**Leveraging phenotypic diversity in a worldwide panel from the Korean genebank to identify new core resources for multi-purposes sesame breeding**

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**Abstract**

Accurate knowledge of phenotypic diversity in a germplasm is a paramount for effective genomic-assisted breeding. A worldwide sesame panel was screened for both agronomic and nutritional characters as part of the South Korean sesame genomic-assisted program. The aim is to identify valuable materials to boot sesame breeding program. Taking advantage of a 506 worldwide accessions, a phenotyping was carried out at Jeonju and Miryang research stations during the cropping season 2018. A significant natural variation of agronomic traits was highlighted for some major traits including plant height, productive axis, length, seed color, number of locules per capsule, and dried seed weight. Following a multivariate analysis, a set of 32 accessions were identified as candidates for yield improvement. Moreover, a core collection composed of 102 accessions was developed, offering a starting point material for genome-wide association studies. From the core collection, protein, oil, sesamolin, sesamin, and fatty acid content were determined for 72 accessions due to the seeds quantity limitation. The accessions T218, T077, T419, T148, TN03, and T414 were pinpointed for lignans, oil content, and fatty acid-oriented sesame breeding. Interestingly, highly leafy-type accessions were also identified, representing a valuable resource for nutraceutical values of sesame leaf investigation.

**Introduction**

Over the last few years, global hunger has begun a rising challenge in the world due to the increasing population growth. By 2050, the global population is expected to exceed 9 billion, increasing the food demand about 70%1. When coupled with the current adverse effects of climate change, the Zero Hunger objective of the Food and Agricultural Organization (FAO) is seriously jeopardized with the addition of more than 80 million of undernourished people in the recent COVID-19 pandemic context2. The projections of the climate change variability on agricultural sector threaten the attainment of the food security and poverty reduction ambitions in developing countries3,4. Therefore, there is an urgent need to develop and deploy crops that combine high yield, nutritional values and strong ability to grow in harsh environments. Besides, crops that can improve the human health through the mitigation of diseases are getting more importance5. The example of the barley cultivar BARLEYTM revealed the presence of resistant starch metabolite that has positive effects on the alleviation of the type-2 diabetes and coronary heart diseases6.

Considered as an orphan crop7, sesame (*Sesamum indicum*) is a nutritional food8 and an excellent source of lignans9 that showed a wide range of benefits for human health including lowering blood cholesterol and glucose, cardiovascular disease prevention10, tumor growth suppression11, anti-carcinogenic properties12 and metabolic syndrome alleviation13. Lignans become marketable compounds with a high economical value estimated to $351.6 million dollars in 2019. The lignans market might approximate more than $500 million dollars by 2027 ([Link 1](https://www.grandviewresearch.com/industry-analysis/lignans-market)). This interest for lignans is noticeable with a growing number of patents in healthy food additives as well as skin care sectors14–17.

Genebank is a reservoir of genetic diversity allowing the identification of promising sources for crop improvement18. South Korea has the second largest sesame genebank in the world with 7,853 accessions ([Link 2](http://genebank.rda.go.kr/plantMain.do)). At the early stage of the Korean genomic-assisted sesame breeding program, the selection of valuable high-quality nutritional and health-beneficial materials is a crucial prerequisite.

From the Korean genbank, sesame core collection development using 2,751 worldwide accessions, was previously performed by including only one African country19. As broad geographic coverage is, genetic resources origin can provide a heuristic view for detection of novel desirable traits. Therefore, we enlarge geographic basis of genotypes covering 35 countries throughout the world by reaching 22 African countries (**Supplementary Table S1**). Despite the characterization of some African accessions from the Chinese genebank20 for lipid content, the two major lignans *viz* sesamin and sesamolin assessment have been neglected.

