INNSPUB

International Journal of Biosciences | IJB |
ISSN: 2220-6655 (Print); 2222-5234 (Online)
Website: https://www.innspub.net
Email contact: info@innspub.net
Vol. 28, Issue: 4, p. 73-84, 2026

RESEARCH PAPER
OPEN ACCESS

Evaluation of the agronomic performance, beta-carotene content and dry matter content of 228 sweet potatoes *(Ipomoea batatas* (L.) Lam) genotypes in Burkina Faso

Nattan Gamsore*[1], Koussao Some[2], Djakaridja Tiama[2], Pauline Bationo_Kando[1]

[1]*Equipe de Génétique et Amélioration des Plantes (EGAP), Laboratoire Biosciences (LaBios), Université Joseph Ki-Zerbo, Ouagadougou, Burkina Faso*
[2]*Institut de l'Environnement et de Recherche Agricole (INERA), Ouagadougou, Burkina Faso*

Key words: Evaluation, *Ipomea batatas*, Family, Genotype, Burkina Faso

Received: March 23, 2026 **Accepted:** April 05, 2026 **Published:** April 11, 2026

DOI: https://dx.doi.org/10.12692/ijb/28.4.73-84

ABSTRACT

Sweet potato [*Ipomoea batatas* (L.) Lam] is a crop cultivated mainly for its root tubers. Unfortunately, sweet potato varieties currently promoted in Burkina Faso produce yields that remain low compared with the species' potential. Additionally, most are white-fleshed, which are nutritionally less rich than orange-fleshed varieties. The aim of this study is to evaluate the agro-morphological performance of 21 families and 228 sweet potato genotypes, derived from crosses between seven parent varieties over two consecutive seasons. The cross design used was a complete diallel without self-pollination. The experiments were conducted at the Centre for Environmental, Agricultural Research and Training (CREAF) experimental station at Kamboinsé during the 2023 and 2024 cropping seasons. The experimental layout followed an alpha lattice design with three replications, five blocks per replication, and twenty-five genotypes per block. Data were collected on agro-morphological variables, beta-carotene content and dry matter content. The analysis of variance revealed a highly significant difference ($p<0.001$) among genotypes and parents over the two years of evaluation. Estimation of heterosis showed families with positive and high heterosis compared with the parents. The BfxTu and HexTu families had the best heterosis for roots tuber yield (RTY). The best families for beta-carotene content (β-CAR) include IrxSo and BfxSo. The BfxJe and JexSo families showed the best heterosis for leaf biomass yield (LBY). The multivariate analyses grouped the 228 genotypes into 4 groups according to their performance. The best groups were cluster 1 for its high beta-carotene content (β-CAR), cluster2 for its high roots tubers yield potential (RDT) and cluster 3, which was characterised by high dry matter content (DMC).

***Corresponding author:** Nattan Gamsore ✉ gamsorenattan@gmail.com

INTRODUCTION

Sweet potato [*Ipomoea batatas* (L.) Lam], a member of the Convolvulaceae family, is currently one of the most important crops grown in a wide range of tropical and subtropical environments (Koussoube *et al.*, 2018). It is grown mainly for its tuberous roots, which contain high-quality carbohydrates and other nutrients (Aliou *et al.*, 2020a). The leaves are also rich in nutrients and are used as vegetables for human and animal consumption in many communities (Nguyen *et al.*, 2021; Padmaja, 2012). This crop is intrinsically undemanding in terms of production inputs. Moreover, sweet potato provides high yields under marginal growing conditions, making it a widely grown crop of choice in sub-Saharan Africa (Kankam *et al.*, 2022). Globally, sweet potato recorded an average yield of 11.90 t/ha compared with 7.03t/ha in Africa in the 2022 cropping season (FAOSTAT, 2024). Sweet potato production in Burkina Faso for the 2021/2022 cropping season was estimated at 115580t, with an average yield of 11.70 t/ha (FAOSTAT, 2024). However, this production is dominated by white-fleshed sweet potato varieties that are less rich in nutrients compared to orange-fleshed varieties that are richer in beta-carotene content.

A Deficiency in β-carotene (provitamin A) affects more than hundreds of millions of children under the age of five worldwide, with the most severe impacts on health observed in developing countries (Somé, 2012). It is with this in mind that sweet potato production, particularly the orange-fleshed variety (OFSP) has long been encouraged as a means of remedying certain health problems, in particular vitamin A deficiency, especially among children under the age of five and women who are pregnant, breastfeeding or of reproductive age.

The number of sweet potato varieties promoted in Burkina Faso remains limited, especially those with orange flesh. Varieties improved in Burkina Faso or introduced for their beta-carotene content have relatively low dry matter content compared with local white-fleshed sweet potato varieties. In addition, these orange-fleshed varieties, which are rich in beta-carotene, have low yield potential compared with white-fleshed varieties.

In view of the above, varietal improvement using traditional methods such as hybridisation is an alternative for developing varieties adapted to local conditions. Inter-varietal crossing enable the exploitation of variability and bring together genes of interest within the same genotype (Chabi *et al.*, 2024). Heterosis, known as hybrid vigour is a phenomenon whereby a hybrid outperforms its parents (Mackay *et al.*, 2011; Mugisa *et al.*, 2022), is a powerful tool for revealing the best crosses in relation to the parents. In this context, new sweet potato genotypes were developed by crossing resistant white-fleshed and orange-fleshed varieties at the Center for Environmental, Agricultural Research and Training (CREAF) at Kamboinsé.

The diallel design was used for the crosses, along with their reciprocals. From these crosses, 228 genotypes grouped into twenty-one families were obtained. It is therefore important to identify the most promising ones in order to obtain high-performance varieties for sweet potato growers in Burkina Faso. It is with this in mind that the present study was initiated, the aim of which is to determine the agro-morphological and beta-carotene performance of the sweet potato genotypes resulting from the crosses.

Specifically, the aim is to identify genotypes with high root tuber yield potential, genotypes with high beta-carotene content, and genotypes that perform well in terms of dry matter content.

MATERIALS AND METHODS

Presentation of the experimental site

The experiments were conducted over a two-year period at the Centre for Environmental, Agricultural and Training Research (CREAF) at Kamboinsé, which is part of the Institute for the Environment and Agricultural Research (INERA). The centre is located 12 km North of Ouagadougou, at latitude 12°28 N, longitude 1°32 W and altitude 296 m, with a tropical climate (Guinko, 1984). The soil at the site is very heterogeneous, deep, of low chemical fertility, with a predominantly sandy-loam texture and a pH ranging from 5 to 6.3 (Guinko, 1984).

During the 2023 cropping season, the minimum temperature recorded was 22.4°C and the maximum 37.8°C, with an annual rainfall of 710 mm (INERA/CREAF, 2024). Rainfall peaked in August (279 mm) and became scarce from September onwards (106.7 mm).

