Management of oat Germplasm in China

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Outline

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

Outline

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
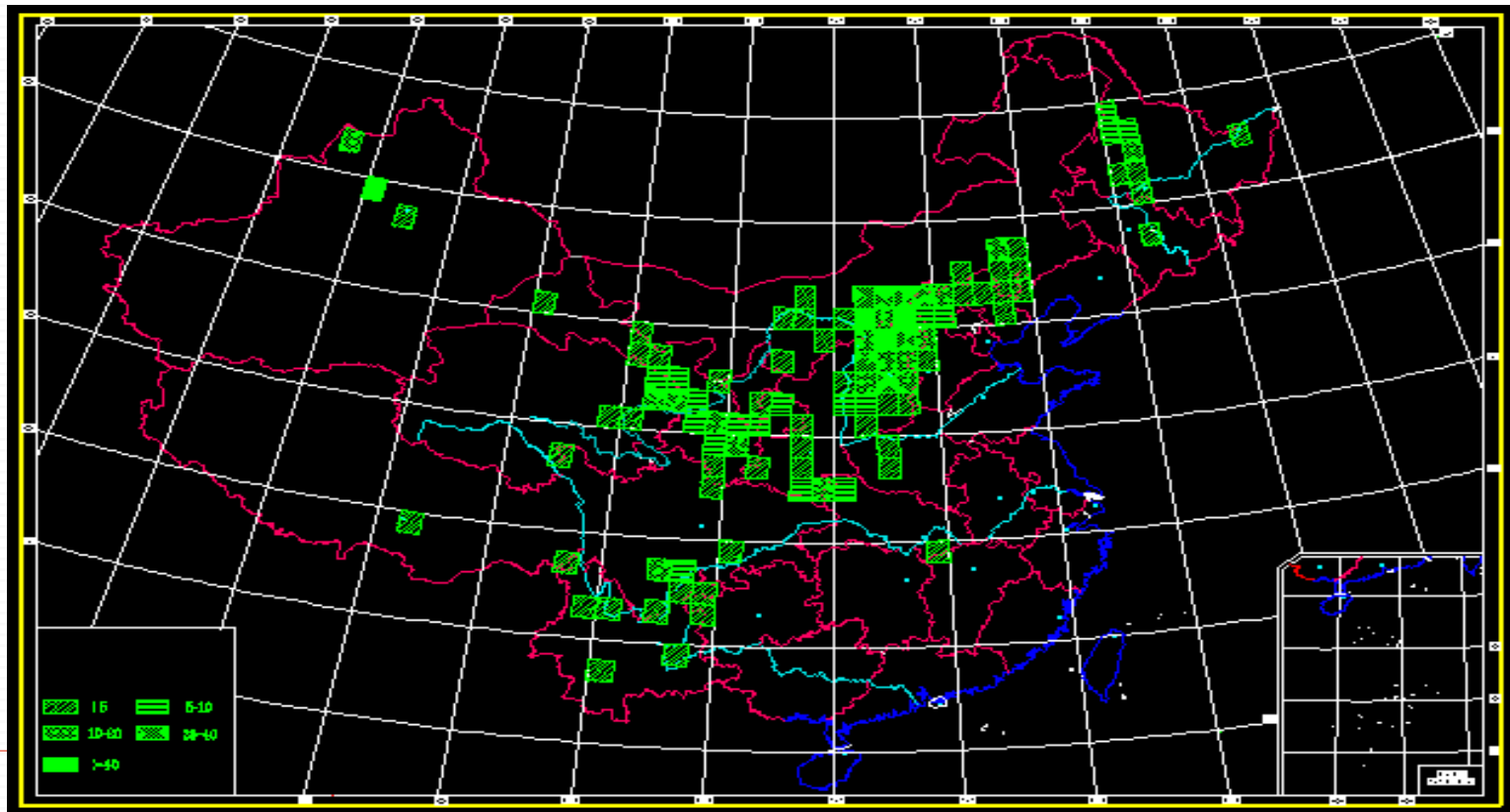
Foreign origins：

