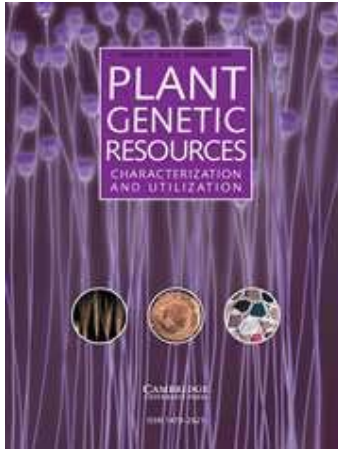


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# Start codon-targeted marker evaluation of genetic relationship and population structure in southern Nigerian fluted pumpkin (*Telfairia occidentalis* Hook F.) collection

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## Abstract

Fluted pumpkin (*Telfairia occidentalis* Hook F.) is an underutilized indigenous leafy vegetable with enormous prospects for food security in sub-Saharan Africa. However, relatively little is known about genetic relationships and population structure in the species. In this study, 32 landraces of fluted pumpkin collected across three southern geographical regions in Nigeria were assessed for genetic diversity and population structure using 8 start codon-targeted (SCoT) makers. The polymorphic information content of the SCoT markers ranged from 0.48 in SCoT36 to 0.94 in SCoT28, with an average of 0.77. Hierarchical cluster dendrogram based on Ward's method and principal component analysis grouped the landraces into four clusters without affiliation to provenance. Overall, the mean values of the population genetic diversity parameters – Nei's gene diversity ( $H$ ) and Shannon's information index ( $I$ ) showed values of  $0.28 \pm 0.01$  and  $0.43 \pm 0.02$ , respectively, implying a narrow genetic base for the landraces. The result was further corroborated by a very close Nei's genetic distance and identity among populations of the landraces. Furthermore, the south-west population exhibited the higher genetic diversity ( $H = 0.31 \pm 0.02$  and  $I = 0.45 \pm 0.03$ ). Population structure analysis inferred three subpopulations for the accessions with varying degrees of allelic admixture. An analysis of molecular variance revealed that almost all the genetic variation occurred within (99%) than between (1%) populations. The findings shed light on the genetic diversity of southern Nigerian fluted pumpkin and have significant implications for the characterisation, conservation, exploitation and improvement of the species.

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## Keywords

Fluted pumpkin genetic diversity population structure SCoT markers *Telfairia occidentalis* underutilized

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## References

Abdin, MZ, Arya, L and Verma, M (2017) Use of SCoT markers to assess the gene flow and population structure among two different populations of bottle gourd. *Plant Gene* 9, 80–86. [Google Scholar](#)

Adeyemo, OA and Tijani, HA (2018) Fluted pumpkin [*Telfairia occidentalis* (Hook F.)]: genetic diversity and landrace identification using phenotypic traits and RAPD markers. *Ife Journal of Science* 20, 391–401. [CrossRefGoogle Scholar](#)

Admas, S, Tesfaye, K, Haileselassie, T, Shiferaw, E and Flynn, KC (2021) Genetic variability and population structure of Ethiopian chickpea (*Cicer arietinum* L.) germplasm. *PLoS ONE* 16, e0260651. [CrossRefGoogle ScholarPubMed](#)

Adu, GB, Awuku, FJ, Amegbor, IK, Haruna, A, Manigben, KA and Aboyadana, PA (2019) Genetic characterization and population structure of maize populations using SSR markers. *Annals of Agricultural Sciences* 64, 47–54. [CrossRefGoogle Scholar](#)

Agarwal, A, Gupta, V, Haq, SU, Jatav, PK, Kothari, SL and Kachhwaha, S (2019) Assessment of genetic diversity in 29 rose germplasms using SCoT marker. *Journal of King Saud University-Science* 31, 780–788. [CrossRefGoogle Scholar](#)

Agatemor, C (2006) Studies of selected physicochemical properties of fluted pumpkin (*Telfairia occidentalis* Hook F.) seed oil and tropical almond (*Terminalia catappa* L.) seed oil. *Pakistan Journal of Nutrition* 5, 306–307. [Google Scholar](#)

Agung, PP, Saputra, F, Zein, MSA, Wulandari, AS, Putra, WPB, Said, S and Jakaria, J (2019) Genetic diversity of Indonesian cattle breeds based on

microsatellite markers. *Asian–Australasian Journal of Animal Sciences* 32, 467–476.[Google ScholarPubMed](#)