The 2024 crop year recorded a cumulative rainfall of 871.3 mm, with a peak of 279.3 mm recorded in August. Temperatures ranged from 23.2°C to 39.1°C (INERA/CREAF, 2024). The rainfall diagram for the experimental site during 2023 and 2024 is in Fig. 1.

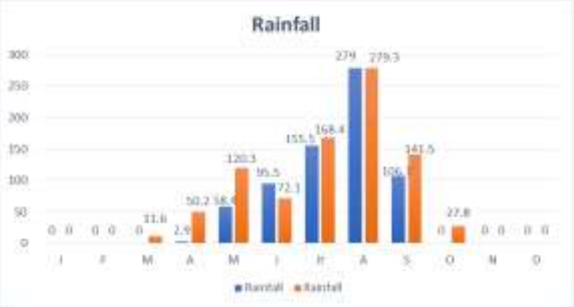


Fig. 1. CREAF rainfall diagram for 2023 and 2024 (INERA, 2024)

Plant material

Table 1 presents the characteristics of the parental varieties used to generate the genotypes evaluated in this study, whereas Table 2 presents the different families generated and the number of genotypes in each family.

Table 1. Origin and characteristics of the parent varieties used

N°	Varieties	Origin	Yied (t/ha)	Flesh colour	Dry matter content
1	BF59 (Bf)	Burkina Faso	35	White	High
2	Heere (He)	Burkina Faso	25	Orange	Low
3	Jewell (Je)	United States	20	Orange	Low
4	Songre (So)	Burkina Faso	16	Orange	Low
5	Tuskegee_orange (Tu)	United States	20	Orange	Low
6	Bagre (Ba)	Burkina Faso	25	Orange	Low
7	Irène (Ir)	Mozambique	25	Orange	Low

Table 2. List of families and number of genotypes resulting from crosses

N°	Families	Number of genotypes per family
1	BaxHe	4
2	BfxHe	14
3	BfxJe	7
4	BfxSo	5
5	BfxTu	6
6	HexBa	2
7	HexBf	2
8	HexJe	12
9	HexSo	21
10	HexTu	6
11	IrxSo	2
12	JexBf	3
13	JexHe	29
14	JexSo	23
15	JexTu	2
16	SoxHe	23
17	SoxTu	16
18	TuxBf	3
19	TuxHe	09
20	TuxJe	10
21	TuxSo	24
Total of genotypes		228

Note: BaxHe= Bagre x Heere= BfxHe= Bf59 x Heere; BfxJe= Bf59 x Jewell;BfxSo= Bf59 x Songre; BfxTu= Bf59 x Tuskegee_orange; HexBa= Heere x Bagre; HexBf= Heere x Bf59; HexJe= Heere x Jewell; HexSo= Heere x Songre; HexTu= Heere x Tuskegee_orange; IrxSo= Irene x Songre; JexBf= Jewell x Bf59; JexHe= Jewell x Heere; JexSo= Jewell x Songre; JexTu= Jewell x Tuskegee_orange; SoxHe= Songre x Heere= SoxTu= Songre x Tuskegee_orange; TuxBf= Tuskegee_orange x Bf59; TuxJe= Tuskegee_orange x Jewell; TuxHe= Tuskegee_orange x Heere;TuxSo=Tuskegee_orange x Songre.

Experimental design

An alpha lattice design with three replications was used. The replications were spaced 2 m apart and each was subdivided into six blocks spaced 1 m apart. Each replicate consisted of 30 ridges 5 m long and 1 m wide, divided into 6 blocks, or 5 ridges per block. Five genotypes from the same family were transplanted onto each ridge. The distance between two consecutive ridges was 1 m and that between two stacks of cuttings was 0.3 m. The experimental set-up was 32 m long and 21 m wide, covering an area of 672 m^2.

Seed germination

Cross-bred seeds were first scarified by family in order to overcome their seed coat dormancy. Following the method proposed by Lebot (2008), the seeds were soaked in 97% sulphuric acid for 30 minutes and then rinsed in tap water for 5 minutes to remove the acid. Next, a flotation technique was used to separate viable from non-viable seeds by immersing the seeds in a beaker containing water. The viable seeds were sown in trays filled with sterilised potting soil and watered every day for 30 days.

Preparing cuttings and setting up the trial

The seedlings were transplanted onto beds in a natural environment and watered every day to accelerate their growth so that the cuttings could be taken to set up the experimentation. From these seedlings, 30 cm cuttings with at least three nodes were taken 45 days after transplanting. The cuttings were labelled before being transplanted. Nine to six cuttings per genotype were cut and stripped with pruning shears, depending on the availability of cuttings for the three replications. The ridges were made on the plot, which had been ploughed with a motorised tractor to a depth of around 30 cm. The cuttings taken were transplanted on 1 August 2023, the same day they were collected. They were transplanted manually, with two nodes inserted into the soil at an angle of approximately 45 degrees to the soil surface to increase the contact surface between the cutting and the soil. Two weeding sessions were carried out two and four weeks after planting using small hoes. NPK 14/23/14 fertiliser at a rate of 350 kg/ha was applied three weeks after transplanting. The water supply was rain-fed and then supplemented by irrigation in October and November, with a frequency of three irrigations per week. The crop was harvested on 15 November 2023, 95 days after transplanting, when most of the leaves of the genotypes had turned yellow. The same experiment was repeated the following year from 15 July to 30 November 2024 on the same site with the same treatments.

Data collection

The various observations and measurements were made on 10 agro-morphological variables:

1. At 60 days after transplanting, the length of the stem (LOT) and the diameter of the main stem (DIT) were measured;
2. At harvest, leaf biomass yield (LBY), number of marketable root tubers per plant (NRT), root tuber yield (RTY), predominant skin colour (PSC), latex production (LP), oxidation (OXY), beta-carotene content (β-CAR) and dry matter content (DMC) were assessed.

The predominant skin colour of the root tubers (PSC) was visually assessed using the following colour score scale: 1= white; 2= cream; 3= yellow; 4= orange; 5= brownish-orange; 6= pink; 7= red; 8= purple-red; 9= dark purple (Human *et al.*, 1999); latex production (LP), oxidation (OXY) were visually observed through a longitudinal section of a medium-sized root tuber and assessed according to the following scores: 1= low; 3= moderate; 7= high; beta-carotene content (β-CAR) was estimated according to the flesh colour chart for tuberous sweet potato roots proposed by Burgos *et al.* (2009). The dry matter content was calculated using the formula: Dry weight/Fresh weight*100.

Data analysis

The data collected was entered into Microsoft Excel, (2016 version) analysed using the software JAMOVI (2.2.28 version). An analysis of variance (ANOVA) with a 95% confidence interval was performed to assess the level of variability of the studied plant material during the two cropping season. Mid-parent heterosis and best-parent heterosis were estimated to identify the best hybrid combinations with regard to the parents. Well-represented variables namely leaf biomass yield (LBY), number of marketable roots per plant (NRT), roots tuber yield (RTY), predominant skin colour of the roots

(PSC), oxidation (OXY), beta-carotene content (β-CAR) and dry matter (DMC) were used to group the genotypes through Hierarchical Ascending Classification based on Ward's distance. The best genotypes were selected on the basis of root tuber yield (RTY > 07 t/ha), beta-carotene content (β-CAR > 1.5 µg/100g) and dry matter content (DM > 30%).