- ➤ 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%

Outline

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 microsatellite-containing sequences and recombines the amplicons by redigestion and ligation

Mol Breeding. 2012, 29:53–59
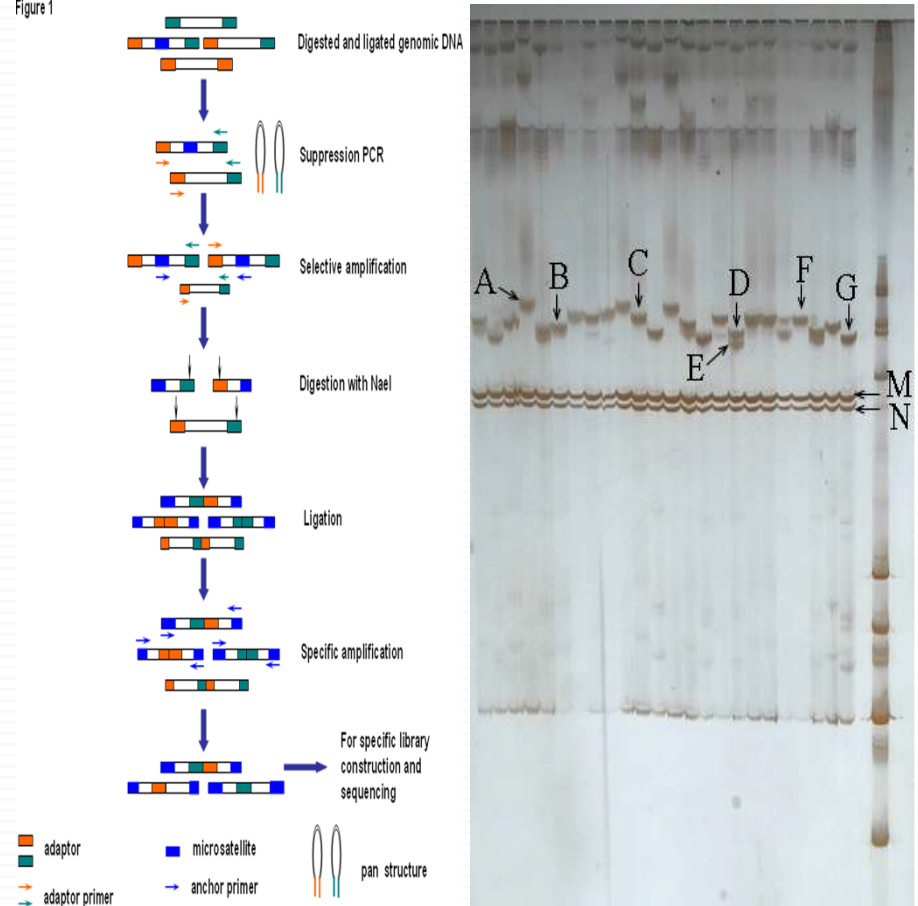
Genetic diversity analysis of oat germplasm
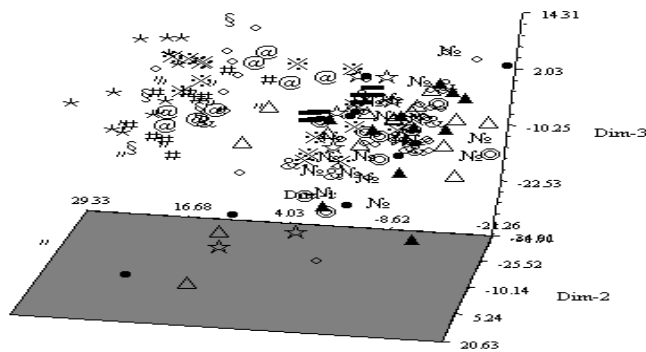
Three dimension distribution

