



Assessment for Parental Traits in Progeny Development among Segregating Population of Sweetpotato Breeding Lines

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Abstract

Progeny development depends on the selection of parents with desirable characteristics which could be genetically incorporated to their future progenies. On this premise, experiment was conducted at the Western experimental field of National Root Crops Research Institute, Umudike, Umuahia Abia State during the 2020 and 2021 cropping season in the rainforest agro-ecology of South-East Nigeria. The objective were to select high yielding and dry matter content breeding lines as parents for progeny development, select breeding lines as parents that are resistant to pathological stresses and select as parents breeding lines with high number of botanical seeds to increase genetic diversity of sweetpotato. Twenty-five breeding lines at AYT (Advance Yield Trial stage) were used. Planting was on the crest of the ridges 0.3m within row and 1.0m between rows in a plot size measuring 3m x 3m and replicated three times in a randomized block design. The breeding lines were subjected to diaelle crossing and all seeds collected from each of the plots were packed in a well labeled envelope. Data collected were on: total number of capsules, total number of seeds, total number of storage roots, and fresh weight of total storage roots, all harvested per plot and percentage dry matter content. Data was also collected on pathological stresses and scored on severity scale of 1 to 9. Data collected were subjected to Analysis of Variance and means were separated using Standard error of difference (S.E.D). Results obtained indicated that the breeding lines selected as parents were resistant/ tolerant to pathological stresses. The high number and weight of storage roots of selected breeding lines agreed with the need for the assessment of breeding lines for selection as parents for breeding programmes. The study identified the following breeding lines for selection as parents: NRSP/UYT/20/22, PO3/36, NRSP/2014/066, NRSP3/017, ERICA, NWA/OP/266, Tio-Joe, NRSP/11 and Smiles. Their performance on the traits evaluated was higher than the check variety and was selected to be valuable source of new parents. They have relatively high dry matter content making them acceptable for use in progeny development.

Keywords: Selection as parents, progeny development, capsules, seeds, sweetpotato and breeding programme

Introduction

Sweetpotato [*Ipomoea batatas* (L) Lam] is an important crop in many parts of the world. Woolfe (1992) reported that it is cultivated in 116 countries. Globally, the crop ranked third among roots and tuber crops after potato and cassava. According to FAOSTAT (2004), the production figure for the crop was about 122 million metric tons, potato 281 million metric tons and cassava 164 million metric tons. China rank first as the world's largest producer of sweetpotato, followed by Uganda and Nigeria (FAOSTAT, 2004). Ajiboye *et al.* (2008) noted that in Nigeria sweetpotato is one of the four major root and tuber crops after cassava, yam and cocoyam. Sweetpotato is widely adapted in all the agro-eco-zones of Nigeria. The crop's input requirements is minimal and has shorter growing period of 3 to 5 months when compared with other roots and tuber crops. According to

Caetano *et al.* (2017), the crop has high root yield per unit area especially when cultivated under fertile soil environment compared with other root crops. Sweetpotato produces more edible energy, protein and dry matter per hectare basis than any other crop (Gasura *et al.*, 2008). It contains vitamins and particularly vitamin A and minerals compared to many fruits (Aritua *et al.*, 1993).

The storage roots could be consumed fresh or processed and the vegetation use as fodder for animals. The crop has potential for use as major source of raw material for industrial purposes (Woolfe, 1992). FAOSTAT (2021) indicated that the yield of sweetpotato has increased from 260,000 to 2.2million metric tons in Nigeria under a period of 15 years. However, yields are still low in farmers' field (6t/ha) compared to yields from research

stations (Gruneberg *et al.*, 2005). The yield potential of sweetpotato may further be increased through breeding and introduction of appropriate technologies that will enhance yield performance. Breeding objectives focus on developing improved sweetpotato varieties with desirable characteristics such as high yielding varieties resistant to pests and diseases. Development of varieties with acceptable culinary and industrial attributes requires the use of parents with proven characteristics. The traits coupled with improved agronomic techniques will help address the constraints of sweetpotato production in the country. Such constraints include: lack/poor quality planting materials, poorly maintained and low soil nutrients, exposure of sweetpotato varieties to pests and diseases leading to susceptibility of crops to biotic stresses. All these obstacles in sweetpotato production need the selection of parents with the desirable characteristics genetically combined and transfer the traits to their progenies. Breeding assists to increase the genetic base of sweetpotato through evaluation and selection for desirable traits for End Users.

