <https://doi.org/10.1007/BF00225376>.
- Getinet A, Sharma S. Niger, *Guizotia abyssinica* (L. f.) Cass. In Promoting the conservation and use of underutilized and neglected crops. 1996.
- Haun W, Coffman A, Clasen BM, Demorest ZL, Lowy A, Ray E, Retterath A, Stoddard T, Juillerat A, Cedrone F, Mathis L, Voytas DF, Zhang F. Improved soybean oil quality by targeted mutagenesis of the fatty acid desaturase 2 gene family. *Plant Biotechnol J*. 2014;12(7):934–40. <https://doi.org/10.1111/pbi.12201>.
- Hu XH, Zhang SZ, Miao HR, Cui FG, Shen Y, Yang WQ, Xu TT, Chen N. High-density genetic map construction and identification of QTLs controlling oleic and linoleic acid in peanut using SLAF-seq and SSRs. *Sci Rep*. 2018. <https://doi.org/10.1038/s41598-018-23873-7>.
- Huang B, Qi F, Sun Z, Miao L, Zhang Z, Liu H, Fang Y, Dong W, Tang F, Zheng Z, Zhang X. Marker-assisted backcrossing to improve seed oleic acid content in four elite and popular peanut (*Arachis hypogaea* L.) cultivars with high oil content. *Breed Sci*. 2019;69(2):234–43. <https://doi.org/10.1270/jsbbs.18107>.
- Hussain Z, Yadav S, Kumar S, Suneja P, Nizar MA, Yadav SK, Yadav SK, Dutta M. Molecular characterization of niger [*Guizotia abyssinica* (L.f.) Cass.] germplasm diverse for oil parameters. *Indian J Biotechnol*. 2015;14(3):344–50.
- Janila P, Variath MT, Pandey MK, Desmae H, Motagi BN. Genomic tools in groundnut breeding program: status and perspectives. *Front Plant Sci*. 2016;7(March):2004–13. <https://doi.org/10.3389/fpls.2016.00289>.
- Kandel H, Porter P. Niger (*Guizotia abyssinica*) (L. f.) Cass. Production in North-west Minnesota. University of Minnesota Extension Service. 2002.
- King AJ, Montes LR, Clarke JG, Itzep J, Perez CA, Jongschaap RE, Visser RG, Loo EN, Van GIA. Identification of QTL markers contributing to plant growth, oil yield and fatty acid composition in the oilseed crop *Jatropha curcas* L. *Biotechnol Biofuels*. 2015. <https://doi.org/10.1186/s13068-015-0326-8>.
- Kushwaha UKS, Mangal V, Bairwa AK, Adhikari S, Ahmed T, Bhat P, Yadav A, Dhaka N, Prajapati DR, Gaur A. Association mapping, principles and techniques. *J Biol Environ Eng*. 2017;2(1):1–9.
- Li C, Miao H, Wei L, Zhang T, Han X, Zhang H. Association mapping of seed oil and protein content in *Sesamum indicum* L. using SSR markers. *PLoS ONE*. 2014. <https://doi.org/10.1371/journal.pone.0105757>.
- Liang Y, Baring MR, Septiningsih EM. Mapping of quantitative trait loci for yield and grade related traits in peanut (*Arachis hypogaea* L.) using high-resolution SNP markers. *Plant Breed Biotech*. 2018;4:454–62.
- Liu YL, Li YH, Zhou GA, Uzokwe N, Chang RZ, Chen SY, Qiu LJ. Development of soybean EST-SSR markers and their use to assess genetic diversity in the subgenus soja. *Agric Sci China*. 2010;9(10):1423–9. [https://doi.org/10.1016/S1671-2927\(09\)60233-9](https://doi.org/10.1016/S1671-2927(09)60233-9).
- Misteru T. Plant regeneration from anther culture of niger (*Guizotia abyssinica* (L.f.) Cass.). 2008; July, 1–83.
- MoA. Ministry of Agriculture Plant Variety Release, Protection, and Seed Quality Control Directorate, Crop Variety Register No.19. Addis Ababa. - Bing. 2016.
