Assessment of genetic diversity among Chinese high-oleic peanut genotypes using miniature inverted-repeat transposable element markers

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Abstract As compared with normal-oleic peanuts, high-oleic peanuts proved to be heart-healthier and had a prolonged shelf life and extended seed longevity. However, there have been concerns about the genetic diversity of present-day high-oleic peanut cultivars, which relied heavily on high-oleic donors with F435 type FAD2 mutations. In the study, a total of 104 high-oleic peanut cultivars/lines/mutants from main breeding teams in China were used to assess their genetic diversity with AhMITE markers. Of all the 31 cultivars tested, those from CTW (Chuan Tang Wang) team had the highest genetic variability. Again, of all the 73 lines studied, those from the same team ranked first in genetic diversity. As compared with cultivars from CTW and C&Y (Xiao Yuan Chi and Shan Lin Yu) teams, greater genetic diversity was detected in new lines of both teams, indicating that recent breeding efforts had resulted in improved genetic diversity in high-oleic peanuts.

Keywords AhMITE · Genetic diversity · High oleate · Groundnut · Mutant · Line · Cultivar

Introduction

As a rich source of edible oil, dietary protein and phytochemicals, peanut is a main cash crop cultivated worldwide, which can be processed into a variety of food products (Bnoku and Yu, 2020).

In a report on the inheritance of high oleic acid in peanut, F2 seeds with at least 70% oleic acid were classified as high-oleic (Moore and Knauf 1989). Likewise, in a similar study, Wang et al. (2013a) adopted the same standard based on the frequency distribution of oleic acid content in F2 seeds. Notably, a qualified health claim was allowed by The US Food and Drug Administration (FDA) (2018) to be placed on the labels of oils with high levels of oleic acid, viz., no less than 70% oleic acid. The industry-accepted standard for high-oleic peanuts is, however, above 74% oleic acid (Davis et al. 2021). High-oleic peanuts are advantageous over their normal-oleic counterpart, having a prolonged shelf life, extended seed longevity and several health benefits (Wang and Zhu 2017; Nkuna et al. 2021). Up to now, much progress has been made in breeding high-oleic peanut cultivars. In China, related studies were mainly carried out at Shandong Peanut Research Institute (SPRI), Kaifeng Academy of Agriculture and Forestry (KFAAF) and
Hebei Academy of Agriculture and Forestry Sciences (HBAAFS). Some high-oleic peanut cultivars were developed by breeders from Henan Academy of Agricultural Sciences (HNAAS) and Chinese Academy of Agricultural Sciences (CAAS) Oil Crops Research Institute (OCRS) (Wang and Zhu 2017). As far as we know, only four research papers (in Chinese) on high-oleic peanut genetic diversity have been published, using high-oleic peanut genotypes with F435 type \textit{FAD2} mutations (G448A in \textit{FAD2A}, 442insA in \textit{FAD2B}). Hu et al. (2013) utilized 12 SSR (simple sequence repeat) primer pairs in the analysis of 5 high-oleic peanut genotypes along with a normal-oleic cultivar (Huayu 22). Similarity coefficient was found to be 0.325–0.750, averaging 0.655. Yu et al. (2017) used 31 SSR primer pairs to assess the genetic diversity of 41 high-oleic peanut cultivars/lines. Similarity coefficient varied from 0.333 to 0.889, with an average of 0.626. In the study by Wang et al. (2020), genetic distance of 25 high-oleic peanut cultivars/lines, as revealed by 140 SSR primer pairs, ranged from 0.057 to 0.624, with a mean value of 0.451. Guo et al. (2020) used 217 SSR primer pairs to study the genetic diversity of 8 high-oleic peanut cultivars bred at KFAAF and found that similarity coefficient was 0.3438–0.9688, with a mean value of 0.6149.