The present study aimed to i) assess the variability of agronomic traits in a worldwide sesame panel, ii) infer a core collection, iii) screen the core collection for sesamolin, sesamin, oil, and protein contents. Ultimately, this research global goal is to provide relevant resources that can serve as starting materials for the Korean genomic-assisted selection initiative for boosting sesame yield, nutritional quality and health benefits.

**Materials and methods**

**Plant material and field experiment**

A total number of 506 accessions (**Supplementary Table S1**) provided by the Korean genebank were tested during summer season 2018 (May-September). The experiment was laid out following Federer’s augmented design21 with 8 blocks at Jeonju (35° 49’ 50.37’’N latitude, 127° 3’ 52.79’’E longitude) and Miryang (35° 29’ 29.70’’N latitude, 128° 44’ 31.98’’E longitude). The inter-row and inter-plant distances were 0.7m and 0.2m respectively. The length of a row was 1.4 m with eight plants. During the experiment, 16 quantitative and five qualitative traits (**Table 1**) were measured on 5 randomly-selected healthy plants. However, for flowering, maturity, biomass and yield data were recorded on the unit plot basis. NPK fertilization was provided by the ratio 2.9:3.1:3.2 kg per acre. The recommended cultivation practices were followed during the experiment.

**Preparation of samples for content analysis**

The harvested seeds were immediately washed with sterile water and air-dried for 3 days at room temperature, and then stored at 4 ºC prior to analysis. Due to the limitation of seed quantity, a total of 72 accessions were processed from the developed core collection (102 accessions, See **Results section**). The list of the accessions is available in the **Supplementary Table S2**.

**Oil quantification**

Oil content was determined by the Soxhlet method using a Büchi B-811 extraction system (Büchi Labortechnik AG, Flawil, Switzerland). Briefly, a 2 g pulverized seeds (60 mesh) was weighed into an extraction thimble (25 × 100 mm) covered by glass wool. The loaded thimble was then inserted into the Büchi B-811 extraction system with an addition of *n*-hexane (150 mL). The mixture was boiled at 105°C for 180 minutes followed by 30 minutes cooling step in a dessicator. The total oil content was calculated on the sesame seeds dry weight basis.

**Fatty acid, sesamin and sesamolin quantification**

*Chemicals.* Acetic acid, palmitic acid methyl ester, stearic acid methyl ester, oleic acid methyl ester, linoleic acid methyl ester, linolenic acid methyl ester, sesamin, sesamolin, and trifluoroacetic acid were purchased from Sigma Chemical Company (St. Louis, MO, USA). Analytical grade n-hexane, methanol, toluene and water were purchased from J.T. Baker (Phillipsburg, NJ, USA).

*Instruments*. High Performance Liquid Chromatography (HPLC) was performed using a Dionex Ultimate 3000 RSLC system equipped with degasser, binary pump, diode-array detector, auto-sampler (Thermo Scientific, Germering, Germany) for sesamin and sesamolin analysis. Lipid was determined using a Buchi B-811 (Büchi, Switzerland) soxhlet extraction system. Nitrogen content was determined by a rapid N exceed® (Elementar Analysensysteme GmbH, Germany). Gas Chromatography (GC) was performed using an Agilent 7890A series (Santa Clara, USA) equipped with flame ionization detector (FID) for fatty acid analysis.

*Preparation of sample and sesamin and sesamolin calibration curve.* The dried seeds of sesame were pulverised (60 mesh) for 3 min using a HR 2860 coffee grinder (Philips, Drachten, Netherlands), and each sample (1.0 g) extracted in 20 ml of 80% methanol for 24 h at room temperature in a shaking incubator.The supernatant was centrifuged at 3,000g for 3 min, and then filtered through a 0.2 μm syringe filter (Whatman Inc., Maidstone, UK) prior to HPLC analysis. For quantification, the peak areas of the isolated compounds were integrated from the HPLC chromatogram at 330 nm using Dionex software. The standard stock solutions were prepared by dissolving in methanol to obtain a 1 mg/ml concentration. Calibration curves were obtained with methanol at eight different concentrations (0, 5, 10, 20, 40, 60, 80, and 100 μg/ml). All calibration curves had coefficients of linear correlation r2 > 0.999.