RESULTS

Average performance of families

Table 3 summarises the results of the analysis of variance between the different families and their parents. The results show a highly significant difference (p<0.001) between the families and their respective parents for roots tuber yield (RTY); predominant skin colour (PSC); beta-carotene content (β-CAR) and dry matter (DMC) content. However a highly significant difference (P<0.01) was observed for leaf biomass yield (LBY) and number of marketable roots tubers per plant (NRT).

The best family for leaf biomass yield (LBY) is HexJe with a yield of 6.69t/ha, while among the parents the highest yield (1.88t/ha) was recorded with the Tu parent. The HexTu family produced more marketable root tubers per plant (NRT=06 root tubers); the male parent He was the best compared to the others with four marketable root tubers per plant. The best root tubers yield was obtained with the BfxHe family (RTY= 22.42/ha), while their parents, He and Tu, had yields of 2.59/ha and 7.02t/ha respectively. The best parent is Je with a root tuber yield of 7.52t/ha.

Table 3. Results of analyse of variance among families and their parents

Families	MSL (cm)	MSD (cm)	LBY (t/ha)	NRT	RTY (t/ha)	PSC	LP	OXY	β-CAR (mg/100g)	DMC (%)
Bf	26,366 a	0,667 a	0,263 abc	3,000 ab	2,591 abc	1,593 b	3,000 a	3,000 a	0,860 b	33,343 b
He	23,723 a	0,815 a	1,419 a	4,000a b	7,020 ab	6,360 ab	4,000 a	3,000 a	9,935 ab	29,707 b
Je	21,705 a	0,778 a	0,241 a	3,000 ab	7,519 ab	5,618 ab	4,000 a	3,000 a	8,950 ab	25,111 b
So	20,320 a	0,721 a	0,697 abc	4,000 ab	5,451 ab	6,429 ab	3,000 a	3,000 a	2,417 ab	27,400 b
Tu	49,043 a	0,536 a	1,878 a	3,000 ab	3,977 abc	7,237 ab	5,000 a	3,000 a	10,942 a	30,462 b
Ba	14,542 a	0,675 a	1,053 a	3,000 ab	5,277 ab	6,951 ab	4,000 a	3,000 a	4,722 ab	32,531 a
Ir	35,046 a	0,528 a	0,975 a	1,000 b	3,773 abc	9,000 a	5,000 a	3,000 a	1,632 ab	29,776 b
HexSo	135,553 a	0,781 a	1,147 a	4,000 ab	10,008 a	5,591 ab	4,000 a	4,000 a	5,010 ab	28,895 b
TuxBf	113,586 a	0,616 a	3,542 a	3,000 ab	8,848 ab	4,399 ab	7,000 a	7,000 a	10,761 a	30,213 b
SoxIr	5,796 a	0,751 a	1,110 a	7,000 a	13,990 a	8,026 ab	7,000 a	5,000 a	0,590 b	24,868 b
BfxTu	28,814 a	0,783 a	1,603 a	4,000 ab	8,319 ab	4,636 ab	4,000 a	3,000 a	2,186 abc	28,309 b
BfxJe	17,645 a	0,674 a	5,853 a	5,000 ab	9,649 a	5,872 ab	4,000 a	4,000 a	4,564 ab	29,678 b
BfxHe	13,906 a	0,746 a	1,162 a	4,000 ab	11,142 a	4,662 ab	4,000 a	4,000 a	4,180 ab	35,122 a
SoxJe	178,844 a	0,928 a	0,838 a	3,000 ab	7,763 ab	6,453 ab	4,000 a	3,000 a	6,975 ab	29,524 b
HexJe	16,344 a	0,726 a	6,688 a	4,000 a	7,940 ab	5,686 ab	4,000 a	4,000 a	4,078 ab	28,831 b
JexTu	4,368 a	0,612 a	6,273 a	2,000 ab	11,177 a	6,200 ab	3,000 a	5,000 a	9,874 ab	32,768 b
TuxHe	103,765 a	0,822 a	1,476 a	3,000 ab	6,919 ab	4,070 ab	4,000 a	5,000 a	6,757 ab	27,456 b
BF x He	34,633 a	0,520 a	0,846 a	4,000 ab	22,418 a	5,153 ab	3,000 a	4,000 a	7,688 ab	31,667 b
JexSo	8,353 a	0,724 a	1,391 a	3,000 ab	10,881 a	6,351 ab	4,000 a	5,000 a	5,905 ab	26,528 b
HexTu	23,489 a	0,763 a	1,077 a	6,000 ab	14,970 a	3,264 ab	4,000 a	4,000 a	3,105 ab	26,944 b
IrxSo	10,870 a	0,654 a	3,933 a	4,000 ab	4,873 abc	8,065 a	3,000 a	4,000 a	4,835 ab	33,044 a
TuxJe	13,628 a	0,701 a	0,976 a	3,000 ab	7,363 ab	7,105 ab	4,000 a	4,000 a	5,985 ab	28,211 b
BaxHe	5,110 a	0,795 a	0,803 a	3,000 ab	7,941 ab	4,084 ab	5,000 a	3,000 a	7,065 ab	29,775 b
SoxHe	10,921 a	0,721 a	1,017 a	3,000 ab	8,537 ab	5,101 ab	4,000 a	4,000 a	4,075 ab	28,196 b
TuxSo	14,507 a	0,754 a	0,836 a	4,000 ab	7,685 ab	4,541 ab	3,000 a	4,000 a	12,614 ab	30,981 b
BfxSo	8,029 a	0,707 a	0,713 a	4,000 ab	7,665 ab	4,021 ab	3,000 a	4,000 a	2,616 abc	32,579 a
JexHe	9,557 a	0,754 a	1,014 a	4,000 ab	8,276 ab	6,013 ab	3,000 a	3,000 a	6,446 ab	26,297 b
JexBa	5,554 a	0,669 a	0,460 a	3,000 ab	7,101 ab	5,026 ab	4,000 a	4,000 a	4,910 ab	28,995 b
SoxTu	25,313 a	0,649 a	0,762 a	2,000 ab	5,750 ab	5,231 ab	3,000 a	3,000 a	2,496 abc	32,293 a
HexBa	6,256 a	0,846 a	0,244 abc	2,000 ab	2,990 abc	6,026 ab	3,000 a	3,000 a	7,855 ab	28,130 b
Minimum	40,368	0,441	0,241	0,932	2,591	1,593	2,874	2,735	0,590	24,868
Maximum	201,178	0,637	6,688	6,865	22,418	9,327	6,930	4,803	12,614	35,1229
Average	35,897	0,513	1,654	3,392	8,125	5,555	3,964	3,622	5,470	29,579
CV	50,497	14,950	70,5090	34,536	48,941	27,704	20,991	14,408	53,160	98,0566
Pr > F	0,977	0,920	0,0023**	0,0029**	0,0001***	0,006**	0,633	0,742	1,3e-05***	2,7e-06***