As the output of continuous breeding efforts, more and more high-oleic peanut cultivars, lines and mutants are currently available. Under such conditions, there still have been concerns about the genetic diversity of present-day high-oleic peanut cultivars, which relied heavily on F435 type high-oleic donors. Miniature inverted-repeat transposable elements (MITEs) are non-autonomous elements of less than 600 bp in length (Shirasawa et al. 2012a). In peanut, the number of \textit{AhMITE1} markers thus far developed has amounted to nearly 4000 (Shirasawa et al. 2012a, b; Gayathri et al. 2018). Being a new type of DNA molecular markers, through have not been widely used, \textit{AhMITE1} markers are most promising. Several reports regarding the identification of true hybrids, mapping, and evolutionary and genetic diversity studies using \textit{AhMITE1} markers all yielded satisfactory results (Hake and Bhat 2017; Hake et al. 2017; Wang and Zhu 2017).

This study aimed to compare the degree of genetic diversity in high-oleic peanut cultivars/lines from different teams in China using \textit{AhMITE1} markers, and to find out if the gene base for high-oleic peanuts has been broadened by recent breeding efforts, through assessment of the levels of genetic diversity in representative high-oleic peanut genotypes.

**Material and methods**

**Peanut material**

Totally 104 high-oleic peanut cultivars/lines/mutants from main breeding teams in China were used in the study. These included 12 cultivars from Chuan Tang Wang (CTW) team, SPRI, 3 cultivars from Xiao Yuan Chi and Shan Lin Yu (C&Y) team, SPRI, 6 cultivars from Jian Zhong Gu (JZG) team, KFAAF, 3 cultivars from Yu Rong Li (YRL) team, HBAAFS, 7 cultivars from other teams, 32 lines from CTW team, 16 lines from C&Y team, and 10 mutants from CTW team (Table 1).

**Primer pairs**

38 \textit{AhMITE} (Miniature Inverted-repeat Transposable Element) primer pairs producing discernable, reproducible and polymorphic bands were utilized to study the genetic diversity among the populations and groups (Tables 2, 3).

**DNA extraction, PCR and electrophoresis**

DNA was extracted from cotyledonary slices of peanut seeds according to a previously reported protocol (Yu et al. 2010). A 20 μl of PCR mixture consisted of 2\texttimes\textit{Taq} PCR Master Mix 10 μl (Tiangen Biotech, Beijing), forward and reverse primers 1 μl each (10 μM), template DNA 1 μl, and sterile double distilled water 7 μl. Thermal cycling profile was 5 min at 94°C for pre-denaturation, 35 cycles of 94°C denaturation for 30 s, 55°C annealing for 30 s, 72°C extension for 40 s, followed by a final extension step of 5 min. PCR was performed on a thermocycler (Model Te-s-B, Bioer, Inc.), and amplification prod-
Table 1 High-oleic peanut genotypes used in this study and their sources