Cluster1 Cluster2 Cluster3 Cluster4 Cluster5
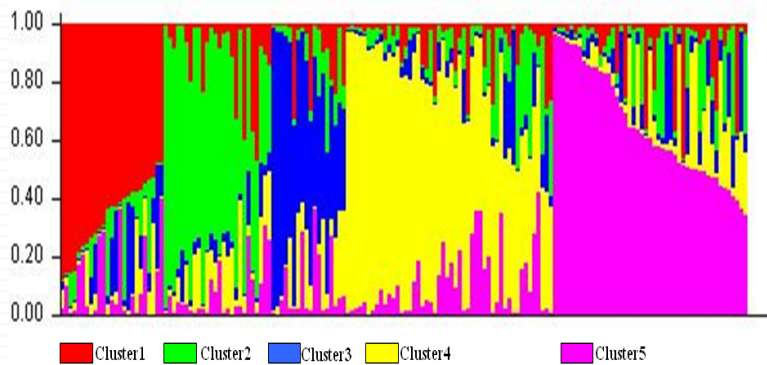
Genetic structure of population

Cluster analysis of oat germplasm

Developing mapping populations

- RIL5 from "578" x "Sanfensan"

- RIL6 from "Xiayoumai" x "Chi38"

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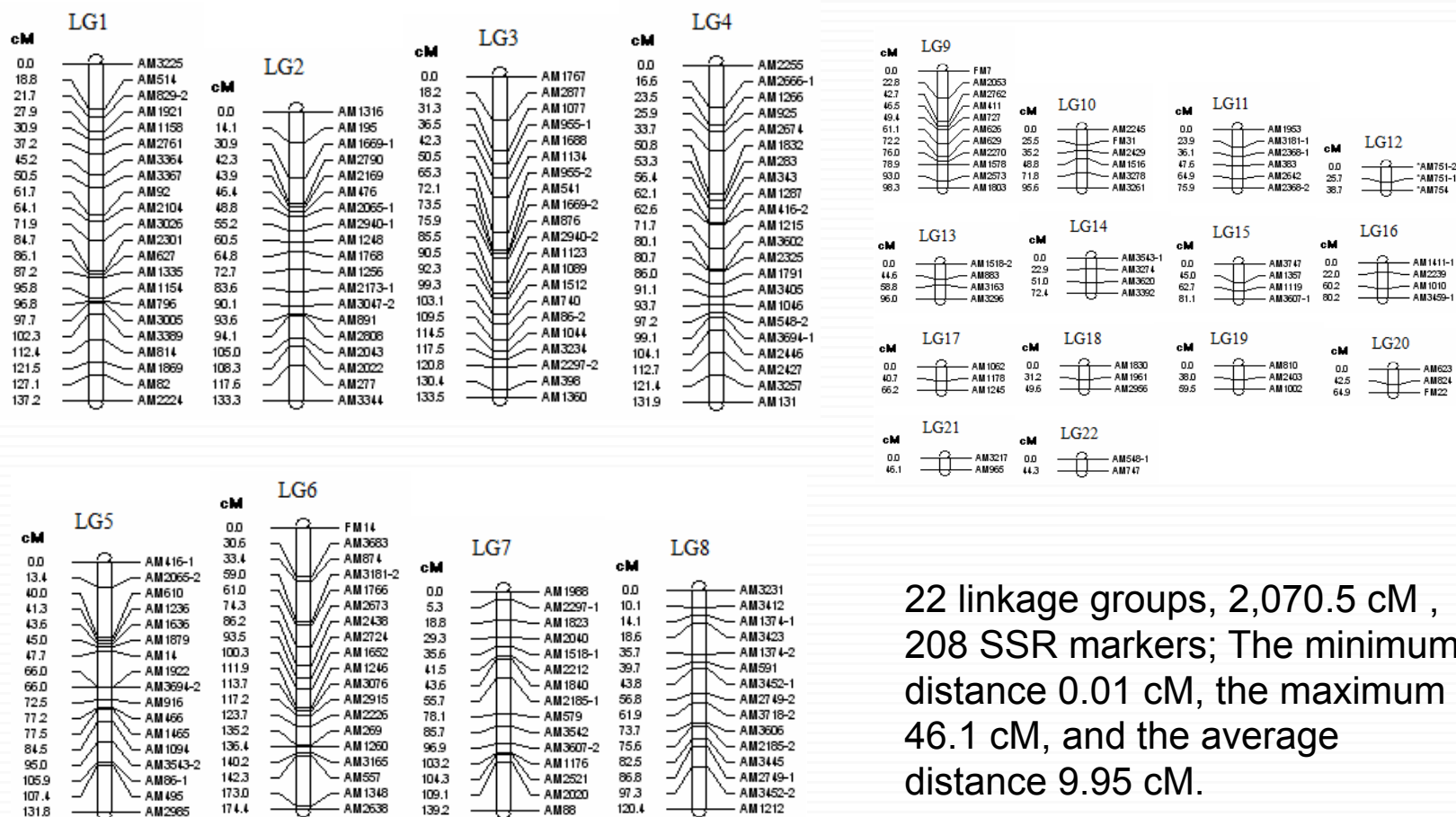
22 linkage groups, 2,070.5 cM , 208 SSR markers; The minimum distance 0.01 cM, the maximum 46.1 cM, and the average distance 9.95 cM.