Airaodion, AI, Ogbuagu, EO, Airaodion, EO, Ekenjoku, JA and Ogbuagu, U (2019) Pharmacotherapeutic effect of methanolic extract of *Telfairia occidentalis* leaves on glycemc and lipidemic indexes of alloxan-induced diabetic rats. *International Journal of Bio-Science and Bio-Technology* 11, 1–17.[Google Scholar](#)

Aisida, SO, Ugwu, K, Nwanya, AC, Bashir, AKH, Nwankwo, NU, Ahmed, I and Ezema, FI (2021) Biosynthesis of silver oxide nanoparticles using leave extract of *Telfairia occidentalis* and its antibacterial activity. *Materials Today: Proceedings* 36, 208–213.[Google Scholar](#)

Ajayi, SA, Dulloo, ME, Vodouhe, RS, Berjak, P and Kioko, JI (2004) Conservation status of *Telfairia* spp. in sub-Saharan Africa. [Regional workshop on plant genetic resources and food security in West and Central Africa], IITA, Ibadan, 26th–30th April.[Google Scholar](#)

Akoroda, MO (1990) Ethnobotany of *Telfairia occidentalis* (cucurbitaceae) among Igbos of Nigeria. *Economic Botany* 44, 29–39.[CrossRefGoogle Scholar](#)

Al-Tamimi, AJ and Al-Janabi, AS (2019) Genetic diversity among bread wheat genotypes using RAPD and SSR markers. *SABRAO Journal of Breeding and Genetics* 51, 325–339.[Google Scholar](#)

Alemu, A, Feyissa, T, Letta, T and Abeyo, B (2020) Genetic diversity and population structure analysis based on the high-density SNP markers in Ethiopian durum wheat (*Triticum turgidum* ssp. durum). *BMC Genetics* 21, 1–12.[CrossRefGoogle ScholarPubMed](#)

Alhariri, A, Behera, TK, Jat, GS, Devi, MB, Boopalakrishnan, G, Hemeda, N F, Teleb, AA, Ismail, E and Elkordy, A (2021) Analysis of genetic diversity and population structure in bitter gourd (*Momordica charantia* L.) using morphological and SSR markers. *Plants* 10, 1860.[CrossRefGoogle ScholarPubMed](#)

An, H, Jo, IH, Oh, YL, Jang, KY, Kong, WS, Sung, JK, So, YS and Chung, JW (2019) Molecular characterization of 170 new gDNA-SSR markers for genetic diversity in button mushroom (*Agaricus bisporus*). *Mycobiology* 47, 527–532.[CrossRefGoogle ScholarPubMed](#)

Anchal, S, Kiran, G and Nitisha, S (2014) Nutritional evaluation of value-added products using dehydrated greens for security of haematinic nutrient. *Food Science Research Journal* 5, 168–173.[Google Scholar](#)

Annicet, NH, Louise, A, N'da

Désiré, P, Paul, AK, Konan, KC and Arsene, ZBI (2016) Genetic diversity and population structure of maize landraces from Côte d'Ivoire. *African Journal of Biotechnology* 15, 2507–2516.[Google Scholar](#)

Athinodorou, F, Foukas, P, Tsaniklidis, G, Kotsiras, A, Chrysargyris, A, Delis, C, Kyratzis, AC, Tzortzakis, N and Nikoloudakis, N (2021) Morphological diversity, genetic characterization, and phytochemical assessment of the cypriot tomato germplasm. *Plants* 10, 1698.[CrossRefGoogle ScholarPubMed](#)

Brown, AHD and Weir, BS (1983) Measuring genetic variability in plant populations. In Tanksley, SD, Orton, TJ (eds), *Isozymes in Plant Genetics and Breeding, Part A*. Amsterdam: Elsevier Science Publishers, pp. 219–239.[CrossRefGoogle Scholar](#)

Cheng, J, Kao, H and Dong, S (2020) Population genetic structure and gene flow of rare and endangered *Tetraena mongolica* Maxim. revealed by reduced representation sequencing. *BMC Plant Biology* 20, 1–13.[CrossRefGoogle ScholarPubMed](#)

