

Technical Working Party on Automation and Computer Programs TWC/36/10**Thirty-Sixth Session
Hanover, Germany, July 2 to 6, 2018****Original:** English
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SELECTION OF SIMILAR VARIETIES FOR MAIZE USING A DNA DATABASE*Document prepared by an expert from China**Disclaimer: this document does not represent UPOV policies or guidance*

The Annex to this document contains a copy of a presentation on “Selection of similar varieties for maize using a DNA database”, to be made at the thirty-sixth session of the Technical Working Party on Automation and Computer Programs (TWC).

[Annex follows]

SELECTION OF SIMILAR VARIETIES FOR MAIZE USING A DNA DATABASE

Presentation prepared by an expert from China

**Selection of similar varieties for maize
using a DNA database**

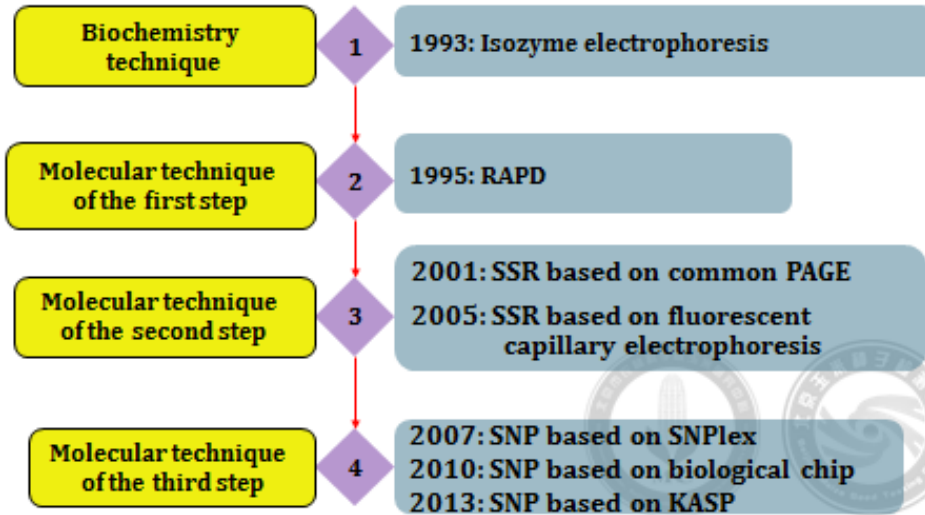
Yang Yang, Wang Fengge, Yi Hongmei, Tian Hongli,
Wang Rui, Zhao Jiuran

The Maize Research Center, Beijing Academy of
Agriculture and Forestry Sciences, China