*HPLC determination of sesamin and sesamolin contents.* The quantification of sesamin and sesamolin contents in the seeds of sesame accessions was carried out using Ultimate 3000 HPLC analysis. A 10μl sample of the 80% methanol extract was injected into an analytical YMC-Triart C18 column (50 mm × 2 mm, 2 μm, YMC Co., LTD, Kyoto, Japan). The mobile phase was composed of 0.1% TFA in 60% methanol. The column temperature was maintained at 25 ◦C and the flow rate was 0.3 mL/min. The detector was held at a fixed wavelength of 290 nm.

*Gas chromatography determination of fatty acid contents.* Fatty acid components were elucidated using the gas chromatography Agilent 7890A (Santa Clara, USA) machine. Before analysis, fatty acid methyl esters (FAMEs) were prepared for gas chromatographic analysis by methylation of the extracted fat using water:methanol:toluene (1:20:10, v/v). The FAMEs were extracted with 2 mL hexane and 1 ºL was injected into the gas-chromatograph, in split mode (split ratio 1:50). Fatty acid analysis was carried out on an Agilent gas chromatograph (Model 7890A GC) fitted with an automatic sampler (Model 7683B Injector) and FID detector. The conditions used were the following: HPFFAP capillary column (30 m × 0.318 mm I.D., 0.25 μm film thickness; Agilent Technologies), temperature programmed from 150 ºC for 1 min, then 150 to 230 ºC at 2.5 ºC/min, then held for 2 min. Carrier gas was nitrogen, column flow 1.0 mL/min, inlet and detector were set at 250 and 260 ºC, respectively.

**Protein content quantification**

The protein quantification was performed following Dumas combustion method in a rapid N exceed® (Elementar Analysensysteme GmbH, Germany) analyzer with 1 g sample weight. The crude protein was determined by multiplying the total nitrogen content by a factor of conversion 6.25 as described by Biancarosa et al.22

**Data analysis**

The collected data were fully analyzed with the open-source statistical software R v.4.0.223. For reproducibility purpose, the data as well as the accompanying R code are made accessible (See **Data and code availability** section).

*Data diagnosis and descriptive statistics*. Using the dlookr v.0.4.224 and pastecs25 packages, the outliers identification, data frequency distribution, Shapiro-wilk normality test and descriptive statistics were performed using *find\_outliers()*, *plot\_normality()*, *normality()*, and *stats.desc()* functions, respectively.

*Diversity index analysis*. For the qualitative traits, (branching type, capsule hairiness, flower color, inflorescence type and seed color) Shannon-Weaver26 (Eq. ) and Simpson27 (Eq. ) diversity indexes were calculated with the function *diversity()* of the package vegan28. The equations of the two indexes are:

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| --- | --- | --- |
|  |  | (1) |

and

|  |  |  |
| --- | --- | --- |
|  |  | (2) |

where n is the number (n) of observations regarding one particular qualitative traits modality i divided by the total number of observations (N)

*Variability of agronomic traits:* Considering that Africa or Asia continents are predicted to be the center of diversity candidates, we performed a one-way analysis of variance with the factor continent of origin. A generalization of Welch's method using trimmed means was employed since homoscedasticity assumption of our dataset was not satisfied. The one-way analysis of variance was run using the function *ggbetweenstats()* of the ggstatsplot v.0.7.0 package29 with the option type = "robust". For categorical variables, a Pearson Chi-square test was carried out with the function *ggpiestats()*, in order to depict the variation between Africa and Asian continents.

*Correlation among traits*. In order to assess correlation between agronomic parameters, Spearman correlation test were performed with the function *ggcorrmat()* of the package ggstatsplot v.0.7029.