Chukwudi, UP and Agbo, CU (2016) Characterization and preliminary evaluation of local germplasm of *Telfairia occidentalis* Hook F. accessions in Enugu, Nigeria. *Agro-Science* 15, 15–22.[CrossRefGoogle Scholar](#)

Chukwudi, UP, Agbo, CU, Ene, CO, Uba, CU and Enyi, JI (2017) Analysis of leaf yield components in fluted pumpkin (*Telfairia occidentalis* Hook F.) grown in derived savannah agro-ecology. *Notulae Scientia Biologicae* 9, 386–391.[CrossRefGoogle Scholar](#)

Collard, BC and Mackill, DJ (2009) Start codon targeted (SCoT) polymorphism: a simple, novel DNA marker technique for generating gene-targeted markers in plants. *Plant Molecular Biology Reporter* 27, 86–93.[CrossRefGoogle Scholar](#)

Cyril-Olutayo, MC, Agbedahunsi, JM and Akinola, NO (2019) Studies on the effect of a nutritious vegetable, *Telfairia occidentalis*, on HbSS blood. *Journal of Traditional and Complementary Medicine* 9, 156–162.[CrossRefGoogle ScholarPubMed](#)

Dhutmal, RR, Mundhe, AG and More, AW (2018) Molecular marker technique: a review. *International Journal of Current Microbiology and Applied Sciences* 6, 816–825.[Google Scholar](#)

Doyle, JJ and Doyle, JL (1990) Isolation of plant DNA from fresh tissue. *Focus* 12, 13–15.[Google Scholar](#)

Earl, DA and VonHoldt, BM (2012) STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method. *Conservation Genetics Resources* 4, 359–361.[CrossRefGoogle Scholar](#)

El-Moneim, A, ELSarag, EI, Aloufi, S, EI-

Azraq, AM, Alshamrani, SM, Safhi, FAA and Ibrahim, AA (2021) Quinoa (*Chenopodium quinoa* Willd.): Genetic diversity according to ISSR and SCoT markers, relative gene expression, and morpho-physiological variation under salinity stress. *Plants* 10, 2802.[CrossRefGoogle Scholar](#)

Elhaik, E (2021) Why most principal component analyses (PCA) in population genetic studies are wrong. *BioRxiv*, 1–54. [Google Scholar](#)

Eltaher, S, Sallam, A, Belamkar, V, Emara, HA, Nower, AA, Salem, KF, Pol and, J and Baenziger, PS (2018) Genetic diversity and population structure of F3: 6 Nebraska winter wheat genotypes using genotyping-by-sequencing. *Frontiers in Genetics* 9, 76. [CrossRefGoogle ScholarPubMed](#)

Etminan, A, Pour-Aboughadareh, A, Noori, A, Ahmadi-Rad, A, Shooshtari, L, Mahdavian, Z and Yousefiazar-Khanian, M (2018) Genetic relationships and diversity among wild *Salvia* accessions revealed by ISSR and SCoT markers. *Biotechnology & Biotechnological Equipment* 32, 610–617. [CrossRefGoogle Scholar](#)

Evanno, G, Regnaut, S and Goudet, J (2005) Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular Ecology* 14, 2611–2620. [CrossRefGoogle ScholarPubMed](#)

Ezenwata, IS, Onyemeka, RM, Makinde, SCO and Anyaegbu, CF (2019) A analysis of variation among genotypes of fluted pumpkin (*Telfairia occidentalis* Hook F.) using factor analysis and principal component analysis (PCA). *International Journal of Engineering Applied Sciences and Technology* 4, 211–216. [CrossRefGoogle Scholar](#)

Ezzat, A, Adly, M and El-Fiki, A (2019) Morphological, agronomical and molecular characterization in irradiated Cowpea (*Vigna unguiculata* (L.) Walp.) and detection by start codon target markers. *Journal of Radiation Research and Applied Sciences* 12, 403–412. [CrossRefGoogle Scholar](#)

Falush, D, Stephens, M and Pritchard, JK (2003) Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies. *Genetics* 164, 1567–1587. [CrossRefGoogle ScholarPubMed](#)