The development of new genotypes involve setting breeding objectives, generating the required genetic diversity through hybridization, recombining the first generations, followed by various forms of selection in subsequent generations to increase the frequency desired characteristics and to fix these, leading to a new variety that is reasonably uniform and stable. Sweetpotato improvement programmes have been even less successful for the extreme arid and high altitude areas of the country partly because of the allocation of limited research resources by national and international programmes and partly due to a failure to use well adapted material as parents for sweetpotato improvement for varied End-Users. Nigeria has many genetically diverse, sweetpotato landraces but little use has been made of them in the national breeding programmes. Concerted efforts should be considered for the use of alternative approaches to address the problems of the limited sweet potato varietal choice available to farmers. Traditionally, the development of sweet potato varieties has been the task of breeders, and farmers are merely the recipients of finished products.

To develop better adapted varieties for the marginal complex environments and, in some cases, for highly productive environments, plant breeders have become increasingly aware that their initial primary concern with yields was not always sufficient to guarantee broad adoption by farmers. It has become apparent that breeding objectives need to incorporate other criteria, such as local consumption preferences. This has led to farmer-participatory evaluation aimed at establishing what additional characteristics were required, such as taste, colour/appearance and other household requirements, e.g. ease of cooking and of storage. There are traits lacking in sweetpotato landraces that limited their use as parents that could be found in the recombined breeding lines that should be harnessed for next generation of sweetpotato improvement. The

principal objective of the sweetpotato breeding programmes was to generate botanical seeds through which variation in sweetpotato plants could be developed, and this will act as raw material for selection (Akoroda, 2008). Seedlings could then be evaluated to select genotypes that merited utility traits for various end-users. Therefore the objectives of this study were: to select high yielding and dry matter content breeding lines as parents for progeny development, to select as parents breeding lines that are resistant to pathological stresses and to select as parents breeding lines with high number of botanical seeds to increase genetic diversity of sweetpotato.

Materials and Methods

Germplasm

The breeding lines were developed by the pedigree breeding method. One hundred and fifty (150) to 200 lines derived from each population were crossed to the corresponding base population as the Advance yield trial. The high yield performance of the lines per se, their combining abilities for storage root yield, pests and disease rating scale and other desirable agronomic characters across the two locations were used as criteria for selecting 25 breeding lines, which were advanced to Advanced yield trial. These genotypes were selected to evaluate them for desirable parental characteristics and to use them for future progeny development.

Evaluation

The experiments was conducted at the Western experimental field of National Root Crops Research Institute, Umudike, Abia State during the 2020 and 2021 cropping season in the rainforest agro-ecology of Southeastern Nigeria. The site for the experiment was slashed, ploughed, harrowed and ridged. The area was then divided into plots and the plots were grouped into blocks. The trial was arranged in a randomized complete block design with three replications. Each of the 25 breeding lines at AYT (Advance Yield Trial stage) were planted manually on the crest of the ridges 0.3m within row and 1.0m between rows in a plot size measuring 3m x 3m which gave a total of 75 plots. Two months after planting, the plots were staked to enhance the flowering, ease of pollination, reduce soil borne diseases and ease in dry capsule collection from the plants. The plots were kept weed free throughout the trial. The breeding lines were subjected to diallel crossing and all seeds collected from each of the breeding lines were packed in a well labeled envelope. No fertilizer was applied to prevent the crop from growing too luxuriantly and delay flowering.

Collection of Agronomic Data

The following data were collected: total number of capsules harvested per plot, total number of seeds harvested per plot, total number of storage roots, and fresh weight of total storage roots all collected per plot. Data were also collected on pathological stresses and scored on severity scale of 1 to 9 (Toker *et al.*, 1999). Where: 1 = Immune, 2 = Highly Resistant, 3 = Resistant, 4 = Moderately Resistant, 5 = Tolerant, 6 = moderately

susceptible, 7 = Susceptible, 8 = highly susceptible, 9 = highly susceptible. Data on dry matter content were realized by oven drying of sliced two hundred grammes of fresh roots for 48 hours in an oven until a constant weight is obtained. The weight was then calculated as follows: The percentage loss in weight was expressed as percentage moisture content on dry weight basis. This was repeated three times to obtain triplicate values.