*Path coefficient analysis for yield and yield relative components*. As correlation alone doesn’t automatically mean causative effect, we executed the path coefficient analysis following Dewey and Lu30, to unravel direct or indirect effect between dried seed weight and relative yield components with the function *path.analysis ()* of the package agricolae v.1.3-331.

*Classification of the accessions based on the agronomic traits*. In order to group accessions based on agronomic traits, a principal component analysis followed by hierarchical agglomerative clustering were done using the function *PCA()* and *HCPC()* of the packages FactoMineR v.2.432 and factoextra v.1.0.733 respectively. The Euclidean distance-based similarity followed by Ward classification method was employed for the clustering stage. To delineate the traits that characterize each cluster, a v test was carried out as described by Lê et al.32. Prior the principal component analysis, data were standardized using the *scale()* function of the rstats23 package. The visualization of the multivariate analysis was rendered using the function *fviz\_pca\_biplot()* of the factoextra package v.1.0.733.

*Core collection inference and quality evaluation*. The R version of Core Hunter 334 *viz* corehunter v3.2.1 was employed to determine a core collection by applying the average-entry-to-nearest-entry distance scheme based on Gower’s distance metric35. The Core Hunter phenotypic data was generated from the comma-separated values excel file format of the data using the *phenotypes()* function. Then, the core collection was inferred with the function *samplecore()*. The quality of the inferred core collection with regard to the worldwide panel was assessed with the following metrics suggested by Hu et al.36 and Kim et al.37:

* the coincidence rate of range CRR (%) (Eq.),

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| --- | --- | --- |
|  |  | (3) |

where RCi is the range of the core collection for the agronomictrait i, and RWi is the range of the worldwide panel for the trait i;

* the variable rate VR (%) (Eq. )

|  |  |  |
| --- | --- | --- |
|  |  | (4) |

where CVCi is the coefficient of variation of the core collection for the agronomictrait i, and CVWi is the coefficient of variation of the worldwide panel for the trait i;

* the variance difference percentage VDP (%) (Eq. )

|  |  |  |
| --- | --- | --- |
|  |  | (5) |

where σCi is the variance of the core collection for the agronomictrait i, and σWi is the variance of the worldwide panel for the trait i;

* the mean difference percentage MDP (%) (Eq. )

|  |  |  |
| --- | --- | --- |
|  |  | (6) |

where µCi is the variance of the core collection for the agronomictrait i, and µWi is the variance of the worldwide panel for the trait i.

Besides, the means difference significance between the core and the whole accessions sets were computed following a Student t-test (for productive axis length), Wilcoxon test (for capsule number, plant height, branch number, stem diameter, dried biomass, dried seed weight, thousand seed weight, number of days to 50% flowering, number of days to maturity, number of days between flowering and maturity, capsule length, capsule width) or generalized linear model with a poisson error distribution (for harvest index, number of capsule per leaf axil, number of locules per capsule).

*Geographical map*: The map was rendered with sf v.0.9-838, ggspatial v.1.1.539, and ggplot2 v.3.3.340 packages. The world shape file was retrieved from the University of California UC DAVIS geographic map data web repository ([Link 3](https://biogeo.ucdavis.edu/data/gadm3.6/gadm36_shp.zip)).

**Results**

**Natural traits variation in the worldwide sesame panel**

The range, mean, standard deviation, and coefficient of variation of measured traits are presented in the **Table 1**. The highest coefficient of variation was observed for dried seed weight (74.09%) followed by harvest index (72.39%), number of branches per plant (71.53%), number of capsules per plant (64.49%), and number of capsule per leaf axil (53.87%). Most of yield-related traits exhibited a wide range of variation indicating that phenotypic-based selection is appropriate for those traits.