Note: Ba= Bagre ; Bf= BF59 ; He= Heere ; Je= Jewell ; So=Songre ; Tu= Tuskegee_orange ; Ir= Irène ; BaxHe= Bagre crossed with Heere= BfxHe= Bf59 crossed with Heere; BfxJe= Bf59 crossed with Jewell; BfxSo= Bf59 crossed with Songre; BfxTu= Bf59 crossed with Tuskegee_orange; HexBa= Heere crossed with Bagre; HexBf= Heere crossed with Bf59; HexJe= Heere crossed with Jewell; HexSo= Heere crossed with Songre; HexTu= Heere crossed with Tuskegee_orange; IrxSo= Irene crossed with Songre; JexBf= Jewell crossed with Bf59; JexHe= Jewell crossed with Heere; JexSo= Jewell crossed with Songre; JexTu= Jewell crossed with Tuskegee_orange; SoxHe= Songre crossed with Heere= SoxTu= Songre crossed with Tuskegee_orange; TuxBf= Tuskegee_orange crossed with Bf59; TuxJe= Tuskegee_orange crossed with Jewell; TuxHe= Tuskegee_orange crossed with Heere;TuxSo=Tuskegee_orange crossed with Songre; MSL= main stem length; MSD= main stem diameter; LBY= leaf biomass yield; NRT= number of root tubers per plant; RTY= root tubers yield; PSC= predominant skin colour; LP= latex production; OXY= oxidation; β-CAR= beta-carotene content. DMC= dry matter content; CV= coefficient of variation; Pr > F= pvalu; ***= difference very highly significant (*p* < 0.001); **= difference highly significant (*p* < 0.01); *= difference significant (*p* < 0.1).

Table 4. Average heterosis (HMP) of the studied families

Families	MSL (cm)	MSD (cm)	LBY (t/ha)	NRT	RTY (t/ha)	PSC	LP	OXY	β-CAR (mg/100g)	DMC (%)
BfxHe	38,286	- 29,823	0,568	25,548	- 49,680	29,591	- 8,310	- 3,999	42,437	15,062
HexBf	- 67,305	13,572	- 80,292	- 44,277	- 51,380	- 9,456	- 21,218	- 16,554	7,186	- 9,605
BfxJe	- 26,589	- 6,702	238,314	68,148	90,875	62,853	- 1,640	18,483	- 6,948	5,140
JexBf	- 69,356	- 7,865	- 28,867	12,906	10,980	- 20,021	- 0,479	22,332	- 28,168	0,604
BfxTu	- 23,579	30,136	49,709	57,352	153,294	5,001	19,212	9,197	- 62,954	- 8,393
TuxBf	- 31,060	- 26,755	- 58,885	- 27,423	- 0,537	6,443	- 5,613	0,868	58,975	- 6,378
HexJe	- 28,045	- 8,914	103,435	9,996	9,223	- 5,061	- 9,135	15,454	- 56,814	5,189
JexHe	- 47,267	3,764	56,759	47,731	29,352	- 4,317	- 13,457	7,925	- 5,711	- 8,756
HexSo	- 38,456	1,646	8,441	- 3,398	60,508	- 12,571	7,521	17,961	- 18,875	1,195
SoxHe	- 50,410	- 6,179	- 3,895	- 14,212	36,911	- 20,233	12,095	25,632	- 34,018	- 1,252
HexTu	- 35,441	12,949	- 34,652	65,877	172,235	- 51,989	- 13,787	12,766	- 70,254	- 10,437
TuxHe	- 42,727	38,598	19,059	- 27,238	63,660	- 41,953	- 0,967	20,571	- 34,036	- 12,062
JexSo	- 60,247	- 3,426	196,548	- 21,713	67,791	5,430	8,186	23,610	3,905	1,037
SoxJe	- 15,081	23,773	78,645	- 24,825	19,707	7,131	- 2,833	4,199	22,734	12,449
SoxTu	- 55,596	16,659	- 8,499	- 20,389	57,305	- 22,326	1,469	8,584	- 47,698	3,744
TuxSo	- 74,898	12,443	- 33,135	20,946	81,151	- 38,600	4,740	21,819	- 34,005	- 7,425
JexTu	1,567	- 10,092	- 73,154	- 65,323	- 13,347	- 24,583	- 20,995	2,977	- 77,568	19,495
JexTu	- 87,652	- 6,899	- 74,238	- 46,868	- 79,516	- 3,543	- 35,264	53,423	- 0,721	- 3,665
BaxHe	0,657	- 17,535	- 4,708	- 25,379	- 35,830	25,977	- 22,736	- 9,992	- 51,547	8,966
IrxSo	- 60,733	4,815	11,560	39,925	5,656	2,376	- 16,247	15,020	138,839	- 0,133
BfxSo	21,447	105,703	193,622	119,886	226,189	160,530	109,884	125,777	207,155	90,588

Note: Ba= Bagre ; Bf = BF59 ; He = Heere ; Je= Jewell ; So =Songre ; Tu = Tuskegee_orange ; Ir = Irène ; BaxHe= Bagre crossed with Heere= BfxHe= Bf59 crossed with Heere; BfxJe= Bf59 crossed with Jewell;BfxSo= Bf59 crossed with Songre; BfxTu= Bf59 crossed with Tuskegee_orange; HexBa= Heere crossed with Bagre; HexBf= Heere crossed with Bf59; HexJe= Heere crossed with Jewell; HexSo= Heere crossed with Songre; HexTu= Heere crossed with Tuskegee_orange; IrxSo= Irene crossed with Songre; JexBf= Jewell crossed with Bf59; JexHe= Jewell crossed with Heere; JexSo= Jewell crossed with Songre; JexTu= Jewell crossed with Tuskegee_orange; SoxHe= Songre crossed with Heere= SoxTu= Songre crossed with Tuskegee_orange; TuxBf= Tuskegee_orange crossed with Bf59; TuxJe= Tuskegee_orange crossed with Jewell; TuxHe= Tuskegee_orange crossed with Heere;TuxSo=Tuskegee_orange crossed with SongreMSL= main stem length; MSD= main stem diameter; LBY= leaf biomass yield; NRT= number of root tubers per plant; RTY= root tubers yield; PSC= predominant skin colour; LP= latex production; OXY= oxidation; β-CAR= beta-carotene content. DMC= dry matter content.

Regarding the average latex production and oxidation, the TuxBf family displayed the highest scores (LP=score 7; OXY=score 7). The male parent Tu (LP=5) recorded the highest latex production. The same parent Tu recorded the highest average beta-carotene content (β-CAR= 10.94mg/100g). When used as a male parent, crossing it with So (TuxSo) gave a high beta-carotene content (β-CAR= 12.61mg/100g). For dry matter (DM) content, the Bf parent had the highest dry matter content (DMC=33.34%). Crossing this parent with the He parent (BfxHe) produced the best dry matter content (DMC=35.12%) among the families.