Statistical Analysis

Analyses of variance for each year and combined across the years were performed for total number of capsules harvested per plot, total number of seeds harvested per plot, and total number of storage roots harvested per plot. Data collected were subjected to Analysis of Variance and means were separated using Standard error of difference (S.E.D) with PROC GLM in SAS (SAS Institute, 2001).

Results and Discussion

Results

The result of the total number of storage roots, total weight of storage roots, percentage dry matter content, total number of capsules, total number of seeds generated and pathological reactions of the breeding lines evaluated in 2020 cropping season are presented in Table 1.

Total number, weight of storage roots and Percentage dry matter content

Total number of storage roots varied greatly from 7.0 (NWAOP/227) to 41.0 roots (Smiles) per plot with mean of 21.3 number of roots per plot. This gave 31.3% coefficient of variation. High degree of variation was an indication of possibility for selection of parents from the breeding lines. High number of storage roots per plot is a function of yield. Parent genotypes with high number of storage roots could transfer such desirable trait to their progenies. Also high number of storage roots leads to heavy weight of fresh matter accumulation. The result in Table 1 showed that total weight of storage roots ranged from 2.5t/ha (Erica) to as heavy as 16.1t/ha (Smiles) with mean of 8.2t/ha and coefficient of variation of 41.2% which was an indication of high variation in total storage root weight. The percentage dry matter content of the storage roots of the breeding lines ranged from 28.2 to 33.2% with a mean of 30.5%. This showed that the breeding lines have high percentage of dry matter content. High matter content is a good trait that should be incorporated into future progenies (Table 1).

Total number of capsules and seeds

The result in Table 1 showed that the total number of capsules with seeds harvested from the sweetpotato genotypes varied greatly from 109 to 733 capsules with mean of 328.8 capsules. The coefficient of variation of 34.2% indicated that capsule production varied greatly among the breeding lines. The genotype that gave the highest number of capsules was Tio-Joe with total number of harvested capsules numbering 733 followed by NWA/OP/266 with total of 634 harvested capsules

while the least number of harvested capsules was obtained from the genotype (NRSPO/50) which gave a total of 109 harvested capsules. Capsules obtained from all the breeding lines indicated that all the genotypes flowered to produce seeds.

However, total number of botanical seeds collected was 9196 with mean of 459.8 seeds. This varied greatly from 76 seeds as produced by NWA/OP/227 to as high as 1107 as was produced by Tio-Joe with coefficient of variation of 38.2% which indicated a high degree of variation. The breeding lines that produced more number of seeds during the 2020 cropping season included the following: NWA/OP/226 (968 seeds), Tio-Joe (1107 seeds), SPO/3/11(1032 seeds), NWA/OP/231 (852 seeds), Smiles (972 seeds), UMUSPO/3 (653 seeds) and NWA/OP/598 (598 seeds).

Pathological Reactions

The pathological reactions of the genotypes indicated that the genotypes had a mean severity score of 1.0 for sweetpotato virus disease (SPVD, *alternaria* and nematode infestation. Although the SPVD did occur in the field the check varieties UMUSPO/3 had SPVD severity score of 3.3.

The results of the total number of storage roots, total weight of storage roots, percentage dry matter content, total number of capsules, total number of seeds generated and pathological reactions of the breeding lines evaluated in 2021 cropping season are presented in Table 2.

Total number, weight of storage roots and dry matter content of the breeding lines

The number of storage roots produced by the sweetpotato genotypes ranged from 7.0 for NRSP3/31 to as high as 38.3 for NWA/OP/227 with mean of 26.3. This was followed by NRSP/UY/20/44 and ERICA with mean storage roots of 36.0 respectively. The coefficient of variation of 38.9% indicated high degree of variation in the number of storage roots among the sweetpotato breeding lines. Number of storage roots is a function of yield. However, the weight of the storage roots ranged from 8.0 (NWA/OP/227) to 15.1t/ha (NRSPO/50). This was followed by Tio-Joe with mean yield of 14.4t/ha with grand mean weight of 12.3t/ha. This yield varied widely with coefficient of 31.6%. The dry matter yield of the breeding lines ranged from 28.1 to 32.1% with grand mean of 30.4% similar to what was obtained in 2020.