| High-oleic cultivar/line | Source | Oleate (%) | High-oleic cultivar/line | Source | Oleate (%) |
|--------------------------|--------|------------|--------------------------|--------|------------|
| Huayu 961                | CV-CTW | 81.2       | 20L19                    | L-CTW  | 77.7       |
| Huayu 962                | CV-CTW | 82.3       | 20L17                    | L-CTW  | 75.0       |
| Huayu 963                | CV-CTW | 80.1       | 20L15                    | L-CTW  | 76.9       |
| Huayu 964                | CV-CTW | 81.7       | 20L16                    | L-CTW  | 78.7       |
| Huayu 965                | CV-CTW | 81.5       | 20L18                    | L-CTW  | 77.0       |
| Huayu 966                | CV-CTW | 82.0       | 20L24                    | L-CTW  | 78.5       |
| Huayu 661                | CV-CTW | 80.9       | 20L23                    | L-CTW  | 76.0       |
| Huayu 662                | CV-CTW | 80.8       | 20L86                    | L-CTW  | 79.6       |
| Huayu 663                | CV-CTW | 80.6       | 20L104                   | L-CTW  | 83.5       |
| Huayu 664                | CV-CTW | 81.9       | 20L87                    | L-CTW  | 79.4       |
| Huayu 666                | CV-CTW | 81.7       | 20L114                   | L-CTW  | 86.0       |
| Huayu 667                | CV-CTW | 80.3       | 20L125                   | L-CTW  | 80.1       |
| Huayu 917                | CV-C&Y | 77.7       | 20L123                   | L-CTW  | 80.5       |
| Huayu 32                 | CV-C&Y | 77.8       | 20L129                   | L-CTW  | 80.2       |
| Huayu 910                | CV-C&Y | 79.3       | 20L127                   | L-CTW  | 79.8       |
| Kainong 301              | CV-JZG | 74.5       | 20L124                   | L-CTW  | 79.9       |
| Kainong 61               | CV-JZG | 77.7       | 20L111                   | L-CTW  | 83.2       |
| Kainong 71               | CV-JZG | 76.5       | 20L163                   | L-CTW  | 87.8       |
| Kainong 176              | CV-JZG | 76.8       | 20L162                   | L-CTW  | 85.6       |
| Kainong 1715             | CV-JZG | 75.6       | 20L168                   | L-CTW  | 81.2       |
| Kainong 1768             | CV-JZG | 75.9       | 20L192                   | L-CTW  | 82.7       |
| Jihua 11                 | CV-YRL | 80.7       | 20S18                    | L-CTW  | 80.1       |
| Jihua 16                 | CV-YRL | 79.3       | 20S80                    | L-CTW  | 80.0       |
| Jihua 18                 | CV-YRL | 76.7       | 20S85                    | L-CTW  | 80.2       |
| Zhonghua 24              | CV-Other-BSL | 78.9 | 20S77                    | L-CTW  | 87.8       |
| Rihua OL1                | CV-Other-DWZ | 81.3 | 20S78                    | L-CTW  | 88.3       |
| Rihua OL2                | CV-Other-DWZ | 81.1 | Huayu 618                | L-C&Y | 84.1       |
| Huayu 51                 | CV-Other-JC | 80.3 | Huayu 9118               | L-C&Y | 81.6       |
| Huayu 52                 | CV-Other-JC | 81.5 | Huayu 9121               | L-C&Y | 80.6       |
| DF05                     | CV-Other-XYZ | 77.6 | Huayu 9128               | L-C&Y | 74.7       |
| Yuhua 37                 | CV-Other-XYZ | 77.0 | Huayu 9130               | L-C&Y | 77.8       |
| Huayu 960                | L-CTW  | 81.7       | Huayu 9131               | L-C&Y | 76.0       |
| Huayu 967                | L-CTW  | 82.5       | Huayu 917                | L-C&Y | 79.8       |
| Huayu 968                | L-CTW  | 80.6       | Huayu 9115               | L-C&Y | 81.0       |
| Huayu 969                | L-CTW  | 79.4       | Huayu 9116               | L-C&Y | 78.4       |
| Huayu 660                | L-CTW  | 80.7       | Huayu 9117               | L-C&Y | 82.0       |
| Huayu 665                | L-CTW  | 79.1       | Huayu 9118               | L-C&Y | 81.6       |
| Huayu 668                | L-CTW  | 81.1       | Huayu 9119               | L-C&Y | 80.2       |
| Huayu 669                | L-CTW  | 81.0       | Huayu 9121               | L-C&Y | 80.6       |
| Huayu 9620               | L-CTW  | 80.6       | Huayu 9123               | L-C&Y | 82.0       |
| Huayu 9621               | L-CTW  | 80.6       | Huayu 9124               | L-C&Y | 82.0       |
| Huayu 9622               | L-CTW  | 80.5       | Huayu 9125               | L-C&Y | 75.1       |
| Huayu 9623               | L-CTW  | 80.3       | CTWE                     | Mutant-CTW | 81.8 |
| Huayu 9624               | L-CTW  | 80.4       | FB4                      | Mutant-CTW | 80.3 |
| Huayu 9625               | L-CTW  | 79.3       | 20L74                    | Mutant-CTW | 85.9 |
ucts were resolved on 1% (w/v) agarose gels with GelGreen dye (Biotium, California) under 1× TAE buffer, 120 V and 20 min electrophoresis conditions.