Mapping QTLs for important traits

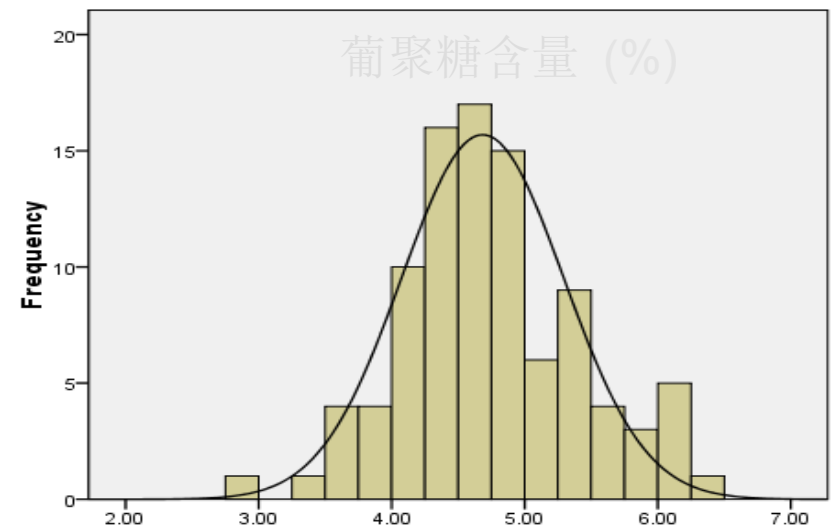- Grain length, width and weight