Famuwagun, AA, Odunlade, TV, Taiwo, KA, Gbadamosi, SO, Oyedele, DJ and Adebooye, OC (2017) Some chemical compositions and sensory properties of wheat bread fortified with fluted pumpkin leaf slurry. In Taiwo, KA, Akponikpe, PBI and Aluko, RE (eds), *African Vegetables Forum*. Leuven, Belgium: International Society for Horticultural Science, pp. 117–128. [Google Scholar](#)

Fatokun, C, Girma, G, Abberton, M, Gedil, M, Unachukwu, N, Oyatomi, O, Yusuf, M, Rabbi, I and Boukar, O (2018) Genetic diversity and population structure of a mini-core subset from the world cowpea (*Vigna unguiculata* (L.) Walp.) germplasm collection. *Scientific Reports* 8, 1–10. [CrossRefGoogle ScholarPubMed](#)

Fayeun, LS and Odiyi, AC (2015) Variation and heritability of marketable leaf yield components in fluted pumpkin. *Scientia Agriculturae* 11, 8–14. [Google Scholar](#)

Fayeun, LS, Odiyi, AC, Makinde, SCO and Aiyelari, OP (2012) Genetic variability and correlation studies in the fluted pumpkin (*Telfairia*

- occidentalis* Hook F.). Journal of Plant Breeding and Crop Science 4, 156–160.[Google Scholar](#)
- Fayeun, LS, Ojo, DK, Odiyi, AC, Adebisi, AM, Hammed, LA and Omikunle, AO (2016) Identification of facultative apomixis in fluted pumpkin (*Telfairia occidentalis* Hook F.) through emasculation method. American Journal of Experimental Agriculture 10, 1–10.[CrossRefGoogle Scholar](#)
- Fayeun, LS, Omikunle, AO, Famogbiele, AA and Oyetunde, OA (2018) Phenotypic traits diversity in fluted pumpkin (*Telfairia occidentalis* Hook F.). International Journal of Plant and Soil Science 24, 1–11.[CrossRefGoogle Scholar](#)
- Feng, S, He, R, Lu, J, Jiang, M, Shen, X, Jiang, Y, Wang, ZA and Wang, H (2016) Development of SSR markers and assessment of genetic diversity in medicinal *Chrysanthemum morifolium* cultivars. Frontiers in Genetics 7, 113.[CrossRefGoogle ScholarPubMed](#)
- Fu, YH, Yang, C, Meng, Q, Liu, F, Shen, G, Zhou, M and Ao, M (2019) Genetic diversity and structure of *Coix lacryma-jobi* L. from its world secondary diversity center, Southwest China. International Journal of Genomics 2019, 9815697.[CrossRefGoogle ScholarPubMed](#)
- Gasim, S, Abuanja, I and Abdalla, AW (2019) Genetic diversity of rice (*Oryza sativa* L.) accessions collected from Sudan and IRRI using SSR markers. African Journal of Agricultural Research 14, 143–150.[Google Scholar](#)
- Ghimire, BK, Yu, CY, Kim, SH and Chung, IM (2019) Diversity in accessions of *Panicum miliaceum* L. based on agro-morphological, antioxidative, and genetic traits. Molecules 24, 1012.[CrossRefGoogle ScholarPubMed](#)
- Green, MR and Sambrook, J (2019) Polymerase chain reaction. Cold Spring Harbor Protocols 2019, 436–456.[Google ScholarPubMed](#)
- Horsefall, M Jr. and Spiff, AI (2005) Equilibrium sorption study of Al<sup>3+</sup>, Co<sup>2+</sup> and Ag<sup>+</sup> in aqueous solutions by fluted pumpkin (*Telfairia occidentalis* Hook F.) waste biomass. Acta Chimica Slovenica 52, 174–181.[Google Scholar](#)
- Huang, CL, Chen, JH, Tsang, MH, Chung, JD, Chang, CT and Hwang, SY (2015) Influences of environmental and spatial factors on genetic and epigenetic variations in *Rhododendron oldhamii* (Ericaceae). Tree Genetics & Genomes 11, 1–16.[CrossRefGoogle Scholar](#)
- Huang, R, Chu, QH, Lu, GH and Wang, YQ (2019) Comparative studies on population genetic structure of two closely related selfing and outcrossing *Zingiber* species in Hainan Island. Scientific Reports 9, 1–11.[CrossRefGoogle ScholarPubMed](#)
- Igwe, DO, Afiukwa, CA, Ubi, BE, Ogbu, KI, Ojuederie, OB and Ude, GN (2017) Assessment of genetic diversity in *Vigna unguiculata* L. (Walp)

accessions using inter-simple sequence repeat (ISSR) and start codon targeted (SCoT) polymorphic markers. *BMC Genetics* 18, 1–13.[CrossRefGoogle ScholarPubMed](#)