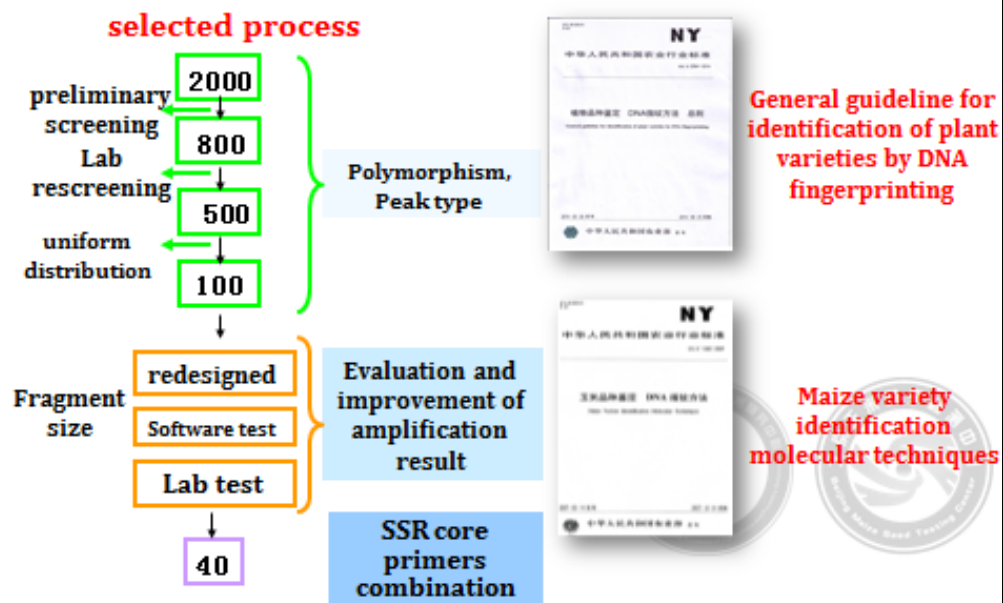
Outline

1 Construction of maize DNA database

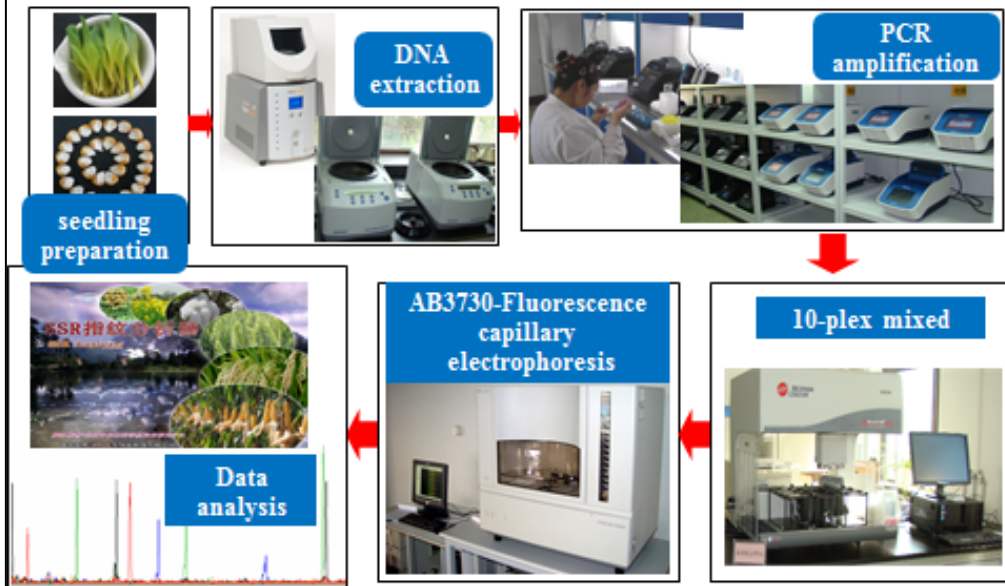
1.1 Four stages of maize variety identification



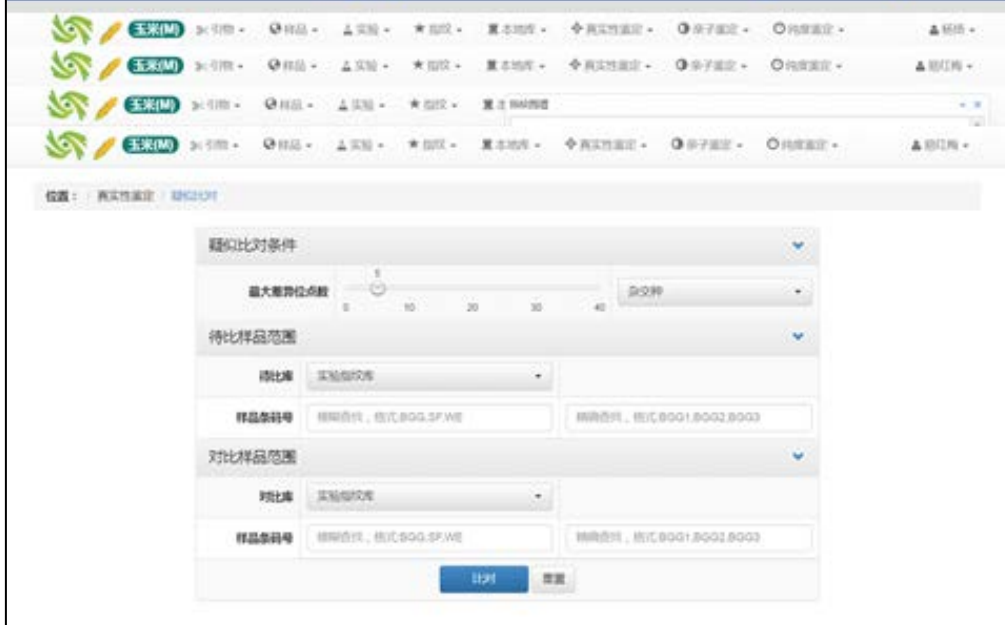
1.2 Selection & standard of core SSR primers in maize