Total number of capsules and Seeds

The total number of capsules and seeds produced by the breeding lines in 2021 was 8057. This ranged from 109 (87/OP/132) to as high as 723 (NRSP/UY/20/32). This was followed by NWA/OP/231 with capsule yield of 604.0 with grand mean of 322.3. The coefficient of 44.2% showed that there was wide variation in capsule yield among the sweetpotato breeding lines. High number of capsules indicated that many of the sweetpotato breeding lines flowered and could be

selected as parents for progeny development. Also the total seed yield of the breeding lines in 2021 was 10358 seeds with mean of 414.3 seeds. This varied from 102 (NRSP/UY/20/99) to 1107 (PO3/36). This was followed by NRSP/2014/066 with total number of seeds of 1032. The high number of seeds is an indication of number for progeny diversity (Table 2).

Pathological reactions: The result of pathological reactions of the breeding lines indicated that the genotypes had mean severity score of 1.2 for sweetpotato virus disease (SPVD), 1.1 for sweetpotato leaf spot/ *alternaria* and 1.0 nematode infestation. This was an indication that the breeding lines were resistant/immune to biological stresses, and good characteristics for genotypes to be selected as parents. However, the SPVD did occur in the field. This was observed on one of the check varieties (UMUSPO/3) which had SPVD severity score of 3.0.

The result of the combined analysis for total number of storage roots, total weight of storage roots, percentage dry matter content, total number of capsules, total number of seeds generated and pathological reactions of the breeding lines evaluated in 2020 and 2021 cropping seasons are presented in Table 3.

Total number of storage roots, weight of storage roots and dry matter content

The result of the combined analysis in Table 3 indicated that the number of storage roots among the sweetpotato breeding lines had high degree of coefficient of variation of 38.9%. This showed that the genotypes differed greatly in the number of storage roots produced. This ranged from 8.0 for NRSP3/31 to 78.5 as produced by NRSP/UYT/20/44 followed by Smiles with 365 roots with grand mean number of 25.9 roots. Also the combined result for the two years showed that the weight of storage roots ranged from 7.3 produced by NRSP03/82 to as heavy as 17.2t/ha as produced by NRSP/UYT/20/44 followed by 14.2t/ha produced by Smiles with grand mean of 11.0t/ha. This high degree of variation of the weight of the storage roots was indicated by the wide degree of the coefficient of variation of 31.6%. High number and heavy weight of fresh storage roots are good characteristics for selecting genotypes that will be good parents for progeny development. The fresh tuber yield of the breeding lines gave storage root dry matter content that ranged from 28.2 to 33.1% with grand mean of 30.5%. This was a good parental trait for progeny development.

Total number of capsules and seeds produced

The result in Table 3 showed the total number of capsules produced was 8223.1. This gave coefficient of variation of 44.2%. This varied from 129.0 for NRSP0/50 to 682.5 (for NRSPUYT /20/32 with mean of 328.9. This was followed by Tio- Joe with 536.0. Also total number of seeds produced was 10,214.3 with mean of 408.6. The coefficient of variation was 35.2%. The number of seeds produced ranged from 141.5 (NRSP0/50) to 852.5 (Tio-Joe). Tio-Joe was followed by Smiles with 709.5. High number of capsules leads to

high number of seeds.

Pathological reactions: The pathological reactions of the breeding lines for the two seasons with the score rate of 1.2 for SPVD, 1.1 for leaf spot and 1.0 for nematode showed that they possess good pathological trait that could be conferred to their progeny if selected as parents.

Discussion

The high number of storage roots produced by the breeding lines in the two seasons which was 8.0 to 78.5 with mean of 25.9 was an indication that this trait could be genetically transferred to their progenies if selected as parents for crosses by the breeding programmes. The wide coefficient of variation of 38.9% indicated wide possibility of selecting good number of breeding lines as parents for the breeding programme. However, breeding lines that produced more number of storage roots above the check varieties should be selected as parents. According to Nwankwo *et al* (2018), number of storage roots is a function of yield. It is the number of roots that gives the farmer(s) the impression of a high yielding variety or varieties. Also the weight of the fresh matter accumulation of the storage roots indicated that those breeding lines with heavy weight higher than the check variety of 11.0t/ha should be selected as parents for breeding programme. Afuape (2014) reported that important traits such as root yield should be selected for consumer targeted breeding for enhanced sweetpotato commercial product development. The high degree of coefficient of variation of 31.6% was an indication of possible selection of parents that will confer their genetic fresh tuber yield potential to their progenies. The dry matter content of these breeding lines was above 28.0% indicating that they would possess acceptable taste, as good sweetpotato taste is associated with high dry matter content (Ndolo *et al.*, 2010). Parents with high dry matter content could incorporate it through gene transfer to their progenies.