Jamnadass, R, Mumm, RH, Hale, I, Hendre, P, Muchugi, A, Dawson, IK, Powell, W, Graudal, L, Yana-Shapiro, H, Simons, AJ and Van Deynze, A (2020) Enhancing African orphan crops with genomics. *Nature Genetics* 52, 56–360.[CrossRefGoogle ScholarPubMed](#)

Jedrzejczyk, I (2020) Genome size and SCoT markers as tools for identification and genetic diversity assessment in *Echinacea* genus. *Industrial Crops and Products* 144, 112055.[CrossRefGoogle Scholar](#)

Jena, RC and Chand, PK (2021) Multiple DNA marker-assisted diversity analysis of Indian mango (*Mangifera indica* L.) populations. *Scientific Reports* 11, 1–15.[CrossRefGoogle ScholarPubMed](#)

Kalpana, D, Choi, SH, Choi, TK, Senthil, K and Lee, YS (2012) Assessment of genetic diversity among varieties of mulberry using RAPD and ISSR fingerprinting. *Scientia Horticulturae* 134, 79–87.[CrossRefGoogle Scholar](#)

Khodaei, L, Azizinezhad, R, Ehteminan, AR and Khosroshahi, M (2021) Assessment of genetic diversity among Iranian *Aegilops triuncialis* accessions using ISSR, SCoT, and CDBP markers. *Journal of Genetic Engineering and Biotechnology* 19, 1–9.[CrossRefGoogle ScholarPubMed](#)

Kimani, EN, Wachira, FN and Kinyua, MG (2012) Molecular diversity of Kenyan lablab bean (*Lablab purpureus* (L.) sweet) accessions using amplified fragment length polymorphism markers. *American Journal of Plant Sciences* 3, 313–321.[CrossRefGoogle Scholar](#)

Kumar, J and Agrawal, V (2019) Assessment of genetic diversity, population structure and sex identification in dioecious crop, *Trichosanthes dioica* employing ISSR, SCoT and SRAP markers. *Heliyon* 5, e01346.[CrossRefGoogle ScholarPubMed](#)

Laurentin, HE and Karlovsky, P (2006) Genetic relationship and diversity in a sesame (*Sesamum indicum* L.) germplasm collection using amplified fragment length polymorphism (AFLP). *BMC Genetics* 7, 1–10.[CrossRefGoogle Scholar](#)

Li, H, Chappell, M and Zhang, D (2020) Assessing genetic diversity and population structure of *Kalmia latifolia* L. in the eastern United States: an essential step towards breeding for adaptability to southeastern environmental conditions. *Sustainability* 12, 8284.[CrossRefGoogle Scholar](#)

Liu, K and Muse, SV (2005) PowerMarker: an integrated analysis environment for genetic marker analysis. *Bioinformatics* 21, 2128–2129.[CrossRefGoogle ScholarPubMed](#)

Luo, Z, Brock, J, Dyer, JM, Kutchan, T, Schachtman, D, Augustin, M, Ge, Y, Fahlgren, N and Abdel-Haleem, H (2019) Genetic diversity and population



structure of a *Camelina sativa* spring panel. *Frontiers in Plant Science* 10, 184.[CrossRefGoogle ScholarPubMed](#)

McBenedict, B, Chimwamurombe, P, Kwembeya, E and Maggs-Kölling, G (2016) Genetic diversity of Namibian *Pennisetum glaucum* (L.) R. Br. (pearl millet) landraces analyzed by SSR and morphological markers. *The Scientific World Journal* 2016, 1439739.[CrossRefGoogle ScholarPubMed](#)

Merheb, J, Pawełkiewicz, M, Branca, F, Bolibok-Brągoszewska, H, Skarzyńska, A, Pląder, W and Chalak, L (2020) Characterization of Lebanese germplasm of snake melon (*Cucumis melo* subsp. *melo* var. *flexuosus*) using morphological traits and SSR markers. *Agronomy* 10, 1293.[CrossRefGoogle Scholar](#)