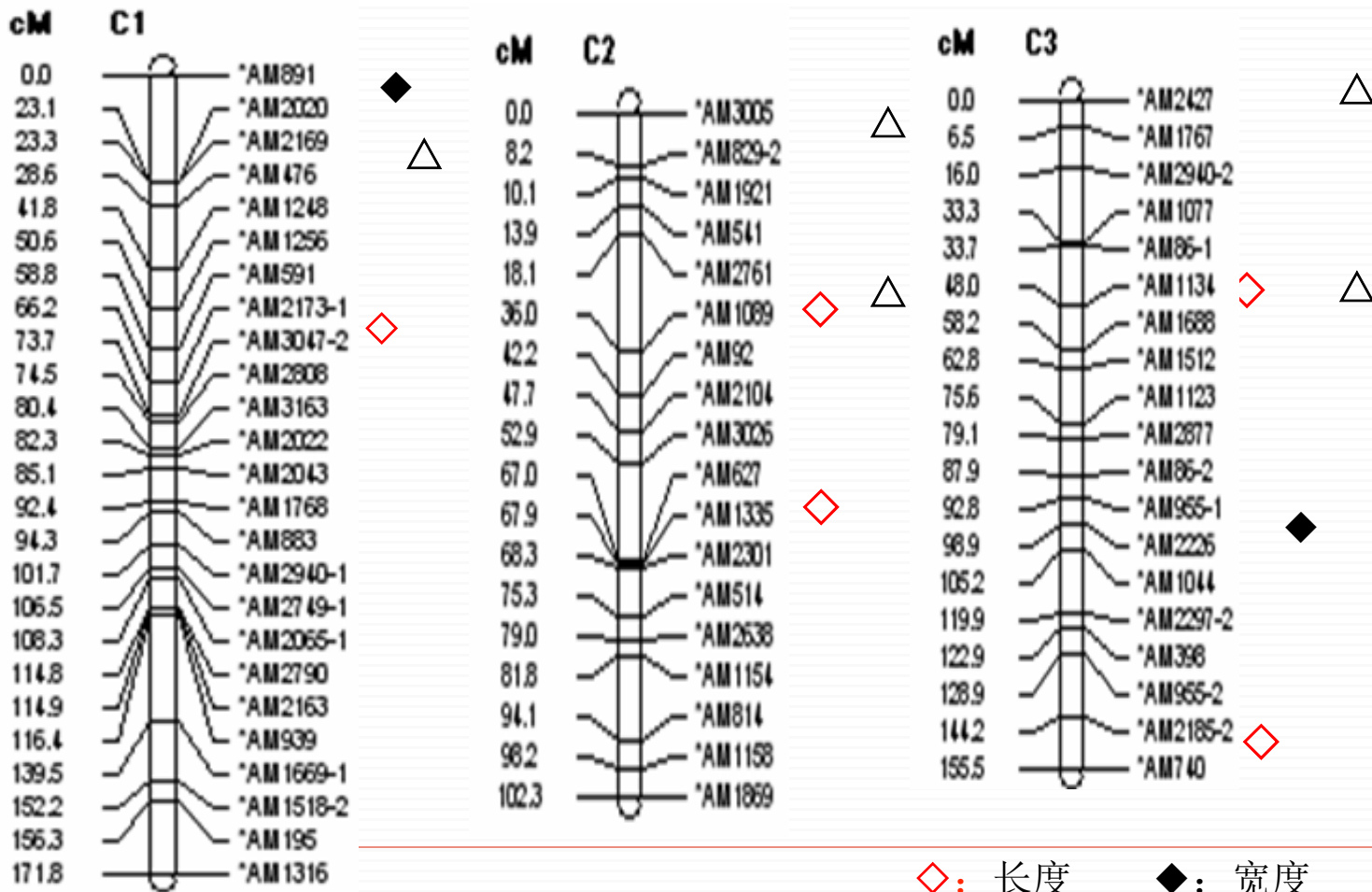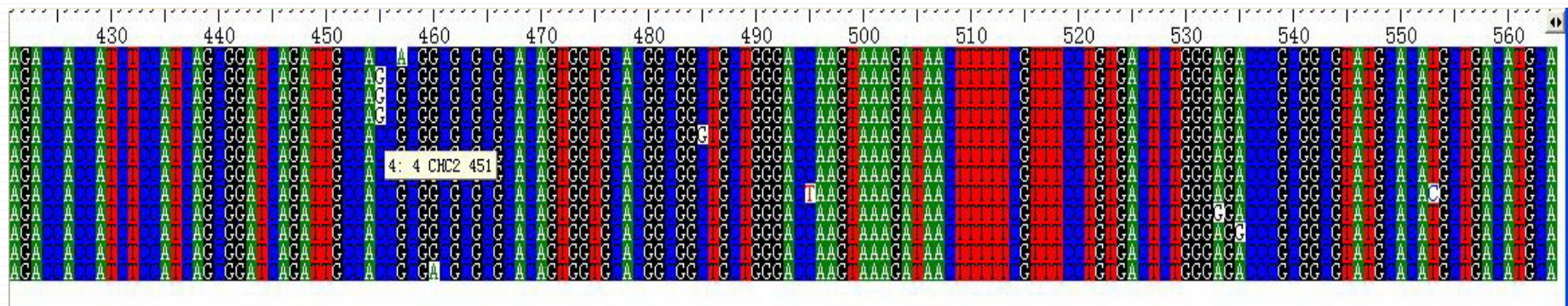

