Management of oat Germplasm in China

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- 1. Introduction
- 2. Oat collection in China
- 3. Agronomic characteristics
- 4. Molecular assessment
- 5. Ploidy level identification
- 6. Future concerns

Introduction

- Oat is a traditional crop in China
 - Over 2000 years
 - Naked type, called Youmai, or Lingdangmai
- Oat is a minor crop in China
 - About 0.5 million ha. annually,
 - Consumed locally in the past, but now nationally
- Oat is considered as health food
 - Reducing blood fat, sugar and cholesterols
 - Prevent from diabetes and other diseases

- Oat plays a very important role in the dry and high altitude areas
 - Food and nutrition supply
 - Income generation
 - Adaptation to climate change
- Naked type is a native of China
 - Large grain, more florets and seed set, early maturity, strong resistance to drought and tolerance to poor soils
 - Thresh easily

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Oat accessions

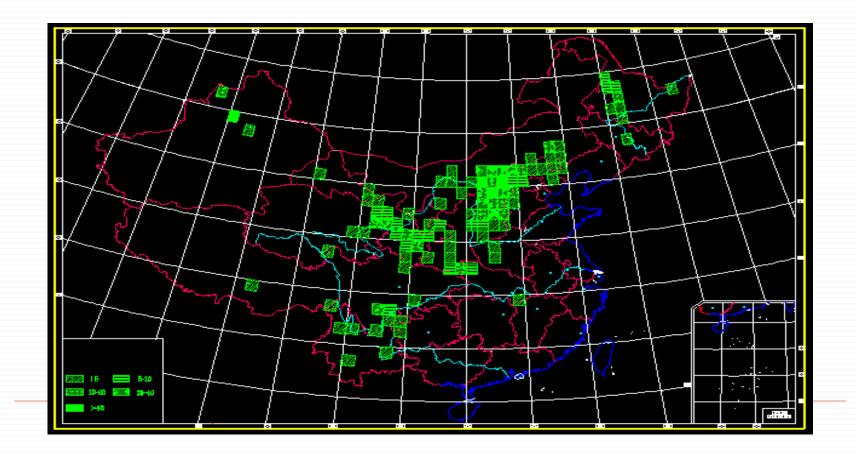
- Over 3550 accessions are conserved in genebank, which is located at CAAS
 - 1,800 accessions of naked oats
 - 1,700 accessions of hulled oats
 - > 50 accessions of wild species

Types of materials

- Landraces, over 80%
 - Traditional, diversified, rich diversity
- Cultivars, 3%
 - High yield, strong resistance, uniformity
- Advanced lines, 15%
 - With special characteristics
- Wild materials, 1.4%
 - Resistance to diseases, rich diversity

Geographic origins

 Domestic origin: more than 20 provinces, mainly from Gansu, Hebei, Inner Mongolia, Ningxia, Qinghai, Shanxi, Shaanxi, Sichuan



Foreign origins:

- America: Agentina, Canada, USA, Chile
- Oceania: Australia, New Zeland
- Asia: Pakistan, Japan, Turkey, Israel
- Europe:
 - Germany, France, Belgium, Netherland, Swiss, Hungary, U.K.
 - Bulgaria, Czech, Romania, Russia
 - Denmark, Sweden, Finland

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Biological characteristics

- Winterness-Springness
 - Springness (>70%), Weak springness(20%), Winterness(<10%)
- Maturity
 - Very early (70 days), Very late (120 days)
- Seedling habits
 - Erect (51%), semi-erect(26%), Prostrate(23%)

Morphological traits

- Plant heights:
 - Range from 50cm to 175cm, average 108.2cm
- Panicle length
 - Range from 12.5 cm to 32 cm, average 20.4 cm
 - Seed weight (1000 seeds)
 - Range from 11g 40g, average 22.8g

Resistance to bio- & abiotic stresses

- Smut is an important disease in naked oat, partly evaluated
 - Resistant 63%
 - Susceptive 37%
- Salt tolerance, partly evaluated at germination stage, among 278 naked types evaluated
 - 17 accessions highly salt tolerant
 - 114 accessions tolerant
 - 106 accessions were moderate tolerant
 - 25 accessions susceptible and
 - 16 accessions highly susceptible.