1.3 The experimental process of SSR database



1.4 The DNA fingerprint database management system



1.5 SSR fingerprint database size



- Total samples: > 50,000
 - ✓ VCU varieties: > 24,000
 - ✓ PVP varieties: > 5,000
 - ✓ other: > 20,000



Outline

1 Construction of maize DNA database

2 Selection of similar varieties by SSR



2.1 Molecular experimental design

The analysis is entirely based on maize DNA database described in the first section.

Data quality:

- (1) Each sample is required more than two groups of independent molecular test.
- (2) Missing rate of all hybrid samples is 0.
- (3) Missing rate of all inbred samples is less than 0.05.

sample type	group name	subgroup count	samples count	0-1 difference loci between each sample in each subgroup	1-5 difference loci between each subgroup	0-1 difference loci between each sample in each group	0-5 difference loci between each sample in each group
hybrid	Z	6	58	√	√		
hybrid	X	1	15			√	
hybrid	D	4	15	√	√		
inbred	C	1	17				√
inbred	Y	1	15				√

Total samples count: 120

Outline

1 Construction of maize DNA database

2 Selection of similar varieties by SSR

3 Verification of similar varieties



3.1 DUS test experimental design

- When: April 2016 to November 2016
- Where: Tiebei district, Gongzhuling city, Jilin province, China -- China agriculture ministry plant new variety protection test (Gongzhuling) sub-center experimental station
- What: Observing and recording characteristics base on the guidelines.
- How: Each sample was planted with two rows of 30 individual plants.



3.2 Verification of similar varieties by SNP & InDel

- Four prevailing genotyping platform

ABI 3730

Illumina iScan

Affymetrix GeneTitan

LGC PHERAstar



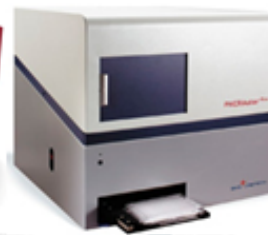
SSR 40



SNP 50k
SNP 3072
SNP 384



SNP 200k
MCIDP 50k
6H90K



SNP 384
SNP 40

Outline

- 1 Construction of maize DNA database
- 2 Selection of similar varieties by SSR
- 3 Verification of similar varieties
- 4 Comprehensive analysis of similar varieties

4.1 Overall data sources and data quality

Missing Rate of different sources Data

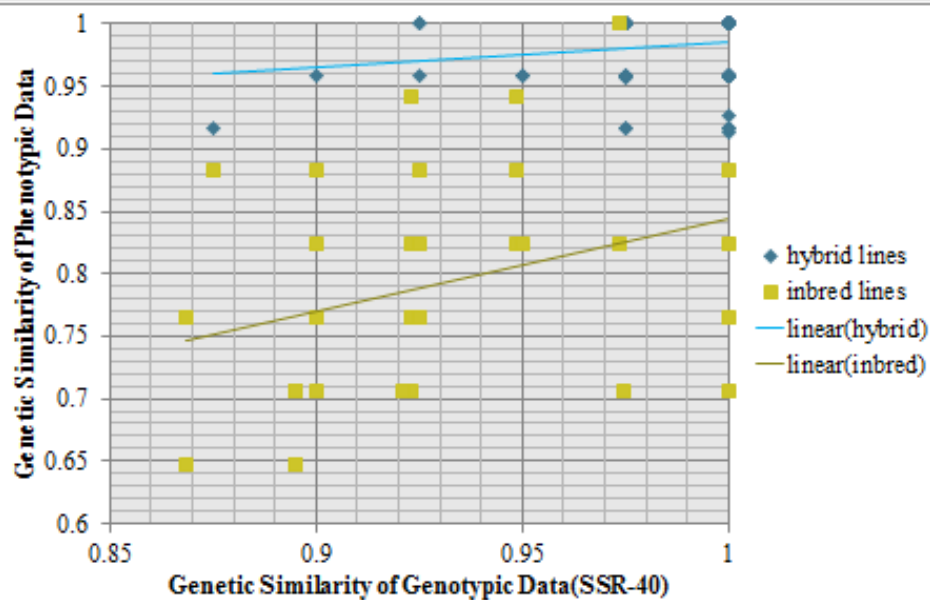
sample type	group name	samples count	SSR-40	SNP-384	SNP-2090	InDel-11520	DUS characteristics count
hybrid	Z	58	√	√	√	√	√
hybrid	X	15	√	√	√	√	√
hybrid	D	15	√	√	√	√	√
inbred	C	17	√	√	√	√	√
inbred	Y	15	√	√	√	√	√
Max missing rate	-	-	0.003	-	0.008	0.009	0.069