Statistical analysis

8 populations inclusive of CV-CTW, CV-C&Y, CV-JZG, CV-YRL, CV-Other, L-CTW, L-C&Y, and Mu-CTW and 3 groups including CV-CTW + CV-C&Y, CV-JZG + CV-YRL + CV-Other, and L-CTW + L-C&Y + Mu-CTW were used in genetic diversity analysis (Table 3).

Each polymorphic band was manually scored as present (1) or absent (0) for each peanut sample. Observed number of alleles, effective number of alleles, Nei’s (1973) gene diversity, Shannon’s information index, number of polymorphic loci, and percentage of polymorphic loci were calculated using the Popgene 1.31 software (Yeh et al. 1999). Analysis of molecular variance (AMOVA) was conducted using GenAlex (Peakall and Smouse 2012). Cluster analysis of populations and genotypes was done with Popgene 1.31 software using Nei’s (1972) genetic distance and UPGMA (unweighted pair group method with arithmetic mean) method and DPS 14.50 package using Jaccard distance and flexible group average cluster method (Tang and Zhang 2013), respectively. Similarity coefficient was calculated with NTSYSpc 2.10e (Applied Biostatistics, Inc., 2000).

Results and analysis

AhMITE polymorphism

38 AhMITE primer pairs generated a total of 75 polymorphic loci (1.97 polymorphic loci per primer pair). AhMITE0017 banding pattern, as an example, was shown in Fig. 1. Among the 8 populations, the mean percentage of polymorphic loci (pp), Nei’s (1973) gene diversity (h), and Shannon’s Information index (i) were 100%, 0.2910 and 0.4518, respectively. Lines from CTW (L-CTW) had the highest level of variability, with pp, h and i being 94.67%, 0.2730 and 0.4211, followed by lines from C&Y (L-C&Y), with pp, h and i being 78.67%, 0.2468, 0.3724, respectively. Cultivars from CTW ranked third (pp, h and i were 68.00%, 0.2461 and 0.3663). CV-Other and Mu-CTW were in the fourth and fifth positions respectively. CV-JZG, CV-C&Y and CV-YRL had relatively low levels of variability (Table 3). Among the 3 groups, Group 3 (L-CTW + L-C&Y + Mu-CTW) and Group 1 (CV-CTW + CV-C&Y) possessed high levels of variability, and Group 2 (CV-JZG + CV-YRL + CV-Other) occupied the third position.

Genetic structure of populations

The coefficient of genetic differentiation (Gst) between the cultivars of CTW and C&Y teams was 0.2640 (26.40% of total variation resided between, and 73.60% within the 2 populations) (Table 3).
the cultivars from JZG, YRL and other teams, $G_{st}$ was 0.1826. Among the lines from CTW and C&Y and mutants from CTW team, $G_{st}$ was 0.1127. $G_{st}$ between the 3 above-mentioned groups was 0.0540, indicating that merely 5.40% genetic variation resided between these groups (Table 3).

Likewise, when the 8 populations were used in AMOVA, the results revealed that of the total genetic diversity, 9.2% was attributed to among-population diversity and the rest (90.8%) to within populations (Table 4). Despite that among-population variation