Metry, A, Adeyemo, OA, Grünig, S and Parisod, C (2023) Characterization of a sex-determining locus and development of early molecular assays in *Telfairia occidentalis* Hook F., a dioecious cucurbit. *Genetic Resources and Crop Evolution*, 1–14.[Google Scholar](#)

Minnaar-

Ontong, A, Gerrano, AS and Labuschagne, MT (2021) Assessment of genetic diversity and structure of Bambara groundnut [*Vigna subterranea* (L.) verdc.] landraces in South Africa. *Scientific Reports* 11, 1–9.[CrossRefGoogle ScholarPubMed](#)

Mohammed, HI and Hamza, NB (2018) Genetic diversity analysis of forty pearl millet (*Pennisetum glaucum* (L.) R. Br) accessions from Sudan using agronomical descriptors and DNA molecular markers. *Advances in Bioscience and Biotechnology* 9, 322.[CrossRefGoogle Scholar](#)

Moniruzzaman, M, Saiem, RM, Emon, RM, Haque, MS, Saha, NR, Malek, MA and Khatun, K (2019) Genetic diversity analysis of soybean genotypes using SSR markers for salinity tolerance. *Progressive Agriculture* 30, 1–9.[CrossRefGoogle Scholar](#)

Mostafavi, AS, Omid, M, Azizinezhad, R, Etminan, A and Badi, HN (2021) Genetic diversity analysis in a mini core collection of Damask rose (*Rosa damascena* Mill.) germplasm from Iran using URP and SCoT markers. *Journal of Genetic Engineering and Biotechnology* 19, 1–14.[CrossRefGoogle Scholar](#)

Nadeem, MA, Nawaz, MA, Shahid, MQ, Doğan, Y, Comertpay, G, Yıldız, M, Hatipoğlu, R, Ahmad, F, Alsaleh, A, Labhane, N and Özkan, H (2018) DNA molecular markers in plant breeding: current status and recent advancements in genomic selection and genome editing. *Biotechnology & Biotechnological Equipment* 32, 261–285.[CrossRefGoogle Scholar](#)

Nayak, S, Naik, PK, Acharya, L, Mukherjee, AK, Panda, PC and Das, P (2005) Assessment of genetic diversity among 16 promising cultivars of ginger using cytological and molecular markers. *Zeitschrift für Naturforschung C* 60, 485–492.[CrossRefGoogle ScholarPubMed](#)

- Ndjiondjop, MN, Semagn, K, Gouda, AC, Kpeki, SB, Dro Tia, D, Sow, M, Goungoulou, A, Sie, M, Perrier, X, Ghesquiere, A and Warburton, ML (2017) Genetic variation and population structure of *Oryza glaberrima* and development of a mini-core collection using DArTseq. *Frontiers in Plant Science* 8, 1748. [CrossRefGoogle ScholarPubMed](#)
- Nei, M (1972) Genetic distance between populations. *The American Naturalist* 106, 283–292. [CrossRefGoogle Scholar](#)
- Nkhata, W, Shimelis, H, Melis, R, Chirwa, R, Mzengeza, T, Mathew, I and Shayanowako, A (2020) Population structure and genetic diversity analyses of common bean germplasm collections of East and Southern Africa using morphological traits and high-density SNP markers. *PLoS ONE* 15, e0243238. [CrossRefGoogle Scholar](#)
- Nwangburuka, CC, Denton LA, and Oyelana, O (2014) Genetic variability and heritability of vegetative, fruit and seed yield traits in fluted pumpkin (*Telfairia occidentalis* Hook F.). *African Journal of Biotechnology* 13, 3262–3270. [CrossRefGoogle Scholar](#)
- Odiaka, NI, Akoroda, MO and Odiaka, EC (2008) Diversity and production methods of fluted pumpkin (*Telfairia occidentalis* Hook F.); experience with vegetable farmers in Makurdi, Nigeria. *African Journal of Biotechnology* 7, 944–954. [Google Scholar](#)
- Odiyi, AC, Fayeun, LS, Makinde, SCO and Adetunji, AT (2014) Analysis of variation among fluted pumpkin (*Telfairia occidentalis*) accessions by factor analysis and principal component analysis. *Canadian Journal of Plant Breeding* 2, 80–86. [Google Scholar](#)
- Ogwu, MC, Osawaru, ME and Obahiagbon, GE (2017) Ethnobotanical survey of medicinal plants used for traditional reproductive care by Usen people of Edo State, Nigeria. *Malaya Journal of Biosciences* 4, 17–29. [Google Scholar](#)
- Okoli, BE and Mgbeogu, CM (1983) Fluted pumpkin, *Telfairia occidentalis*: West African vegetable crop. *Economic Botany* 37, 145–149. [CrossRefGoogle Scholar](#)
- Osuji, EE, Munonye, JO, Olaolu, MO, Onyemauwa, CS, Tim-Ashama, AC, Ibekwe, CC, Obasi, IO, Obike, KC, Ebe, FE, Onu, SE and Obi, JN (2022) Econometric analysis of fluted pumpkin production in Nigeria; empirical in-depth analysis. *Journal of Agriculture and Crops* 8, 105–114. [Google Scholar](#)
- Pandey, A, Khan, MK, Isik, R, Turkmen, O, Acar, R, Seymen, M and Hakki, EE (2019) Genetic diversity and population structure of watermelon (*Citrullus* sp.) genotypes. *3 Biotech* 9, 1–14. [CrossRefGoogle ScholarPubMed](#)