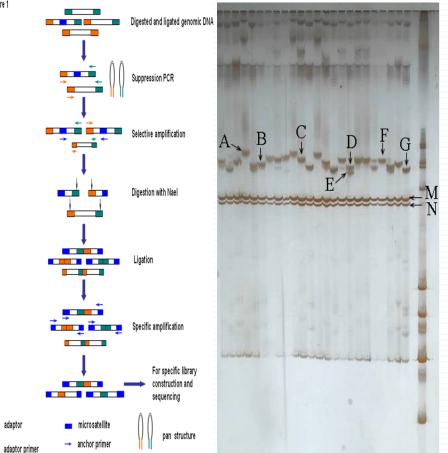
Chemical components

- Protein content:
 - Range from 8.71%-19.9%, average 14.9%
- Fat content:
 - Range from 3.44% 9.82%, average
- ß-glucan content:
 - Range from 2% 7.5%, in total 1010 accessions, 67 accession <3%, 866 accessions between 3% and 4.9%, 75% accessions >4.9%

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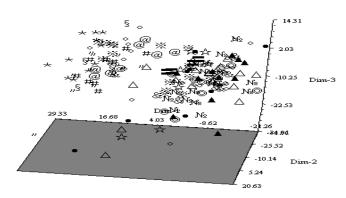
SSR development

- Developed a quick methods for SSR identification
- DNA sequences flanking microsatellites can be isolated rapidly on a large scale.
 - The approach selectively amplifies microsatellitecontaining sequences and recombines the amplicons by redigestion and ligation

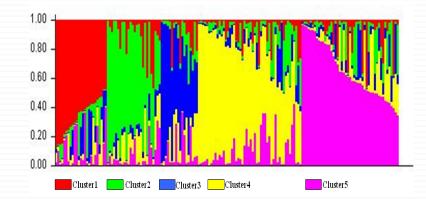


Mol Breeding. 2012, 29:53–59

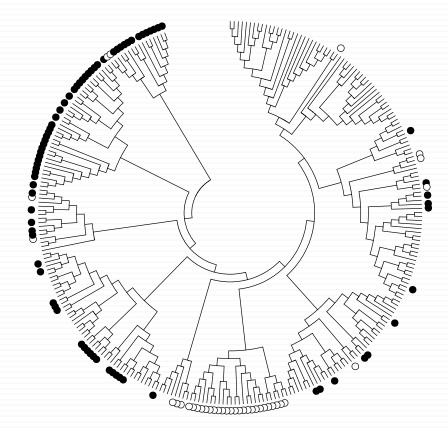
Genetic diversity analysis of oat germplasm



Three dimension distribution



Genetic structure of population



Cluster analysis of oat germplasm

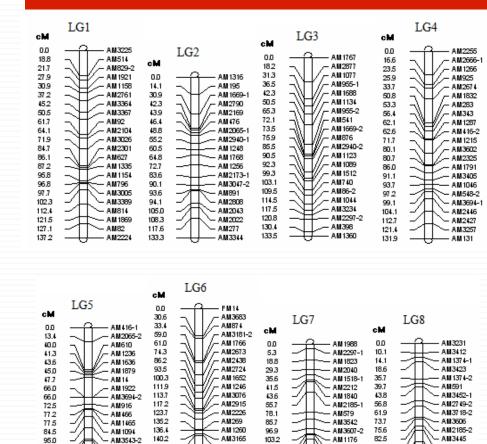
Developing mapping populations

- RIL5 from "578" x "Sanfensan"
- RIL6 from "Xiayoumai" x "Chi38"





Constructing linkage groups



AM557

AM 1348

- AM2638

104.3

109.1

139.2

86.8

97.3

120.4

AM2521

- AM2020

AM88

AM2749-1

- AM3452-2

AM 1212

142.3

173.0

174.4

- AM86-1

- AM2965

- AM 495

105.9

107.4

131.8

22 linkage groups, 2,070.5 cM, 208 SSR markers; The minimum distance 0.01 cM, the maximum 46.1 cM, and the average distance 9.95 cM.