| Primer name | Forward primer (5’ → 3’) | Reverse primer (5’ → 3’) |
|-------------|---------------------------|--------------------------|
| AhTE0001    | aatgtcctagttgcttgc       | acccacatctttgagacaca     |
| AhTE0004    | tgaggctacctcactc          | gcactacgctatgtctc        |
| AhTE0007    | ccaactggttttattcctctct   | ttgtgctgttcaataatctct   |
| AhTE0010    | ggcgtgtctctcacaag        | tggacactgttggtggtgct     |
| AhTE0016    | tgtctgtgttagtgaagaca      | accgacagctctcagctgtct   |
| AhTE0017    | tgcagccaaagaactagact      | caccggtgactcctctctctct  |
| AhTE0018    | aggtgccctagctggttttttt   | gggaagctctcactgacg       |
| AhTE0019    | cctgccctcttggtgca         | aaaaagctctggaggtggtgct   |
| AhTE0020    | tctacagcactattcattttgg   | tgtctggtcttgaattgaaa    |
| AhTE0021    | agtccaagatggaacaagaag    | ttagacactttcatgaaggtgct  |
| AhTE0023    | tgcactgctcaaataacaa      | tcaacgagggcacacaaacaa   |
| AhTE0024    | acagactacacaccacacga      | cgctctcttgctcctctctct   |
| AhTE0025    | tgcctctctctcgcgaaga       | cgggctctctctctctctctct  |
| AhTE0028    | cgatcgactcggtggttttttt   | cctgacactctcaatataacaa  |
| AhTE0031    | taagggctgagttgcatttgg    | ctcagcctctctctctctctct  |
| AhTE0033    | aaagctcgcagagaccaaat     | gaatgtccttgaagctggttga  |
| AhTE0035    | tgcgccaaatatcatgagtgg    | cgggctctctctctctctctct  |
| AhTE0036    | accggagcttggaatgagt      | acaggtgctttgtcctctctct  |
| AhTE0038    | aacagactcggagcaaaat      | ggtgctctctctctctctctct  |
| AhTE0039    | aacagcactcatgaataatgca   | aagggctctctctctctctctct  |
| AhTE0046    | tccacnntctcagttgtag      | tgtgctctctctctctctctct  |
| AhTE0047    | aaaaagctctttgagttgaagctt | ggtgctctctctctctctctct  |
| AhTE0048    | cttccccctccacacatgc      | cattgtgctttctcaggttga   |
| AhTE0049    | atcagcctctccctctctctctct | ctcagctctctctctctctctct |
| AhTE0055    | aaattctgagggacatataatgcc | aagattctctactttgtgagct  |
| AhTE0056    | ttgacaatccatgacatc       | catccagctgtggtctctctct  |
| AhTE0057    | gctgctgctctctctctcctctct | gaaagacgctgctctctctctct |
| AhTE0059    | cgatcgccaaatatctctctct  | tgtgctctctctctctctctct  |
| AhTE0060    | ggggttattgtctgcaatgc     | tccagttgctttgtgctctctct|
| AhTE0067    | cttctcttctctctctctctctct | ggtgctctctctctctctctctct |
| AhTE0089    | tggggtctaatggctctctctct | ctcagctctctctctctctctct |
| AhTE0091    | gctgggctggctgctgctgct    | acctctctctctctctctctct |
| AhTE0101    | gggggttattgtctgcaatgc     | aaaaatttttatgttgtaacttatgc |
| AhTE0463    | acctctctctctctctctctctct | ctcagctctctctctctctctct |
| AhTE0615    | tggctgggttactctctctctctct | ctcagctctctctctctctctct |
| AhTE0660    | aaagatggctcactctctctctctct | acagctctctctctctctctctct |
| AhTE0696    | cttctctctctctctctctctctct | ggtgctctctctctctctctctct |
| AhTE0797    | acccctctacactctctctctctct | tgtgctctctctctctctctctct |

Source: [http://marker.kazusa.or.jp/Peanut marker list/](http://marker.kazusa.or.jp/Peanut marker list/)
was significant, differences within populations can explain the vast majority of \textit{Ah}MITE variation. As shown in Fig. 2, high-oleic peanut lines and mutants from CTW team were grouped together, and cultivars from YRL and JZG teams also had a close relationship. Cultivars from C&Y team were distantly related to other genotypes, however (Fig. 2). As compared with cultivars and lines from C&Y team, cultivars from CTW team were more closely related to the rest other genotypes (Fig. 2).