The coefficient of variation is high for 6 variables: length of main stem (CV=50.49%); leaf biomass (CV=70.5%) and roots tubers(CV=48.94%) yields; number of marketable root tuber per plant (CV=34.53%); beta-carotene content (CV=53.16%) and dry matter content (CV=98.05%).

Table 5. Heterosis in relation to the best parent (BPH) in the studied families

Families	MSL (cm)	MSD (cm)	LBY (t/ha)	NRT	RTY (t/ha)	PSC	LP	OXY	β-CAR (mg/100g)	DMC (%)
BfxHe	31,355	- 36,208	- 40,391	8,466	- 65,552	- 18,973	- 19,290	- 7,973	- 22,615	10,607
HexBf	- 73,631	3,776	- 82,833	- 51,967	- 57,414	- 5,250	- 24,588	- 20,893	- 20,934	- 13,529
BfxJe	- 33,077	- 4,126	382,032	13,565	48,187	- 17,018	2,913	48,617	- 53,291	- 11,942
JexBf	- 74,412	- 13,976	- 56,290	6,842	- 5,562	- 10,531	- 9,550	24,155	- 45,133	- 10,870
BfxSo	- 69,546	-1,991	2,216	- 15,558	40,631	- 37,454	- 3,939	30,353	8,249	- 8,820
SoxBf	- 17,790	19,241	20,211	- 34,029	3,244	14,871	- 13,365	4,880	- 22,061	7,751
BfxTu	- 1,247	46,006	- 14,660	57,600	109,159	- 35,941	- 1,560	9,882	- 80,021	- 9,680
TuxBf	- 46,999	- 17,822	- 76,562	- 27,308	-17,868	-35,062	- 22,060	1,500	- 14,263	- 11,066
HexJe	- 31,106	- 11,007	19,002	- 0,391	13,103	- 10,601	- 3,759	7,955	- 58,956	10,517
JexHe	- 59,714	- 7,571	- 28,514	13,394	17,893	- 5,456	- 12,040	- 4,695	- 35,124	- 11,477
HexSo	- 42,870	- 4,241	- 19,135	0,185	42,568	- 12,094	0,848	10,971	- 49,571	- 2,734
SoxHe	- 53,967	- 11,612	- 28,334	- 11,030	21,608	- 19,797	5,138	18,187	- 58,984	- 5,086
HexTu	- 52,106	- 6,386	- 42,645	43,118	113,239	- 54,897	- 19,965	18,626	- 71,623	- 11,547
TuxHe	- 57,512	14,872	4,495	- 37,221	28,194	-45,470	- 8,063	26,836	- 37,072	- 13,151
TuxJe	- 54,400	29,389	- 49,467	14,830	- 18,932	14,925	- 17,492	39,762	- 47,664	- 3,078
JexTu	- 91,093	14,082	- 85,466	- 43,736	- 70,397	- 14,333	- 36,622	50,396	- 9,761	7,571
TuxSo	- 58,591	49,564	- 56,824	- 8,151	25,299	-32,465	- 32,053	21,450	- 66,915	- 4,209
SoxTu	- 28,175	5,395	- 81,594	- 64,761	- 32,747	- 28,790	- 30,856	1,591	- 86,307	13,491
JexSo	- 61,515	- 6,962	99,548	- 31,298	44,716	13,047	- 3,540	24,418	- 34,019	7,765
BaxHe	-78,461	- 2,456	- 43,375	- 11,447	13,120	-35,787	26,412	- 1,849	- 28,889	- 8,472
IrxSo	- 68,983	- 9,233	- 4,340	- 14,408	- 10,606	- 13,526	- 30,073	13,024	100,073	- 14,782

Note: Ba= Bagre ; Bf= BF59 ; He= Heere ; Je= Jewell ; So=Songre ; Tu= Tuskegee_orange ; Ir= Irène ; BaxHe= Bagre crossed with Heere= BfxHe= Bf59 crossed with Heere; BfxJe= Bf59 crossed with Jewell;BfxSo= Bf59 crossed with Songre; BfxTu= Bf59 crossed with Tuskegee_orange; HexBa= Heere crossed with Bagre; HexBf= Heere crossed with Bf59; HexJe= Heere crossed with Jewell; HexSo= Heere crossed with Songre; HexTu= Heere crossed with Tuskegee_orange; IrxSo= Irene crossed with Songre; JexBf= Jewell crossed with Bf59; JexHe= Jewell crossed with Heere; JexSo= Jewell crossed with Songre; JexTu= Jewell crossed with Tuskegee_orange; SoxHe= Songre crossed with Heere= SoxTu= Songre crossed with Tuskegee_orange; TuxBf= Tuskegee_orange crossed with Bf59; TuxJe= Tuskegee_orange crossed with Jewell; TuxHe= Tuskegee_orange crossed with Heere; TuxSo=Tuskegee_orange crossed with Songre; MSL= main stem length; MSD= main stem diameter; LBY= leaf biomass yield; NRT= number of root tubers per plant; RTY= root tubers yield; PSC= predominant skin colour; LP= latex production; OXY= oxidation; β-CAR= beta-carotene content. DMC= dry matter content.

Average heterosis (HMP) and heterosis relative to the best parent (HBP) in the studied families

The average heterosis of both parents (HMP) and the heterosis relative to the best (HBP) of sweet potato crosses for the agro-morphological variables beta-carotene and dry matter (DM) content are presented in Tables 4 and 5, respectively. Some crosses showed both positive and high average heterosis (HMP). For root tuber yield, the best crosses were BfxTu (HMP= 153.20%), HexTu (HMP= 172.23%), BfxSo (HMP= 226.18%). The IrxSo and BfxSo crosses showed the best average heterosis for beta-carotene content, with values of 138.84% and 207.15% respectively. The BfxSo (MHP= 90.58) and JexTu (MHP= 19.49) families showed positive and high average heterosis for dry matter content. The BfxSo family was the only to show a high and positive average heterosis for all the variables studied.

In terms of heterosis relative to the best parents (HBP), the BfxJe, JexSo and BfxSo families gave high heterosis for leaf biomass yield (BIO). The BfxTu and HexTu families were the best, with values of 109.16% and 113.23% respectively for root tuber yield. For latex production and oxidation, the best heteroses were BaxHe (HBP= 26.41%) and BfxJe (HBP= 48.62%) respectively (Table 5). Only two families showed positive heterosis for beta-carotene content: BfxSo (BPH= 8.25%) and IrxSo (BPH=100.07%). As for the dry matter (DMC) content, the crosses showed low values. Nevertheless, the BfxHe (BPH=10.61) and SoxTu (BPH=13.49) families were the best in terms of this variable.