Plant architecture including branching type is economically important trait that can affect crop productivity41. In the present panel, 61.73% highly branched (n > 10 branches), 5.12% bi-branched and only 0.2 % (the accession TN42) unbranched accessions were recorded (**Table 1**). Most of the tested accessions exhibited white flower (97.4%), followed by pink (2.76%) and purple (0.4%) flowers (**Fig. 1A-C**). The purple color was observed for the wild relative *Sesamum radiatum* (**Fig. 1A**) whereas a typical pronounced pink color was showed by the wild *Sesamum alatum* (**Fig. 1B**). A remarkable diverse (H = 1.72, D = 0.78) seed color was also noted (**Table 2**, **Fig. 1D**), with 33.72% of white seed followed by 21.49% and 9.66 % of black seeds (**Table 1**). Interestingly, we identified some accessions that present six (T418) and eight (T109 and T324) locules per capsule (**Fig. 1 E-F**).

None of the accessions showed determinate growth habit except the induced determinate mutants dt-sel and dt-45 originated from Turkish sesame breeding program42.

An investigation of the variability of the studied traits among continent of origin revealed a significant variation between African- and Asian-originated accessions for all traits (**Fig. 2-6**).

**Relationship among traits**

The coefficients of correlation matrix among agronomic traits were summarized in the **Fig. 7**. A total of 41 positive (p < 0.05) and 45 negative (p < 0.05) coefficients of correlation were highlighted. For yield aspect, the strongest positive correlation was found between dried seed weight and harvest index (r = 0.85, p < 0.001). Similarly, number of days to flowering and number of days to maturation also exhibited a high relationship (r = 0.85, p < 0.001). In term of biomass, a positive relationship was revealed between stem diameter and dried biomass (r = 0.69, p < 0.001). The similar tendency was confirmed between plant height and stem diameter (r = 0.73, p < 0.001) and plant height and dried biomass (r = 0.61, p < 0.001). Meanwhile, the highest negative relationship was detected between plant height and harvest index (r = -0.71, p < 0.001), followed by stem diameter and harvest index (r = -0.69, p < 0.001), and plant height and dried seed weight (r = -0.54, p < 0.001). Overall, biomass traits augmentation seems to have a reduction effect on yield and yield components traits.

In order to clarify the effect of the studied traits with a focus on dried seed weight, a path coefficient analysis was carried out. Details results were presented in the **Table 3**. The traits, number of capsules (0.18), productive axis length (0.14), thousand seed weight (0.02), and number of locules per capsule (0.02) exerted a positive direct effect on dried seed weight. However, number of days to flowering (-1.12), plant height (-0.09), flowering to maturity days (-0.57), branch number (-0.06), and stem diameter (-0.01) exhibited indirect effect on dried seed weight.

Altogether, both correlation and path coefficient analysis pinpointed the positive contribution of the number of capsules, number of locules per capsule, and the productive axis length for dried seed weight.

**Phenotypic-based clustering**

The principal component analysis performed on the quantitative traits revealed that 62.3% of the overall variability was retained by the first four principal components with 34.4%, 10.8%, 8.9% and 8.2% for the principal components 1, 2, 3 and 4 respectively (**Supplementary** **Fig. S1**).

The most contributing trait for the first principal component was harvest index (13.62%) (**Supplementary Fig. S2A**). This first dimension is characterized by some yield-related variables including harvest index (r = 0.87, p < 0.0001), capsule number per leaf axil (r = 0.68, p < 0.0001), and dried seed weight (r = 0.64, p < 0.0001) (**Supplementary Table S3**). The second principal component was highly correlated with the number of capsules per plant (r = 0.79, p < 0.0001) (**Supplementary Table S3**) with the highest contribution (35.87%) to the construction of the principal component 2 (**Supplementary Fig. S3B**). Therefore, the factorial plan (1 × 2) depicted high-yield variables (**Fig. 8A**).