LG11

LG15

LG19

AM 1953

- AM3741

- AM 1357

AM810

- AM2403

- AM 1002

AM 1357 AM 1119 AM 3507-1

AM2368-AM383 AM2542 AM2542

LG12

LG16

"AM751-2 "AM751-1 "AM754

AM 1411-AM 2239 AM 1010 AM 3459-

AM623 AM824 FM22

LG20

- AM1411-1

сM

0.0

257

38.7

сM

0.0 22.0 60.2 80.2

сM

0.0 42.5 64.9

сM

0.0 23.9 36.1 47.6 64.9 75.9

сM

0.0 45.0 62.7 81.1

сM

0.0 38.0 59.5

LG9

LG13

LG17

LG21

AM 1052 AM 1178 AM 1245

AM3217 AM965

- AM2053

- AM411 - AM727

- AM625 0.0

AM629

- AM 1803 95.6

— AM 1518-2

- AM2270

AM 1578 AM 2573

AM2762

сM

25.5 35.2 48.8 71.8

сM

0.0 22.9 51.0 72.4

сM

0.0 31.2 49.6

сM

0.0 44.3

LG10

AM2245 FM31 AM2429 AM1516 AM3278 AM3261

LG14

LG18

LG22

AM548-1

AM3543-1 AM3274 AM3620 AM3620 AM3992

— AM 1830 — AM 1961

- AM2956

сM

0.0

22.8 42.7 46.5 49.4 61.1 72.2 76.0 78.9 93.0 98.3

сM

0.0 44.6 58.8 96.0

сM

0.0 40.7

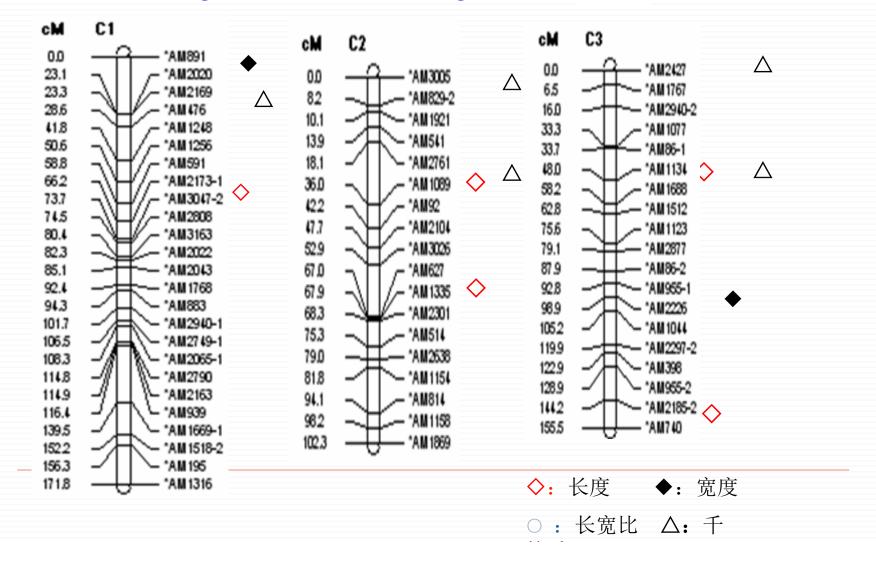
66.2

сM

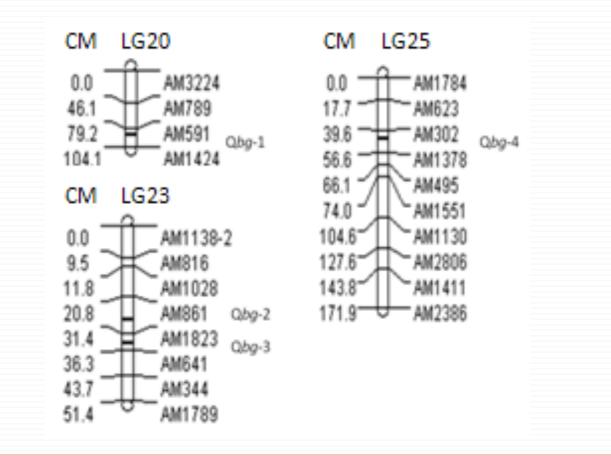
0.0 46,1

Mapping QTLs for important traits

Grain length, width and weight



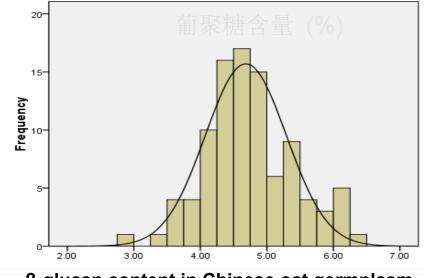
• β-glucan content



CSLH gene diversity and identification of associated marker

Identified 1 SNP associated with βglucan content, additive effective value 0.28

SNP	CC(2	78%) C	G(5%)	GG(17%)	A2	D3	P value
Glucan conte	nt 4.88=	:0.61 4.4	44±0.47	4.33±0.68	0.28	-0.17	0.003