Table 6. Results of analyse of variance of studies genotypes

	MSL (cm)	MSD (cm)	LBY (t/ha)	NRT	RTY (t/ha)	PSC	LP	OXY	β-CAR (mg/100g)	DMC (%)
Minimum	50,072	0,268	0,050	0,000	0,167	1,000	1,000	1,000	0,000	12,121
Maximum	317,000	0,772	8,200	16,000	66,667	9,000	7,000	7,000	14,370	41,460
Average	113,95	0,696	1,202	3,759	8,241	5,924	3,934	3,767	5,210	28,000
CV	32,505	42,104	83,973	68,995	94,595	37,093	32,154	29,278	85,246	17,090
Pr > F (Gen)	3,5e-16 ***	7e-06 ***	5,5e-10 ***	2e-08 ***	2e-09 ***	2e-16 ***	1,4e-12 ***	4,6e-12 ***	2e-16 ***	0,0009***
Pr > F (Year)	1e-09 ***	2e-16 ***	1,1e-11 ***	0,012 *	0,020 *	0,002 **	0,0014 **	2,1e-07 ***	2,9e-05 ***	3,3e-05 ***
Year ×Gen	1,94e-4 ***	0,03 *	0,0024 **	8,2e-08 ***	0,012 *	0,002 **	0,1780	2,9e-05 ***	0,055	0,00092***

Note: MSL= main stem length; MSD= main stem diameter; LBY= leaf biomass yield; NRT= number of root tubers per plant; RTY= root tuber yield; PSC= predominant skin colour; LP= latex production; OXY= oxidation; β-CAR= beta-carotene content. DMC= dry matter content; CV= coefficient of variation; Pr > F (Gen)= p value between genotypes; Pr > F (Year)= pvalue between years; Year x Gen= genotypes by years interaction; ***= difference very highly significant (*p* < 0.001); **= difference highly significant (*p* < 0.01); *= difference significant (*p* < 0.1).

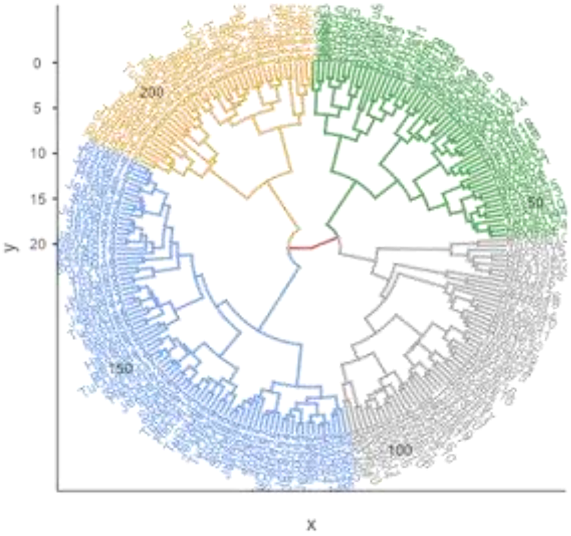
Performance of the studied genotypes

All the results of the descriptive analysis shown in Table 6 revealed a significant to highly significant difference (*p*> 0.001) among genotypes for all variables. The effect of the year revealed a very highly significant difference (*p*> 0.001) for stem length (MSL), stem diameter (MSD), leaf biomass yield (LBY), oxidation (OXY), beta-carotene content (β-CAR) and dry matter (DMC) content. However, a significant difference (*p*> 0.05) among genotypes was observed for root tuber yield components. The genotype x year interaction was highly significant for main stem length (MSL), number of marketable root tubers per plant (NRT), oxidation (OXY) and dry matter (DM) content. The coefficient of variation values was high (CV > 30%) for all variables (except for oxidation (CV= 29.27%), and dry matter content (CV= 17.09%)). Stem length (LOT) varied from 50.072cm (TuxHe1) to 317cm (BfxJe1), with an average of 113.95cm. The SoxHe2 and HexSo19 genotypes had the lowest and highest values (0.268 and 0.772 cm) of stem diameter (DIT) respectively. 6.74% of genotypes showed good stem growth (LOT> 150cm) compared with 13.38% that gave a diameter greater than 0.5cm. Leaf biomass yields ranged from 0.050t/ha to 8.200t/ha for the HexSo16 and BfxHe10 genotypes respectively. The SoxHe14 genotype did not produce any root tubers, while the HexSo10 genotype recorded the highest average number (16) of tuberous roots (NBT). With an average of 5.07t/ha, root tuber yield (TRY) varied from 0 t/ha (SoxHe14) to 66.67t/ha (HexSo11). Seventeen point seventeen per cent of genotypes showed high root tuber yields (RTY > 20t/ha). The beta-carotene content (β-CAR) varied from 0 mg/100g (BfxHe1) to 14.37mg/100g (JexSo8) with an average of 5.21 mg/100. The lowest dry matter content (12.12%) was recorded with the HexSo15 genotype, while the highest content (41.46%) was obtained with the BFxJe1 genotype. The frequency of the best genotypes is 60.61% for beta-carotene (β-CAR>5 mg/100g) and 22.56% for dry matter content (DM>30%).

Organisation of 228 genotypes

The CAH dendrogram, with truncation at level 15, structured the 228 genotypes into four distinct clusters (Fig. 2).

Cluster 1 (G1) consists of 98 genotypes characterised by high beta-carotene content (β-CAR), low dry matter (DMC), and low root tuber yield (RTY).



🟦 =Cluster 1; 🟧 =Cluster 2; 🟩 =Cluster 3;
⬜ = Cluster 4

Fig. 2. Dendrogram resulting from the hierarchical ascending classification (HAC) of 228 sweet potato genotypes

Cluster 2 (G2) contains 44 genotypes characterised by high number of marketable root tubers per plant (NMT), good root tuber yield (RTY) and leaf biomass yield (LBY), and low beta-carotene (β-CAR). Cluster 3 (G3) includes 41 genotypes distinguished from the others by high latex production (LP), high oxidation (OXY), and high dry matter (DMC). 10 genotypes out of the 228 studied showed the best average performances for root tuber yield (TRY), beta-carotene content (β-CAR) and matter content (MS).

Heterosis performance of the top ten genotypes for yield, beta-carotene content, and dry matter content

Table 7 indicates substantial variation in heterosis among the ten best genotypes across root tuber yield, beta-carotene content, and dry matter content. For root tuber yield, BfxSo4 (204.985% HMP; 141.625% HBP) and BfxJe5 (203.950% HMP; 172.400% HBP) showed the highest heterosis, followed by SoxTu9 (118.147% HMP; 82.250% HBP), whereas JexSo10 (−4.167% HMP; −25.000% HBP) and JexHe25 (−4.000% HMP; −24.400% HBP) exhibited negative values. For beta-carotene content, strong positive heterosis was observed in JexHe25 (150.979% HMP; 56.314% HBP), BaxHe4 (123.462% HMP; 77.461% HBP), and BfxSo4 (122.386% HMP; 200.667% HBP), while HexJe6 (−5.1676% HMP; −5.840% HBP) and SoxHe13 (−13.986% HMP; −74.977% HBP) showed negative heterosis. Dry matter content showed positive heterosis in all genotypes, with BaxHe4 (53.078% HMP; 31.944% HBP) and JexHe25 (41.641% HMP; 30.000% HBP) recording the highest values, indicating their superior performance across traits.