The third principal component was strongly correlated to two phenological traits including days to flowering (r = 0.74, p < 0.0001) and days to maturation (r = 0.71, p < 0.0001) (**Supplementary Table S3**) with their relative contribution of 38.50% and 35.70% (**Supplementary Fig. S2C**), respectively. Thus, the factorial plan (1 × 3) highlighted high values of flowering and maturation days (late flowering and maturation characteristics) (**Fig. 8B**).

Productive axis length, plant height, capsule width and capsule length contributed to construction of the fourth principal component with 23.22%, 19.90%, 12.05% and 11.09% respectively (**Supplementary Fig. S2-D**). The fourth principal component is positively correlated to the productive axis length (r = 0.55, p < 0.0001), plant height (r = 0.51, p < 0.0001), capsule width (r = 0.40, p < 0.0001), and capsule length (r = 0.38, p < 0.0001) (**Supplementary Table S3**). This dimension of the principal component analysis presented sesame plant growth rate-related parameters (**Fig. 8C**).

The hierarchical classification of the accessions resulted in three clusters (**Fig. 9**). The cluster 1, 2, and 3 grouped 35.37%, 41.50%, and 23.12% of the total number of accessions, respectively. The quantitative traits that described each cluster are summarized in the **Table 4**.

The cluster 1 encompassed the accessions that exhibited high biomass and low yield. The cluster 2 is characterized by late maturing and moderately yield-performing accessions while the cluster 3 representing the elite accessions harboring high-yield attributes (**Table 4**, **Fig. 10**). Most accessions of the cluster 3 (69.23%) originated from eastern Asia (**Fig. 10**). Interestingly, African representatives (13.67% for northern Africa, 3.42% for eastern Africa, 1.71% for western Africa, 1.71 % for southern Africa) are the second largest group that exhibited high-yield performance (**Fig. 10**).

**Core collection inference**

From 506 accessions, the Core Hunter 3 program generated a core collection encompassing 102 accessions. The number of retained accessions following geographical position is presented in the **Fig. 11**. The top 3 most contributing regions were eastern Asia (n = 34), followed by the northern Africa (n = 30) and the eastern Africa (n = 10) (**Fig. 11**).

The evaluation of the core collection quality revealed a variation of the coincidence rate of range (CRR) per trait from 50% to 100% with an overall value of 78.04% (**Table 5**). The variable rate per (VR) trait was ranging from 89.65% to 116.87% with an overall VR of 100.49%. More interestingly, there was no significant difference (p > 0.05) between the core and the worldwide collection for all traits. This result was supported by the low overall mean difference (3.61%) and variance difference (14.39%) percentages (**Table 5**).

**Identification of candidate genotypes for oil, protein, fatty acid, sesamin and sesamolin contents**

Out of 102 accessions of the core collection, we were able to extracted and quantify oil, fatty acid and lignans contents for 72 accessions due to the seed quantity limitation. The oil and lignans content of the 72 accessions are presented in the **Supplementary Table S2**.

The hierarchical classification based on oil, lignans, fatty acid and the agronomic traits resulted in three clusters (**Fig. 12A**). The cluster 1 grouped the accessions that show not only high-yield attributes but also are rich in proteins and alpha linoleic acid content (**Table 6**). The cluster 2 highlighted the accessions that exhibit higher yield while the cluster 3 is characterized by oil rich accessions with higher sesamin, sesamolin, and linoleic acid contents (**Table 6**).

Based on their relative contributions to the construction of the first factorial plan, the accessions T218, T077, T419, and T148 (**Fig. 12B**) appeared as valuable candidates for lignan-oriented breeding. The accession TN03 and T415 were highlighted for oleic acid and protein contents respectively (**Fig. 12B**).

**Discussion**

The present study reports a comprehensive view of the phenotypic variability of a worldwide sesame panel from the Korean genebank and the development of a multi-purpose core collection regarding agronomic and nutritional traits.

The wide range variability observed among the accessions for the studied traits provide a scope for selection and set a path for the identification of novel genotypes with desirable traits.