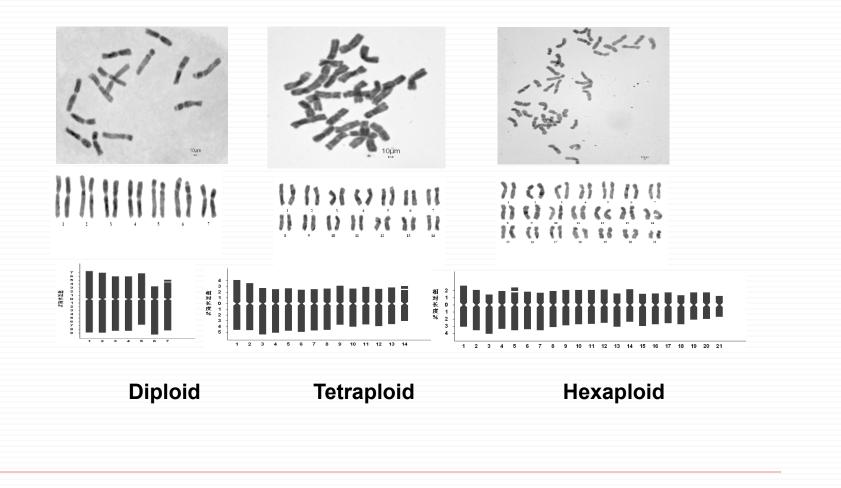


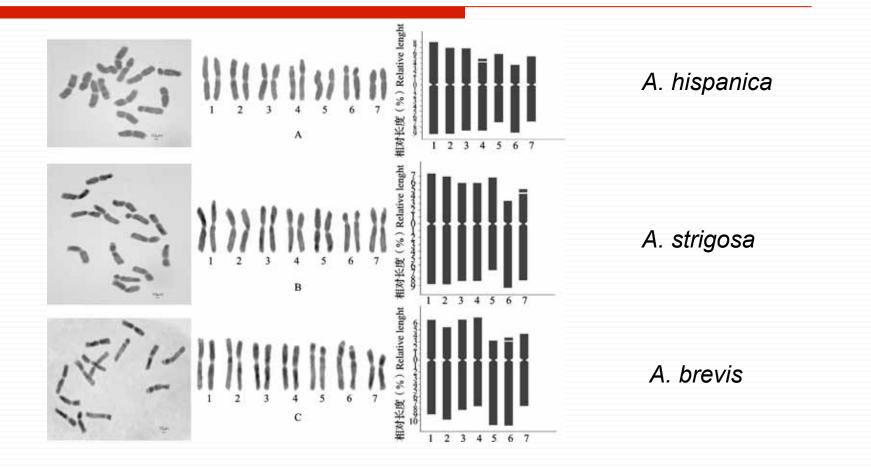
β-glucan content in Chinese oat germplasm

A A A	:30 1 1 A	440 AG GGA	450 AGAT C	460 A A CC C C	G A AG GG G	480 A CC CC TC	490 CCCA	500 AAGTAAAGAT	510 AA TITTI G	520	530 CCCCACA	540 G GG G	550 ATC A ATC	560 TGA ATC
A A A		AG GGA AG GGA	AGA G AGA G	AC C CC C C AC C CC C C	G A AG GG C G A AG GG G G A AG GG G G A AG GG G	A GG GG G A GG GG G	GGGGA	AAG AAAGA AAG AAAGA	AA IIIII G	G GA	I GGGAGA GGGAGA	G GG G G GG G	A G A A G A G A A G	IGA AIG GA AIG
A A A A A A	T A	AG GGA AG GGA	AGAT G AGAT G	AC G GG G G	Ğ A AĞ ĞĞ Ğ G A AG GG G	A ĞĞ ĞĞ Ğ A GG GG <mark>G</mark> G	GGGA	AAGTAAAGAT	AA TTTTT G	G GA	CGGGAGA CGGGAGA	G GG G	AGAAG	GA A G
A A A	t t Å	AG GGA	AGA G	A G GG G G A 4: 4 CHC2 451	7 A AG GG G	A GG GG IG	GGGA	AAGTAAAGAT	AA IIIII G	G GA	GGGAGA	G GG G	AGAAG	GA A G
A A A A A A		AG GGA AG GGA	AGA G AGA G	17	G A AG GG G G A AG GG G	A GG GG GG	CCC 1	AAGTAAAGAT TAAGTAAAGAT	AA G	G GA G GA	I GGGAGA GGGAGA	G GG G G GG G	A G A A G A G A ACG	GAAG GAAG
A A A	T T A	AG GGA	AGA G	A G GG G G	G A AG GG G	A GG GG GG	GGGA	AAGTAAAGAT	AA TTTTT Ğ	ĞĞÂ	GGGGGGA	G GG G	AGAAG	GA A G
A A A A A A	T T A	AG GGA AG GGA	AGA G AGA G	A G GG G G A G GG G G A G GA G G	G A AG GG G G A AG GG G G A AG GG G	A GG GG G A GG GG G	GGGA	AAG AAAGA AAG AAAGA		G GA	GGGAGG GGGAGA	G GG G G GG G	A G A A G A G A A G	GAAG GAAG
A A A	TTA	AG GGA	AGATTG	A G GA G G	G A AG GG G	A GG GG 📕	- CCCA	AAGAAAGA	AA TTTTT G	G GA	GGGAGA	Ğ ĞĞ Ğ	ATG A ATG	GA ATC GA ATC