Genotype grouping

Based on \textit{Ah}MITE profiling, the 104 high-oleic peanut genotypes fell into two categories (I and II). Each category was further divided into two sub-categories (I-a, I-b, II-a, and II-b) (Fig. 3). Most of the lines from C&Y team were found in category I, whereas all the cultivars and most of the lines from CTW team were found in category II. All the cultivars from CTW team were in II-b, and 5 of the 6 cultivars from JZG team were in I-b. The mutants from CTW team could be

Table 3 Statistical analysis of genetic diversity in high-oleic peanut from different breeding teams in China

| Group/population                      | Sample size | \(na\) | \(ne\) | \(h\)   | \(i\)   | \(np\) | \(pp\) | \(G_{st}\) |
|--------------------------------------|-------------|--------|--------|--------|--------|--------|--------|---------|
| CV-CTW + CV-C&Y                      | 15          | 1.8933 | 1.4760 | 0.2884 | 0.4392 | 67     | 89.33  | 0.2640  |
| CV-CTW                              | 12          | 1.6800 | 1.4221 | 0.2461 | 0.3663 | 51     | 68.00  |
| CV-C&Y                              | 3           | 1.5200 | 1.3486 | 0.2010 | 0.2969 | 39     | 52.00  |
| CV-JZG + CV-YRL + CV-Other          | 16          | 1.8267 | 1.4227 | 0.2615 | 0.4017 | 62     | 82.67  | 0.1826  |
| CV-JZG                              | 6           | 1.6267 | 1.3508 | 0.2096 | 0.3178 | 47     | 62.67  |
| CV-YRL                              | 3           | 1.5200 | 1.3416 | 0.1985 | 0.2942 | 39     | 52.00  |
| CV-Other                            | 7           | 1.6667 | 1.3855 | 0.2285 | 0.3442 | 50     | 66.67  |
| L-CTW + L-C&Y + Mu-CTW              | 73          | 2.0000 | 1.4567 | 0.2839 | 0.4410 | 75     | 100.00 | 0.1127  |
| L-CTW                               | 47          | 1.9467 | 1.4432 | 0.2730 | 0.4211 | 71     | 94.67  |
| L-C&Y                               | 16          | 1.7867 | 1.4256 | 0.2468 | 0.3724 | 59     | 78.67  |
| Mu-CTW                              | 10          | 1.6667 | 1.3706 | 0.2215 | 0.3357 | 50     | 66.67  |
| Total                                | 104         | 2.0000 | 1.4665 | 0.2910 | 0.4518 | 75     | 100.00 | 0.0540  |

\(na\) = observed number of alleles, \(ne\) = effective number of alleles, \(h\) = Nei’s (1973) gene diversity, \(i\) = Shannon’s information index, \(np\) = number of polymorphic loci, \(pp\) = percentage of polymorphic loci

CV-CTW + CV-C&Y = Cultivars from Chuan Tang Wang, and Xiao Yuan Chi and Shan Lin Yu teams, CV-JZG + CVYRL + CV-Other = Cultivars from Jian Zhong Gu, Yu Rong Li, Jing Chen, Bo Shou Liao, Dian Wen Zhang, and Xin You Zhang teams, L-CTW + L-C&Y + Mu-CTW = Lines from Chuan Tang Wang and Xiao Yuan Chi and Shan Lin Yu teams, and mutants from Chuan Tang Wang team.

![Fig. 1](image1.png)

\textit{Ah}MITE0017 banding pattern of 96 of 104 peanut materials used in the study (Size of the 6 bands of D2000 DNA marker (Tiangen, Beijing) on the far left, from top to bottom was 2, 1, 0.75, 0.5, 0.25, and 0.1 kbp)

Fig. 1: Genetic diversity analysis of peanut from different breeding teams in China

Table 4 AMOVA of 104 peanut genotypes of 8 populations using 38 \textit{Ah}MITE primer pairs

| Source of variation | Degree of freedom | Sum of squares | Variance component | % total variance |
|---------------------|------------------|---------------|--------------------|------------------|
| Among populations   | 7                | 157.799       | 1.082              | 9.2%**           |
| Within populations  | 96               | 1021.557      | 10.641             | 90.8%            |
| Total               | 103              | 1179.356      | 11.724             | 100%             |
found in 3 of the 4 sub-categories (3 in I-b, 5 in II-a, and 2 in II-b). Cultivars from YRL team and lines from CTW team were in 3 of the 4 sub-categories (Fig. 3). Lines from CTW and C&Y teams were more genetically diversified than cultivars from both teams.