The mean total number of capsule of 8223.1 for the two years showed that greater number of the genotypes flowered and would be used as parents in breeding programmes. The high coefficient of variation of 44.2% indicated that large number of the breeding lines could be used for crosses. The total number of seeds collected was 10,214.3. High number of capsules results into high number of seed yield. Not all pollinated capsules produce the same quantity of seeds. From the results obtained, genotypes that produce high number of capsules produced high number of seeds. High number of seeds and capsules is an indication of high compatibility of the parents with other genotypes in the same crossing block. Capsules contained the botanical seeds carrying genes for variation, the higher the number of seeds, the higher the genetic diversity. One seed is a potential variety. Breeding programme is the mainstay of crop development and substantially contributing to crop improvement using quality seeds that carry genetic material from parents with good characteristics. Therefore genotypes with number of

seeds above the grand mean were selected for use as parents in the hybridization block. Capsules contain botanical seed for the development of sweetpotato progenies which will give rise to new sweetpotato genotypes which individually possess different characteristics desired by various end-users. For the fact that most of the new genotypes flowered; is an indication that they are out crossing, and could be used as parents for sweetpotato hybridization block.

Crop improvement depends partly to improving parents for progeny development, so the availability and use of improved varieties and seeds play an important role in technological development and the seed system in the agricultural sector. Most of the breeding lines presented relative resistant/immune to the pathological stresses. However, the check variety (with SPVD severity rate of 3.4) was severely infected which indicated that infection did occur during the field trial, and that some of the high yielding breeding lines for selection as parents may be resistant to the pathological stresses.

Conclusion

The study suggested that some of the breeding lines for selection as parents were resistant/tolerant to pathological stresses. The high yields of number and weight of storage roots of most breeding lines agreed with the need for the assessment of breeding lines for parents for breeding programme. The study identified the following breeding lines for selection as parents for breeding programmes: NRSP/UYT/20/22, PO3/36, NRSP/2014/066, NRSP3/017, ERICA, NWA/OP/266, Tio-Joe, NRSP/11 and Smiles. Their performance in the traits evaluated was higher than the check variety and was selected to be valuable source of new parents. They have relatively high dry matter content making them acceptable for use in progeny development.

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Table 1: Total number of storage roots, total weight of storage roots, percentage dry matter content, total number of capsules, total number of seeds generated and pathological reactions of the breeding lines used as parents in 2020 cropping season