Table 7. Median heterosis (HMP) and heterosis in relation to the best parents (HBP) for yield, beta-carotene content and dry matter content of the 10 best genotypes

N°	Genotypes	RTY (t/ha)		β-CAR (mg/100g)		DMC	
		HMP	HBP	HMP	HBP	HMP	HBP
1	HexJe6	37.000	23.300	- 5.1676	- 5.840	14.448	10.980
2	BfxSo4	204.985	141.625	122.386	200.667	20.227	9.391
3	BfxJe5	203.950	172.400	29.589	20.103	1.577	0.060
4	JexSo10	- 4.167	- 25.000	6.425	- 25.000	0.877	11.393
5	SoxTu5	17.176	19.500	13.815	7.529	1.745	0.768
6	BaxHe4	131.452	66.625	123.462	77.461	53.078	31.944
7	SoxHe13	105.375	61.500	- 13.986	- 74.977	20.136	14.987
8	JexSo15	21.306	66.700	14.039	6.830	3.389	22.210
9	JexHe25	- 4.000	- 24.400	150.979	56.314	41.641	30.000
10	SoxTu9	118.147	82.250	20.243	0.667	19.872	12.245

Note: HMP= average heterosis; HBP= heterosis in relation to the best parent; RTY= root tuber yield; β-CAR= beta-carotene content. DMC= dry matter content; HexJe= Heere crossed with Jewell; BfxSo= Bf59 crossed with Songre; BfxJe= Bf59 crossed with Jewell; JexSo= Jewell crossed with Songre; SoxTu= Songre crossed with Tuskegee_orange; BaxHe= Bagre crossed with Heere; JexHe= Jewell crossed with Heere.

DISCUSSION

The desirable traits targeted for improvement in sweet potatoes include, among others, yield components, beta-carotene content and dry matter content. Moreover, a high variability has been observed between families and parents as well as between genotypes for these traits.

This variability could be attributed to the high rate of heterozygotes and the polyploidy (2n=6X=90) of sweet potato on one hand (Alam *et al.*, 2024), and the fact that the genotypes used are derived from crosses of genetically different parents on the other hand. This significant variability within the population provides a solid foundation for selecting genotypes with desirable traits to support the sweet potato breeding program in Burkina Faso.

Furthermore, the exploitation of heterosis is a powerful tool in agriculture as it helps meet the food and nutritional needs in many countries by rapidly increasing crop yields and quality (Al-Mamun *et al.*, 2023). However, unlike cereal crops such as maize and wheat, where major genetic gains have been made in recent years through controlled crosses, heterosis in root crops such as sweet potato has not yet been fully exploited, as they are generally reproduced by cloning (Nikiema, 2016). In this study, positive heterosis was obtained for the different variables, which offers the possibility of selecting progenies that perform better than their corresponding parents for breeding programs. Aliou *et al.* (2020b) reported that the improvement in hybrid performance compared to their parents can be explained by favourable allelic interactions at heterozygous loci that exceed homozygous states or by the fact that deleterious and recessive alleles at different loci in the parents' genomes are masked in the hybrids, thus producing better phenotypes. According to (Jiang *et al.*, 2017), heterosis is mainly attributed to non-additive effects such as dominance, overdominance and epistasis.

Dominance is when favourable dominant alleles from maternal and paternal lines accumulate in hybrids, subsequently leading to their better performance compared to parental genotypes.

In the case of overdominance, heterozygous hybrids perform better than their homozygous parents due to favourable intra-locus allelic interactions. Epistasis leads to heterosis when favourable underlying interactions occur between different loci, resulting in better hybrid performance (Liu *et al.*, 2020; Mugisa *et al.*, 2022). For tuber root yield, the families BfxTu, HexTu, and BfxSo were the best for average heterosis, while the best families for heterosis compared to the best parents were BfxTu and HexTu. Grüneberg *et al.* (2022) also reported positive heterosis, with maximums of 566.23% and 233.11% respectively for the average of the parents and compared to the best parent on sweet potato genotypes for root tuber yields.

The IrxSo and BfxSo families exhibited the best heterosis for beta-carotene content. The high levels of heterosis are explained by the self-compatibility of the sweet potato, which makes it a halogamous plant. (Grüneberg *et al.*, 2022; Mackay *et al.*, 2011) have reported that the level of heterosis is higher in cross-pollinated plants than in self-pollinated plants. These crosses are therefore the best candidates for improving new sweet potato varieties for beta-carotene content. The dry matter content showed weakly positive heterosis for certain families. The best families for both heterosis are the BfxSo and SoxTu families. These results are similar to those of Fekadu *et al.* (2018) who found positive but relatively weak heterosis for dry matter content.

Moreover, the structuring of diversity reveals that individuals in group 1, characterised by a high beta-carotene content, are potential candidates in sweet potato breeding programs for vitamin A, given that beta-carotene is converted in the human body into vitamin A. Somé (2012) estimated that vitamin A deficiency has become a major public health concern, prompting increased efforts to promote orange-fleshed sweet potatoes, which are very rich in beta-carotene. According to Beal *et al.* (2017), vitamin A deficiency causes irreversible negative consequences on cognitive ability and physical work in humans. In 2011, Sub-Saharan Africa was the main region in the world with the highest vitamin A deficiency, with nearly half of children under 5 years old affected by this deficiency (Beal *et al.*, 2017). The consumption of orange-fleshed sweet potatoes remains one of the best alternatives to address this form of malnutrition. Indeed, according to Somé *et al.* (2012), the average consumption of 125 g of orange-fleshed sweet potato would be sufficient to provide the daily intake of vitamin A recommended for children and breastfeeding women.

However, the genotypes of group 2 characterised by a high yield potential and those of group 3, which stand out from the others due to their high dry matter content (DMC>30%), can be exploited to increase the productivity and profitability of sweet potatoes. Indeed, most sweet potato varieties cultivated in sub-Saharan Africa have a low dry matter content (25 to 30%), whereas for processing, industries require a dry matter content >30% (Mourtala *et al.*, 2023).

As a result, sweet potato breeding in Sub-Saharan Africa aims to develop varieties with orange flesh, >30% dry matter content as well as a high potential for tuber root yield (Cervantes-Flores *et al.,* 2011).