- Mondal S, Sutar SR, Badigannavar AM. Assessment of genetic diversity in cultivated groundnut (*Arachis hypogaea* L.) with differential responses

- to rust and late leaf spot using ISSR markers. *Indian J Genet Plant Breed*. 2009;69(3):219–24.
- Nagella P, Hosakatte NM, Ravishankar KV, Hahn EJ, Paek KY. Analysis of genetic diversity among Indian niger [*Guizotia abyssinica* (L. f.) Cass.] cultivars based on randomly amplified polymorphic DNA markers. *Electr J Bio*. 2008;11:140.
- Oladosu Y, Rafii MY, Abdullah N, Hussin G, Rahim HA, Miah G, Usman M. Principle and application of plant mutagenesis in crop improvement: a review. *Biotechnol Biotechnol Equip*. 2016;30(1):1–16. <https://doi.org/10.1080/13102818.2015.1087333>.
- Padgett SR, Kolacz KH, Delannay X, Re DB, LaVallee BJ, Tinius CN, Rhodes WK, Otero YI, Barry GF, Eichholtz DA, Peschke VM, Nida DL, Taylor NB, Kishore GM. Development, identification, and characterization of a glyphosate-tolerant soybean line. *Crop Sci*. 1995;35(5):1451–61. <https://doi.org/10.2135/cropsci1995.0011183X003500050032x>.
- Petros Y, Merker A, Zeleke H. Analysis of genetic diversity of *Guizotia abyssinica* from Ethiopia using inter simple sequence repeat markers. *Hereditas*. 2007;144(1):8–24. <https://doi.org/10.1111/j.2007.0018-0661.01969.x>.
- Rahman M, Jiménez M M. De. Designer oil crops. In: *Breeding oilseed crops for sustainable production*. Elsevier Inc. 2016. <https://doi.org/10.1016/B978-0-12-801309-0/00015-X>.
- Rai SK, Charak D, Bharat R. Scenario of oilseed crops across the globe. *Plant Archives*. 2016;16(1):125–32.
- Ramadan MF. Niger seed oil. In *Gourmet and health-promoting specialty oils*. AOCS Press. 2009. <https://doi.org/10.1016/B978-1-893997-97-4.50015-2>.
- Ramadan MF. Functional properties, nutritional value, and industrial applications of niger oilseeds (*Guizotia abyssinica* cass.). *Crit Rev Food Sci Nutr*. 2012;52(1):1–8. <https://doi.org/10.1080/10408398.2010.486083>.
- Sahin EC, Kalenderoğlu A, Aydın Y, Evci G, Uncuoğlu AA. SSR markers suitable for marker assisted selection in sunflower for downy mildew resistance. *Open Life Sci*. 2018;13(1):319–26. <https://doi.org/10.1515/biol-2018-0039>.
- Semagn K, Bjørnstad Å, Ndjondjop MN. Progress and prospects of marker assisted backcrossing as a tool in crop breeding programs. *Afr J Biotechnol*. 2006;5(December):2588–603.
- Singh AS, Kumari S, Modi AR, Gajera BB, Narayanan S, Kumar N. Role of conventional and biotechnological approaches in genetic improvement of castor (*Ricinus communis* L.). *Ind Crops Prod*. 2015;74:55–62. <https://doi.org/10.1016/j.indcrop.2015.05.001>.
- Song C, Li W, Wang Z, Pei X, Liu Y, Ren Z, He K, Zhang F, Sun K, Zhou X, Ma X, Yang D. Genome resequencing reveals genetic variation between the parents of an elite hybrid upland cotton. *Agronomy*. 2018;8(12):1–16. <https://doi.org/10.3390/agronomy8120305>.
- Sood A, Chauhan RS. Genomics of disease resistance in castor bean. 2018; p. 105–113. https://doi.org/10.1007/978-3-319-97280-0_6.
- Tadele Z. African orphan crops under abiotic stresses. *Scientifica*. 2018;2018:1–19.