4.2 Correlation between phenotype and genotype

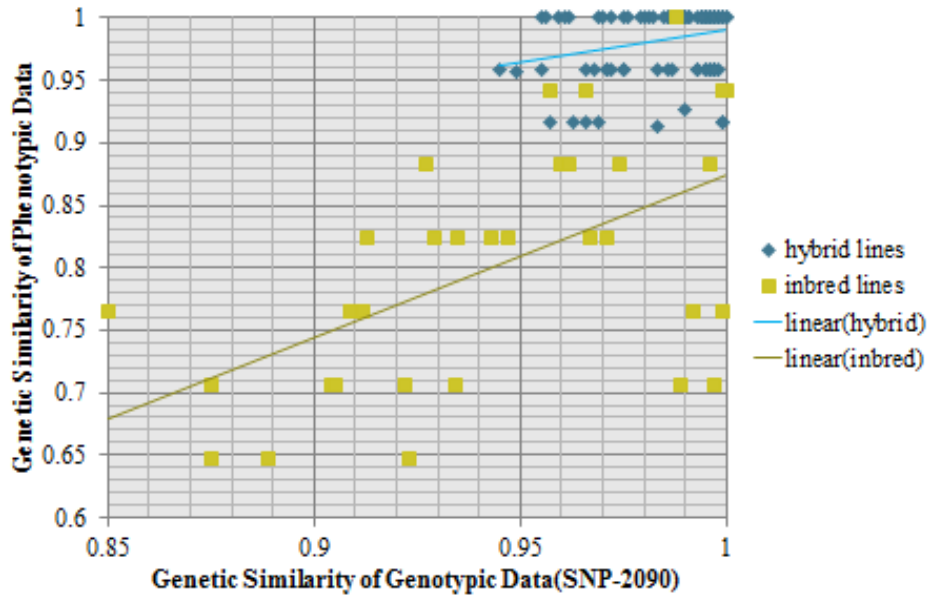
The correlation coefficient of different sources Data

	SSR-40 vs DUS	SNP-2090 vs DUS	InDel-11520 vs DUS	SSR-40 vs SNP-2090	SSR-40 vs InDel-11520	SNP-2090 vs InDel-11520
hybrid lines	0.177	0.259	0.253	0.474	0.418	0.982
inbred lines	0.317	0.551	0.574	0.757	0.780	0.994
Total	0.667	0.721	0.738	0.788	0.788	0.994