Peakall, R and Smouse, PE (2012) GenAEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research: an update. *Bioinformatics* (Oxford, England) 28, 2537–2539.[Google ScholarPubMed](#)

Perrier, X and Jacquemoud-Collet, J (2006) DARwin software. Available at <http://darwin.cirad.fr/> (accessed 18 July 2021).[Google Scholar](#)

Popoola, JO, Bello, OA, Olugbuyiro, JA and Obembe, OO (2017) Simple sequence repeats (SSR) analysis of genetic intraspecific relationships of *Moringa oleifera* populations from Nigeria. *Science International* (Lahore) 29, 645–657.[Google Scholar](#)

Pritchard, JK, Stephens, M and Donnelly, P (2000) Inference of population structure using multilocus genotype data. *Genetics* 155, 945–959.[CrossRefGoogle ScholarPubMed](#)

Rajesh, MK, Sabana, AA, Rachana, KE, Rahman, S, Jerard, BA and Karun, A (2015) Genetic relationship and diversity among coconut (*Cocos nucifera* L.) accessions revealed through SCoT analysis. *3 Biotech* 5, 999–1006.[CrossRefGoogle ScholarPubMed](#)

Ramakrishnan, M, Ceasar, SA, Duraipandiyar, V, Al-Dhabi, NA and Ignacimuthu, S (2016) Assessment of genetic diversity, population structure and relationships in Indian and non-Indian genotypes of finger millet (*Eleusine coracana* (L.) Gaertn) using genomic SSR markers. *SpringerPlus* 5, 1–11.[CrossRefGoogle ScholarPubMed](#)

Rao, VR and Hodgkin, T (2002) Genetic diversity and conservation and utilization of plant genetic resources. *Plant Cell, Tissue and Organ Culture* 68, 1–19.[Google Scholar](#)

Ren, R, Ray, R, Li, P, Xu, J, Zhang, M, Liu, G, Yao, X, Kilian, A and Yang, X (2015) Construction of a high-density DArTseq SNP-based genetic map and identification of genomic regions with segregation distortion in a genetic population derived from a cross between feral and cultivated-type watermelon. *Molecular Genetics and Genomics* 290, 1457–1470.[CrossRefGoogle Scholar](#)

Salgotra, RK and Stewart, CN Jr. (2020) Functional markers for precision plant breeding. *International Journal of Molecular Sciences* 21, 4792.[CrossRefGoogle ScholarPubMed](#)

Samarina, LS, Malyarovskaya, VI, Reim, S, Yakushina, LG, Koninskaya, N G, Klemeshova, KV, Shkhalakhova, RM, Matskiv, AO, Shurkina, ES, Gabueva, TY and Slepchenko, NA (2021) Transferability of ISSR, SCoT and SSR markers for *Chrysanthemum* × *Morifolium* Ramat and genetic relationships among commercial Russian cultivars. *Plants* 10, 1302.[CrossRefGoogle Scholar](#)