REFERENCES

Alam Z, Khan Md AH, Hossain M, Karim M, Saif H, Mustakim AAMM, Molla M, Islam M, Akhter S, Akter S. 2024. Genetic variability and diversity analysis for some agronomic traits of a sweet potato (*Ipomoea batatas* L.) collection: insights for breeding superior genotypes. Heliyon **10**, e38616. https://doi.org/10.1016/j.heliyon.2024.e38616

Aliou B, Dorcus CG, Justus O, Diaga D, Thiago M, Reuben TS, Robert OMM, Mercy K. 2020a. Heterosis and combining ability for storage root, flesh color, virus disease resistance and vine weight in sweet potato [*Ipomoea batatas* (L.) Lam.]. African Journal of Agricultural Research **15**(2), 187–202. https://doi.org/10.5897/AJAR2019.14498

Aliou B, Dorcus CG, Justus O, Diaga D, Thiago M, Reuben TS, Robert OMM, Mercy K. 2020b. Heterosis and combining ability for storage root, flesh color, virus disease resistance and vine weight in sweet potato [*Ipomoea batatas* (L.) Lam.]. African Journal of Agricultural Research **15**(2), 187–202. https://doi.org/10.5897/AJAR2019.14498

Al-Mamun M, Rafii MY, Misran AB, Berahim Z, Ahmad Z, Khan MMH, Oladosu Y. 2023. Heterosis and combining ability estimate on yield and yield-related traits in a half diallel crosses of kenaf (*Hibiscus cannabinus* L.) in Malaysia. Journal of Natural Fibers **20**(1), 2192541. https://doi.org/10.1080/15440478.2023.2192541

Beal T, Massiot E, Arsenault JE, Smith MR, Hijmans RJ. 2017. Global trends in dietary micronutrient supplies and estimated prevalence of inadequate intakes. PLoS One **12**(4), e0175554. https://doi.org/10.1371/journal.pone.0175554

Burgos G, Carpio R, Sanchez C, Sosa P, Porras E, Espinoza J, Gruneberg W. 2009. Guide for using the RHS color chart for selecting for high β-carotene sweetpotatoes. ISTRC, Lima, Peru.

Cervantes-Flores JC, Sosinski B, Pecota KV, Mwanga ROM, Catignani GL, Truong VD, Watkins RH, Ulmer MR, Yencho GC. 2011. Identification of quantitative trait loci for dry-matter, starch, and β-carotene content in sweetpotato. https://hdl.handle.net/10568/67671

Chabi NKA, Tchemadon GC, Hounkpatin OL, Jimmy PK, Afouda LAC. 2024. Knowledge and management strategies of farmers to safeguard sweet potato (*Ipomoea batatas* L.) against viral diseases in Benin. Hosts and Viruses **11**, 1–8. https://doi.org/10.17582/journal.hv/2024/11.1.8

FAOSTAT. 2024. Statistics on production and international trade of food products (report).

Fekadu G, Hussein S, Laing M. 2018. Combining ability, heterosis, and heritability of storage root dry matter, beta-carotene and yield-related traits in sweetpotato. HortScience **53**(2), 167–175. https://doi.org/10.21273/HORTSCI12280-17

Grüneberg WJ, De Boeck B, Diaz F, Eyzaguirre R, Low JW, Reif JC, Campos H. 2022. Heterosis and responses to selection in orange-fleshed sweetpotato (*Ipomoea batatas* L.) improved using reciprocal recurrent selection. Frontiers in Plant Science **13**, 793904. https://doi.org/10.3389/fpls.2022.793904

Guinko S. 1984. Végétation de la Haute Volta. Thèse de doctorat, sciences naturelles. Université de Bordeaux III.

Human C, Laurie SM, van Heerden SM. 1999. Use of colour charts for the estimation of beta-carotene content in sweet potato (*Ipomoea batatas* (L.) Lam). ARC-Roodeplaat Vegetable and Ornamental Plant Institute, Pretoria, South Africa.

INERA/CREAF. 2024. Données pluviométriques. Institut de l'Environnement et de Recherches Agricoles, Ouagadougou (rapport).

Jiang Y, Schmidt RH, Zhao Y, Reif JC. 2017. A quantitative genetic framework highlights the role of epistatic effects for grain-yield heterosis in bread wheat. Nature Genetics **49**(12), 1741–1746. https://doi.org/10.1038/ng.3974

Kankam F, Abayateye V, Akpatsu IB. 2022. Preliminary study on evaluation of sweet potato genotypes for resistance to sweet potato virus disease (SPVD). Ghana Journal of Science, Technology and Development **8**(2), 33–43. https://doi.org/10.47881/373.967x

Koussoube S, Traore F, Some K, Dabire-Binso C, Sanon A. 2018. Perception paysanne des principales contraintes et pratiques culturales en production de patate douce au Burkina Faso. Journal of Applied Biosciences **126**, 1–10. https://doi.org/10.4314/jab.v126i1.2

Lebot V. 2008. Tropical root and tuber crops: cassava, sweet potato, yams, aroids. Tropical Root and Tuber Crops **1**, 1–413.

Liu J, Li M, Zhang Q, Wei X, Huang X. 2020. Exploring the molecular basis of heterosis for plant breeding. Journal of Integrative Plant Biology **62**(3), 287–298. https://doi.org/10.1111/jipb.12804

Mackay I, Horwell A, Garner J, White J, McKee J, Philpott H. 2011. Reanalyses of the historical series of UK variety trials to quantify the contributions of genetic and environmental factors to trends and variability in yield over time. Theoretical and Applied Genetics **122**(1), 225–238. https://doi.org/10.1007/s00122-010-1438-y

Mourtala IZ, Innocent N, Habibou M, Oselebe H. 2023. Recent progress in breeding for beta-carotene, dry matter content and sugar in sweet potato [*Ipomoea batatas* (L.) Lam]: A review. European Journal of Agriculture and Food Sciences **5**(1), 6–13. https://doi.org/10.24018/ejfood.2023.5.1.551

Mugisa I, Karungi J, Musana P, Odama R, Alajo A, Chelangat DM, Anyanga MO, Oloka BM, Gonçalves dos Santos I, Talwana H, Ochwo-Ssemakula M, Edema R, Gibson P, Ssali R, Campos H, Olukolu BA, da Silva Pereira G, Yencho C, Yada B. 2022. Combining ability and heritability analysis of sweetpotato weevil resistance, root yield, and dry matter content in sweetpotato. Frontiers in Plant Science **13**, 956936. https://doi.org/10.3389/fpls.2022.956936

Nguyen HC, Chen CC, Lin KH, Chao PY, Lin HH, Huang MY. 2021. Bioactive compounds, antioxidants, and health benefits of sweet potato leaves. Molecules **26**(7), 1820.

Nikièma J. 2016. Exploitation of heterosis in sweetpotato (*Ipomoea batatas* L. (Lam)) via progeny testing and use of molecular markers. Master's thesis, Kwame Nkrumah University of Science and Technology.

Padmaja G. 2012. Food uses and nutritional benefits of sweet potato. Fruit, Vegetable and Cereal Science and Biotechnology **1**, 115–123.

Somé K. 2012. Genetic improvement of sweetpotato (*Ipomoea batatas* [L.] Lam) for beta-carotene and yield in Burkina Faso. Thesis, West Africa Centre for Crop Improvement, University of Ghana.