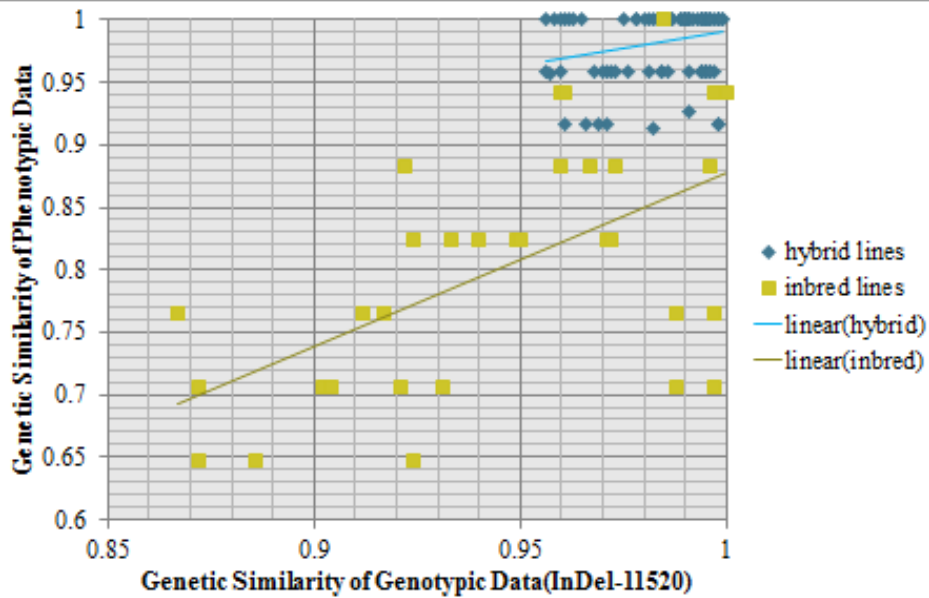
4.2 Correlation between phenotype and genotype



4.2 Correlation between phenotype and genotype



4.2 Correlation between phenotype and genotype



4.3 Five Characteristics with significant difference in S.V.

① 23.7% of paired similar varieties with significant difference in 'Ear: anthocyanin coloration of silks'



代码1: 无或极弱



代码3: 弱



代码5: 中



代码7: 强



代码9: 极强



4.3 Five Characteristics with significant difference in S.V.

② 20.6% of paired similar varieties with significant difference in 'Tassel: anthocyanin coloration of glumes excluding base'

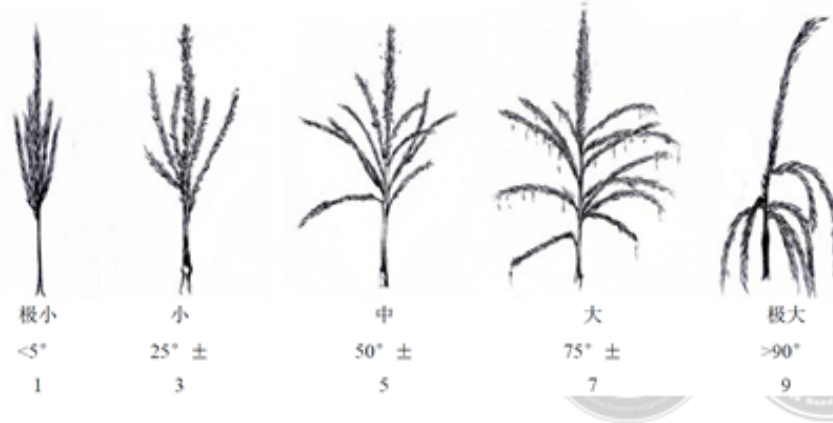


代码1: 无或极弱 代码3: 弱 代码5: 中 代码7: 强 代码9: 极强



4.3 Five Characteristics with significant difference in S.V.

③ 15.3% of paired similar varieties with significant difference in 'Tassel: angle between main axis and lateral branches'



4.3 Five Characteristics with significant difference in S.V.

④ 11.5% of paired similar varieties with significant difference in 'Tassel: anthocyanin coloration of anthers'



4.3 Five Characteristics with significant difference in S.V.

- ⑤ 7.6% of paired similar varieties with significant difference in 'Ear: anthocyanin coloration of glumes of cob'



代码1: 无或极弱 代码3: 弱 代码5: 中 代码7: 强 代码9: 极强

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...ATGAG... ACAGGCCA... TCGGGCTC... GTCGACCG... TCGT...  
...CTGAG... ACAGGCCA... TCGAGCTC... GTCAACCG... TGGG...  
...GTGAG... ACAGGCCA... TCGGGCTC... GTCGACCG... TCGT...  
...CTGAG... ACAGGCCA... TCGGGCTC... GTCGACCG... TGGT...
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Thanks for the help of Tang Hao, Yang Kun, Yang Yang, Han Yuxi, Wang Fenghua, Zhou Haitao, etc.

**Thanks for your
attention!**