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Cytological identification





Chromosomes shape(left),karyotype and karyotype pattern(right) of 3 diploid oat species

Molecular identification

Identified 3 SSR markers associated with ploidy of oat species

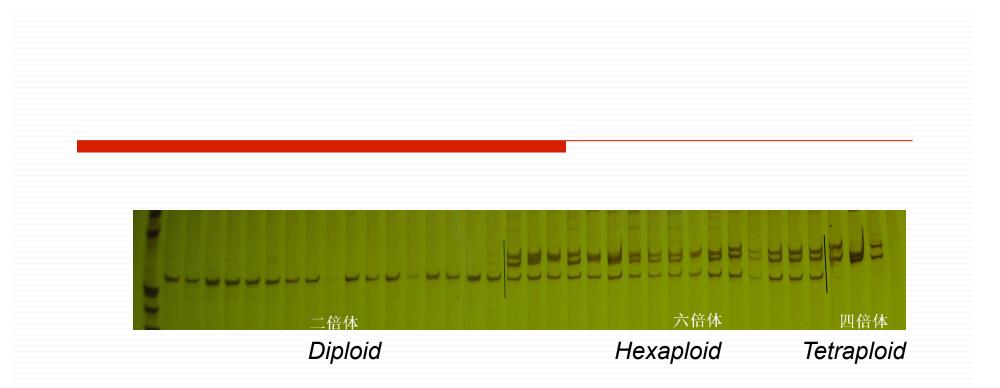


Diploid

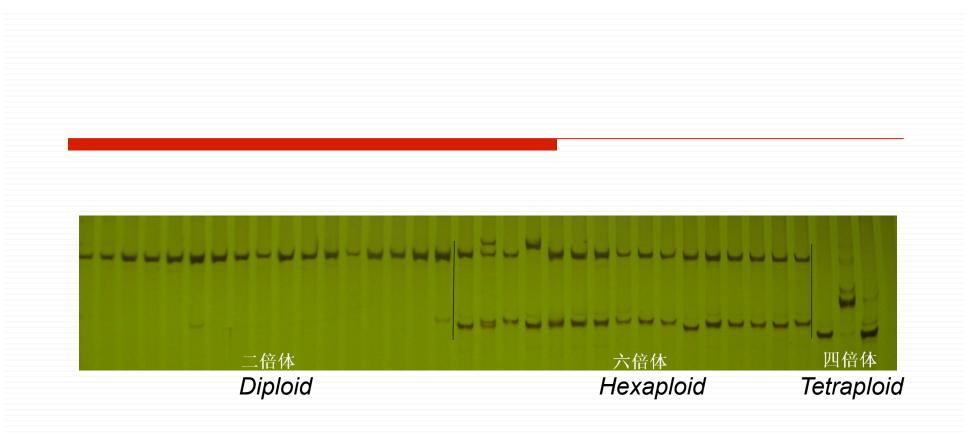
Hexaploid

Tetraploid

Band pattern of Primer AM63 on different ploidy of oat



Band pattern of Primer AM447 on different ploidy of oat



Band pattern of Primer AM1403 on different ploidy of oat

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- Multiplication trials for climate change
- Resistance to biotic and abiotic stresses
- Comparison study of linkage groups
- Genotyping by sequencing
- Contributing to CORE project

Thank you !