Conclusions and discussion

Genetic similarity coefficient of the 104 high-oleic peanut genotypes in the present study, as calculated by NTSYSpc 2.10e ranged from 0.4400 to 0.9333, with a mean value of 0.6953 (detailed data unshown), comparable to that in a previous study using AhMITE markers to analyze 115 peanut cultivars/lines (mean value = 0.6902) (Wang et al. 2013b). In earlier reports on high-oleic peanut, where only SSR markers were exploited, the minimum similarity coefficient was in the range of 0.3250–0.3438, and the average similarity coefficient ranged from 0.6149–0.6550 (Hu et al. 2013; Yu et al. 2017; Guo et al. 2020). However, in contrast to co-dominant markers, dominant markers tended to underestimate genetic diversity (Qian and Ge 2001), thus making a comparison between level of genetic diversity in the present study using AhMITE markers with that in the previous studies using SSR markers difficult. In the present study, with the 38 AhMITE markers from at least 10 of the 21 (≥ 47.62%) linkage groups of the cultivated peanut (Shirasawa et al. 2012b), it was still possible to assess the genetic diversity of high-oleic peanut genotypes from representative breeding teams at gene, population and group levels.

In this study, of all the 8 populations, lines from CTW ranked first in genetic variability, followed by lines from C&Y, and cultivars from CTW occupied the third position. CTW team and C&Y team have succeeded in broadening the gene base in high-oleic peanut, as new lines from both teams had higher levels of genetic diversity. Over 90% of the total genetic diversity could be ascribed to within population diversity. Like the situation in the 8 populations, as shown by G\textsubscript{st} of individual groups, for each group, within populations variation predominated (over 70% of total).

With the identification/creation of new high-oleic peanut mutants in CTW team (Nkuna et al., 2021; Wang and Zhu 2017), more and more natural and induced mutants were used in breeding. Also, more exotic germplasm lines were used in hybridization in the development of these lines. These were the reasons why the lines from CTW team had the highest genetic diversity and why the lines and mutants from the team had a close relationship. Since all of the 3 cultivars from YRL used the same high-oleic peanut donor (Kaixuan 01–6) from JZG team (Wang and Zhu 2017), cultivars from YRL and JZG were also closely related.

Compared to other types of molecular markers, handling of AhMITE markers in the laboratory is much easier and only requires fewer resources (Gayathri et al. 2018). AhMITE markers have shown considerably high polymorphisms (Hake and Bhat 2017). Thus, they have been considered a potent and convenient tool in genetic research. Since the genotypes used in the present report were of diverse origin, the generated information may provide a basis for
To summarize, much variability resided within populations in this study. Of the high-oleic peanut cultivars, those from CTW team had the highest genetic variability. Of all the high-oleic peanut lines tested, those from CTW team ranked first in genetic diversity. As compared with high-oleic cultivars from CTW and C&Y teams, greater genetic diversity was detected in new lines of both teams, indicating that recent breeding efforts were effective in improving the genetic diversity of high-oleic peanuts.

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Conflict of interest All of the authors of “Assessment of genetic diversity among Chinese high-oleic peanut genotypes using Miniature Inverted-Repeat Transposable Element Markers” here declare that there is no conflict of interest.

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Fig. 3 Dendrogram of 104 high-oleic peanut genotypes using Jacard distance and flexible group average cluster method

Further association studies on agronomically important traits. Using AhMITE markers, this study demonstrated the possibility of broadening the narrow gene base of high-oleic peanut, which is of global importance. In a world with erratic climates, it is imperative to explore novel germplasm resources of diversity and useful alleles to develop climate-resilient high-oleic peanut varieties. AhMITE markers may find wide use in the appraisal of parental lines, and marker-aided selection in peanut.
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