Shannon, CE and Weaver, W (1949) *The Mathematical Theory of Communication*. Urbana: University of Illinois Press.[Google Scholar](#)

Shayanowako, AIT, Shimelis, H, Laing, MD and Mwadzingeni, L (2018) Genetic diversity of maize genotypes with variable resistance to *Striga asiatica* based on SSR markers. *Cereal Research Communications* 46, 668–678. [CrossRefGoogle Scholar](#)

Shekhawat, JK, Rai, MK, Shekhawat, NS and Kataria, V (2018) Start codon targeted (SCoT) polymorphism for evaluation of genetic diversity of wild population of *Maytenus emarginata*. *Industrial Crops and Products* 122, 202–208. [CrossRefGoogle Scholar](#)

Srivastava, A, Gupta, S, Shanker, K, Gupta, N, Gupta, AK and Lal, RK (2020) Genetic diversity in Indian poppy (*P. somniferum* L.) germplasm using multivariate and SCoT marker analyses. *Industrial Crops and Products* 144, 112050. [CrossRefGoogle Scholar](#)

Uba, CU, Oselebe, HO, Tesfaye, AA and Abteu, WG (2021) Genetic diversity and population structure analysis of Bambara groundnut (*Vigna subterrene* L.) landraces using DaRT SNP markers. *PLoS ONE* 16, e0253600. [CrossRefGoogle ScholarPubMed](#)

Uguru, MI and Onovo, JC (2011) Evidence of polyploidy in fluted pumpkin (*Telfairia occidentalis* Hook F.). *African Journal of Plant Science* 5, 287–290. [Google Scholar](#)

Wada, E, Feyissa, T, Tesfaye, K, Asfaw, Z and Potter, D (2021) Genetic diversity of Ethiopian cocoyam (*Xanthosoma sagittifolium* (L.) Schott) accessions as revealed by morphological traits and SSR markers. *PLoS ONE* 16, e0245120. [CrossRefGoogle ScholarPubMed](#)

Wang, Z, Kang, M, Liu, H, Gao, J, Zhang, Z, Li, Y, Wu, R and Pang, X (2014) High-level genetic diversity and complex population structure of Siberian apricot (*Prunus sibirica* L.) in China as revealed by nuclear SSR markers. *PLoS ONE* 9, e87381. [CrossRefGoogle ScholarPubMed](#)

Xanthopoulou, A, Ganopoulos, I, Kalivas, A, Nianiou-Obeidat, I, Ralli, P, Moysiadis, T, Tsaftaris, A and Madesis, P (2015) Comparative analysis of genetic diversity in Greek Genebank collection of summer squash (*Cucurbita pepo*) landraces using start codon targeted (SCoT) polymorphism and ISSR markers. *Australian Journal of Crop Science* 9, 14–21. [Google Scholar](#)

Xu, S, Böttcher, L and Chou, T (2020) Diversity in biology: definitions, quantification and models. *Physical Biology* 17, 031001. [CrossRefGoogle ScholarPubMed](#)

Yang, S, Xue, S, Kang, W, Qian, Z and Yi, Z (2019) Genetic diversity and population structure of *Miscanthus lutarioriparius*, an endemic plant of China. *PLoS ONE* 14, e0211471. [CrossRefGoogle ScholarPubMed](#)

Zhao, J, Solís-Montero, L, Lou, A and Vallejo-Marín, M (2013) Population structure and genetic diversity of native and invasive populations

of *Solanum rostratum* (Solanaceae). PLoS ONE 8, e79807.[CrossRefGoogle ScholarPubMed](#)

Zheng, Y, Xu, S, Liu, J, Zhao, Y and Liu, J (2017) Genetic diversity and population structure of Chinese natural bermudagrass [*Cynodon dactylon* (L.) Pers.] germplasm based on SRAP markers. PLoS ONE 12, e0177508.[CrossRefGoogle ScholarPubMed](#)

Zhu, L, Zhu, H, Li, Y, Wang, Y, Wu, X, Li, J, Zhang, Z, Wang, Y, Hu, J, Yang, S, Yang, L and Sun, S (2021) Genome wide characterisation, comparative and genetic diversity analysis of simple sequence repeats in cucurbita species. Horticulturae 7, 143.[CrossRefGoogle Scholar](#)

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