Name of Variety	Total number of storage root	Total weight of storage root	% Dry matter content	Total Number of capsules harvested	Number of seeds collected	SPVD	Leaf Spot	Nematode
NRSP/UY/20/44	27.8	21.0	29.8	228	167	1.3	1.0	1.0
NRSP/UY/20/32	28.2	14.4	30.0	321	153	1.0	1.3	1.0
UTY/20/017	32.0	10.2	30.3	149.0	147	1.0	1.3	1.3
NRSP/UY/221	16.5	13.3	31.4	241	202	1.0	1.1	1.0
NRSP/UY/20/22	38.3	13.7	30.8	320	168	1.0	1.3	1.0
NRSP/UY/20/99	31.0	14.4	33.0	221	187	1.0	1.2	1.0
PO3/36	36.0	13.3	29.8	242.0	184	1.0	1.2	1.2
NRSP/2014/066	38.0	12.5	31.3	244.0	432	1.0	1.0	1.0
87/OP/132	29.0	14.1	33.2	339.0	378	1.4	1.0	1.0
NWA/OP/227	15.0	9.4	28.4	138.0	76	1.1	1.0	1.0
NRSP3/017	19.0	11.2	30.2	366.0	432	1.3	1.0	1.0
ERICA	7.0	2.5	30.3	233.0	166	1.2	1.0	1.0
NWA/OP/226	17.0	9.7	30.4	634.0	968	1.0	1.2	1.2
NRSP3/187	13.0	6.3	32.1	444.0	102	1.0	1.1	1.1
TIO-JOE	15.0	4.0	30.2	733.0	1107	1.0	1.0	1.0
NRSP3/11	14.0	5.0	30.1	454.0	1032	1.0	1.0	1.0
NRSP3/31	9.0	3.0	30.2	174.0	219	1.0	1.0	1.0
NRSP3/119	11.0	2.6	34.1	345.0	290	1.4	1.1	1.1
NWA/OP/231	34.0	13.1	30.3	426.0	852	1.1	1.1	1.1
SMILES	41.0	16.1	30.2	535.0	972	1.0	1.0	1.0
NRSP03/47	12.0	4.2	33.2	244.0	332	1.2	1.2	1.2
NRSP0/50	14.0	6.7	28.2	109.0	118	1.0	1.0	1.0
NWA/OP/241	23.0	9.4	29.1	229.0	598	1.0	1.0	1.0
NRSP03/82	13.0	5.3	28.3	219.0	138	1.0	1.0	1.0
UMUSPO/3	14.0	4.8	28.2	319.0	653	3.0	1.0	1.0
(chk)								
Total	426.0	163.4	763.1	6576	9196	29.0	27.1	26.2
Mean	21.3	8.2	30.5	328.8	459.8	1.2	1.1	1.0
SE	4.2	2.6	5.6	16.6	19.6	=	=	=
Range	7-41	2.5-16.1	28.2-33.2	109-733	76-1107	1-3	1-1.2	1-1.2
CV%	31.3	41.2	=	34.2	38.2	=	=	=

Table 2: Total number of storage roots, total weight of storage roots, percentage dry matter content, total number of capsules, total number of seeds generated and pathological reactions of the breeding lines used as parents in 2021 cropping season

Variety	Total number of storage root	Total weight of storage root	Dry matter content	Total Number of capsules harvested	Number of seeds collected	SPVD	Leaf Spot	Nematode
NRSP/UY/20/44	36.0	13.3	30.8	404.0	378	1.3	1.0	1.0
NRSP/UY/20/32	38.0	12.5	31.0	723.0	176	1.0	1.3	1.0
UTY/20/017	29.0	14.1	32.3	454.0	332	1.0	1.3	1.3
NRSP/UY/221	25.0	9.4	30.4	174.0	266	1.0	1.1	1.0
NRSP/UY/20/22	19.0	11.2	30.7	345.0	967	1.0	1.3	1.0
NRSP/UY/20/99	27.8	12.5	32.0	426.0	102	1.0	1.2	1.0
PO3/36	28.2	10.7	28.8	535.0	1107	1.0	1.2	1.2
NRSP/2014/066	32.0	9.3	30.3	244.0	1032	1.0	1.0	1.0
87/OP/132	16.5	14.0	32.2	109.0	219	1.4	1.0	1.0
NWA/OP/227	38.3	8.0	29.4	229.0	290	1.1	1.0	1.0
NRSP3/017	31.0	13.0	31.2	219.0	852	1.3	1.0	1.0
ERICA	36.0	12.6	29.5	319.0	972	1.2	1.0	1.0
NWA/OP/226	38.0	13.1	30.0	242.0	332	1.0	1.2	1.2
NRSP3/187	29.0	21.0	32.1	244.0	218	1.0	1.1	1.1
TIO-JOE	15.0	14.4	30.0	339.0	598	1.0	1.0	1.0
NRSP3/11	19.0	10.2	30.1	168.0	138	1.0	1.0	1.0
NRSP3/31	7.0	13.3	31.2	366.0	653	1.0	1.0	1.0
NRSP3/119	17.0	13.7	32.1	233.0	187	1.4	1.1	1.1
NWA/OP/231	33.0	14.4	31.3	604.0	131	1.1	1.1	1.1
SMILES	35.0	12.3	31.2	528	447	1.0	1.0	1.0
NRSP3/47	17.0	13.5	30.2	321	212	1.2	1.2	1.2
NRSP3/50	33.0	15.1	28.2	149.0	168	1.0	1.0	1.0
NWA/OP/241	15.0	9.4	28.1	241	188	1.0	1.0	1.0
NRSP3/82	24.0	9.2	29.3	320	180	1.0	1.0	1.0
UMUSPO/3 (chk)	19.0	8.5	28.4	221	213	3.0	1.0	1.0
Total	647.8	308.7	760.8	8057	10358	29.0	27.1	26.1
Mean	26.3	12.3	30.4	322.3	414.3	1.2	1.1	1.0
SE	5.09	3.5	5.6	17.7	20.5	=	=	=
Range	7.0-38.3	8.0-15.1	28.1-32.1	109.0-723	102-1107	1.0-3	1.0-1.3	1.0-1.2
CV%	38.9	31.6	=	44.2	35.2	=	=	=