- Tadele Z. Mutagenesis and TILLING to Dissect gene function in plants. 2016; 499–508. <https://doi.org/10.2174/138920291766616052010>.
- Tsehay S, Ortiz R, Johansson E, Bekele E, Tesfaye K, Hammenhag C, Geleta M. New transcriptome-based SNP markers for Noug (*Guizotia abyssinica*) and their conversion to KASP markers for population genetics analyses. *Genes*. 2020;11(11):1373.
- Tsehay S, Ortiz R, Geleta M, Bekele E, Tesfaye K, Johansson E. Nutritional profile of the Ethiopian oilseed crop noug (*Guizotia abyssinica* cass.): opportunities for its improvement as a source for human nutrition. 2021. <https://doi.org/10.3390/foods10081778>.
- USDA. Brazil Sees Record Soybean Exports In October–November 2019. November, 1–38.
- Wang L, Zhang Y, Zh X, Zhu X, Li D, Zhang X. Development of an SSR-based genetic map in sesame and identification of quantitative trait loci associated with charcoal rot resistance. *Sci Rep*. 2017. <https://doi.org/10.1038/s41598-017-08858-2>.
- Werner CR, Voss-fels KP, Miller CN, Qian W, Hua W, Guan C, Snowdon RJ, Qian L. Effective genomic selection in a narrow-genepool crop with low-density markers: Asian rapeseed as an example. *Plant Genome*. 2018. <https://doi.org/10.3835/plantgenome2017.09.0084>.
- Wirtu AH. Genetic gain in grain yield and oil content of Noug (*Guizotia abyssinica*) in Ethiopia. *J BioSci Agric Res*. 2021;27(01):2234–51.
- Won YL, Kim PK, Cha JL, Song YM, Lee K. EMS-induced mutation of an endoplasmic reticulum oleate desaturase gene (FAD2-2) results in elevated oleic acid content in rapeseed (*Brassica napus* L.). *Euphytica*. 2018. <https://doi.org/10.1007/s10681-017-2106-y>.
- Wongyai W, Saengkaewsook W, Veerawudh J. Sesame mutation induction: improvement of non-shattering capsule by using gamma rays and EMS. 2001.
- Yadav S, Hussain Z, Suneja P, Nizar MA, Yadav SK, Dutta M. Genetic divergence studies in niger (*Guizotia abyssinica*) germplasm. *Biomass Bioenerg*. 2012;44:64–9. <https://doi.org/10.1016/j.biombioe.2012.04.011>.
- Yadava DK, Vasudev S, Singh N, Mohapatra T, Prabhu KV. Breeding major oil crops: Present status and future research needs. In *Technological Innovations in Major World Oil Crops*. Springer New York 2012; 1:17–51. https://doi.org/10.1007/978-1-4614-0356-2_2.
- York N, Garden B. Utilization of Commercial Oilseed Crops Author (s): E. H. Pryde Published by: Springer on behalf of New York Botanical Garden Press Stable URL. 2016. <http://www.jstor.org/stable/4254545> Accessed 10 Aug 2016 : 49 UTC Utilization of Commercial Oilseed C. 37(4), 459–477.
- Zhang L, Huang BB, Kai GY, Guo ML. Analysis of intraspecific variation of Chinese *Carthamus tinctorius* L. using AFLP markers. *Yaoxue Xuebao*. 2006;41(1):91–6.
- Zhang J, Song Q, Cregan PB, Liang G. Genome-wide association study, genomic prediction and marker—assisted selection for seed weight in soybean (*Glycine max*). *Theor Appl Genet*. 2016;129(1):117–30. <https://doi.org/10.1007/s00122-015-2614-x>.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Ready to submit your research? Choose BMC and benefit from:

- fast, convenient online submission
- thorough peer review by experienced researchers in your field
- rapid publication on acceptance
- support for research data, including large and complex data types
- gold Open Access which fosters wider collaboration and increased citations
- maximum visibility for your research: over 100M website views per year

At BMC, research is always in progress.

Learn more biomedcentral.com/submissions