The study showed that some accessions (most from western and central African continent) exhibited important leafy biomass, are taller and less productive compared to the Asian representatives. Despite sesame leaves nutritional values have been neglected (mainly due to the oilseed trait) by the scientific community43, it is widely consumed in some African countries including Benin, Togo, Niger, Burkina-Faso, Nigeria, Sudan as leafy-vegetables and employed as remedy 43.

The delay of the flowering and maturation days for these African accessions was also observed. More interestingly, certain did not enter in the maturity stage or even not flower. These observations indicate the photoperiodism sensitivity of some African accessions in our experimental environment (35° N latitude). Therefore, the photosensitivity appears as an adaptative trait for discriminating some African genotypes. Similarly, Bedigian et al.44 reported some tropical accessions that did not flower at the latitude of 40°N. Despite this phenomenon, valuable African representative performed well at 35° N Latitude with early flowering and high yield and nutritional characteristics. Most of those accessions are from eastern and northern Africa, representing acceptable resources as parental genotype for population development in the tested environment.

Wide-range seed color was also observed in the worldwide panel. As suggested by Bedigian et al.45, sesame seed color may undergo intensive selection by human so far. As a result, extensive seed color variability occurred. This observation was in line with others agronomic traits including number of locules per capsule, branching type and number of capsule per leaf axil.

For yield-oriented breeding, the knowledge about the yield components traits that has a direct or indirect impact of yield is paramount for efficient yield-related breeding. Herein, we investigated the cause and effect relationship among yield and yield-component traits. The results highlighted the number of capsules, number of locules per capsule, and the productive axis length as key traits that has a direct effect on dried seed weight. Similar studies carried out in India46, Turkey42, and China44 support the present findings. Therefore, these traits may be considered as index for parental material selection for yield improvement. Specifically, the accessions T109 and T324 that harbor eight locules per capsule constitute valuable candidates as parental genotype.

Meanwhile, we were able to define a core collection that preserve the phenotypic variability from the whole set. The core collection size is about 20% from the initial worldwide set, suggesting that the inferred core set contains the minimum of repetitiveness. Comparable core set size was previously reported for sorghum47 and safflower48 with 24% and 31% respectively. Moreover, a non-significant difference between whole and core set for all traits was noted, supporting the fact that the core set maintained the genetic diversity. It is also valuable to mention a geographical broad representativeness of the inferred core collection in contrast with the previous core collection developed by Park et al.19. These observations support the good quality of the inferred core collection for effective usage in sesame breeding through genome-wide association studies for the dissection of the genetic basis of the desirable traits.

The study presents the first investigation of lignans content from a worldwide set of sesame accessions. The lignans is known to have multiple health benefits for human45. The candidate genotypes provided by this study constitute a valuable resource regarding lignan-oriented breeding. Besides, for nutritional purposes, we also identified candidate rich-protein and lipid content accessions that can serve as parental material for population development. We also suggest as further investigation, to screen the high leafy biomass accessions for leaf nutritional content. It may be a valuable fiber dietary alternative that can help to feed people in the current context of the increasing population.

As part of the Korean genomic-assisted sesame breeding, these initial results pave the way for the identification of genomic regions responsible of the expression of the desirable agronomic traits. Ultimately, the proposed core collection would lay a foundation for association mapping studies for effective sesame breeding regarding oil, protein and lignans contents.

**Data and code availability**

The code and datasets generated during the current study are available in the following zenodo repository: **xxxx [Ref zenodo]**.

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**Author contributions**

YABZ, SUK and KL conceived and designed this study. YABZ, SUK, HJJ and KL conducted the experiments and collected data. YABZ performed data analysis and drafted the manuscript. SUK, SKTA, MN, DF, NAK, NC, NJC and KL supervised the study, provided funding and technical support, and revised the draft of the manuscript. All authors have read and approved the final version of this manuscript.

**Competing interests**

The authors declare no competing interests.

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