Table 3: Total number of storage roots, total weight of storage roots, percentage dry matter content, total number of capsules, total number of seeds generated and pathological reactions of the breeding lines used as parents in 2020 and 2021 cropping season combined

Name of Variety	mean number of storage root	mean weight of storage root	Dry matter content	mean Number of capsules harvested	mean Number of seeds collected	mean SPVD score	mean Leaf Spot score	mean Nematode score
NRSP/UY/20/44	78.5	17.2	30.3	311.6	272.5	1.0	1.0	1.0
NRSP/UY/20/32	33.1	13.5	30.5	682.5	164.5	1.0	1.3	1.2
UTY/20/017	30.5	12.2	31.3	301.5	239.5	1.0	1.3	1.3
NRSP/UY/221	20.6	11.4	30.9	207.5	234.0	1.0	1.1	1.0
NRSP/UY/20/22	28.7	12.5	30.8	332.5	567.5	1.0	1.0	1.0
NRSP/UY/20/99	29.4	13.5	32.5	323.5	144.5	1.0	1.2	1.0
PO3/36	32.1	12.0	29.3	388.5	645.5	1.0	1.2	1.2
NRSP/2014/066	35.0	10.9	30.8	244.0	732.0	1.0	1.0	1.0
87/OP/132	22.8	14.1	32.8	224.0	298.8	1.4	1.0	1.0
NWA/OP/227	26.7	8.5	28.9	218.5	183.0	1.1	1.3	1.0
NRSP3/017	25.0	12.1	30.7	292.5	642.0	1.0	1.0	1.0
ERICA	21.5	7.6	29.9	276.0	569.0	1.2	1.0	1.0
NWA/OP/226	27.5	11.4	30.2	438.0	650.0	1.0	1.2	1.0
NRSP3/187	21.0	13.7	32.5	344.0	160.0	1.3	1.1	1.1
TIO-JOE	15.0	9.2	30.1	536.0	852.5	1.0	1.0	1.0
NRSP3/11	16.5	7.6	30.5	296.0	585.0	1.0	1.0	1.0
NRSP3/31	8.0	8.2	30.7	270.0	436.0	1.0	1.0	1.0
NRSP3/119	14.0	7.9	33.1	289.0	238.5	1.0	1.1	1.1
NWA/OP/231	33.5	13.8	30.8	530.0	491.5	1.1	1.1	1.1
SMILES	36.5	14.2	30.7	531.5	709.5	1.0	1.0	1.0
NRSP03/47	14.5	8.9	31.7	282.5	272.0	1.2	1.0	1.2
NRSP0/50	23.5	10.9	28.2	129.0	141.5	1.0	1.0	1.0
NWA/OP/241	19.0	9.4	28.6	235.0	393.0	1.3	1.2	1.0
NRSP03/82	18.5	7.3	28.8	269.5	159.0	1.0	1.0	1.0
UMUSPO/3	16.5	6.7	28.3	270.0	433.0	3.4	1.0	1.0
(chk)								
Total	647.5	274.7	762.9	8223.1	10214.3	29.0	27.1	26.1
Mean	25.9	11.0	30.5	328.9	408.6	1.2	1.1	1.0
SE	5.2	3.3	5.6	18.5	20.6	=	=	=
Range	8.0-78.5	7.3-17.2	28.2-33.1	129.0-682.5	141.5-852.5	1-3	1-1.3	1-1.2
CV%	38.9	31.6	=	44.2	35.2	=	=	=