◇：长度　◆：宽度

○ ：长宽比　△：千
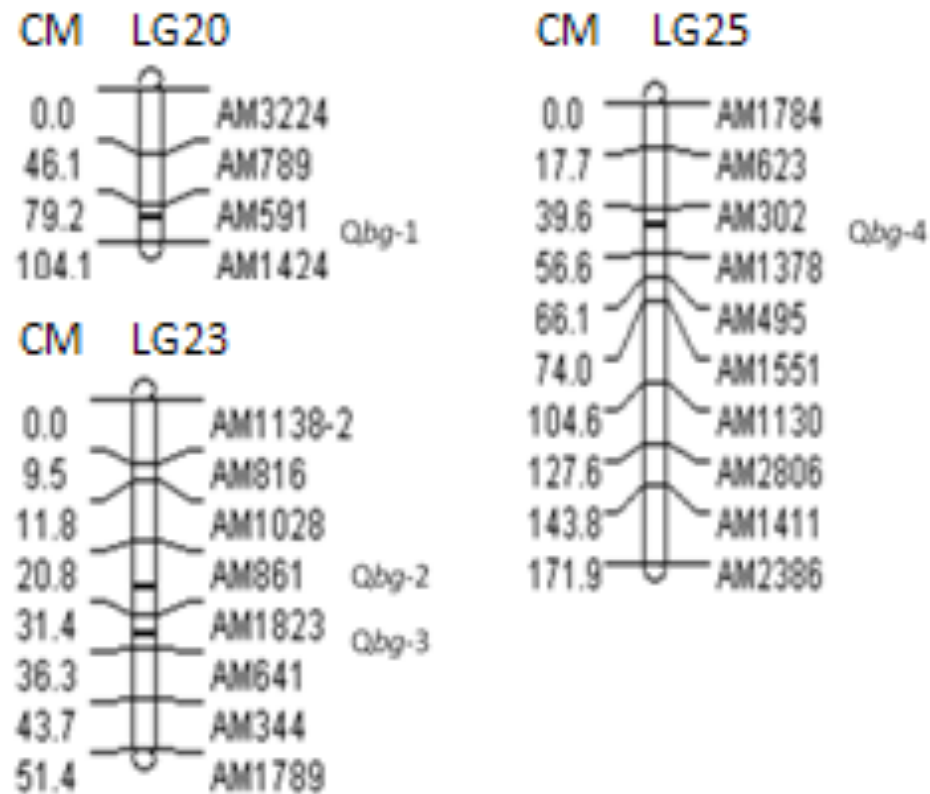
- **β-glucan content**

CSLH gene diversity and identification of associated marker

Identified 1 SNP associated with β-glucan content, additive effective value 0.28

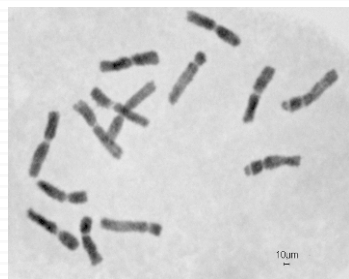| SNP	CC(78%)	CG(5%)	GG(17%)	A2	D3	P value
Glucan content	4.88±0.61	4.44±0.47	4.33±0.68	0.28	-0.17	0.003

葡聚糖含量 (%)
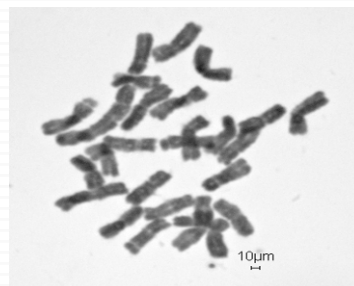
β-glucan content in Chinese oat germplasm

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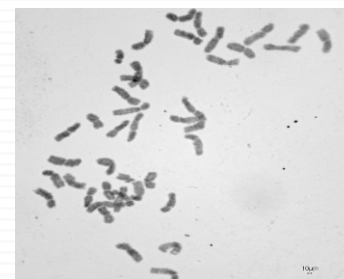5. Ploidy level identification
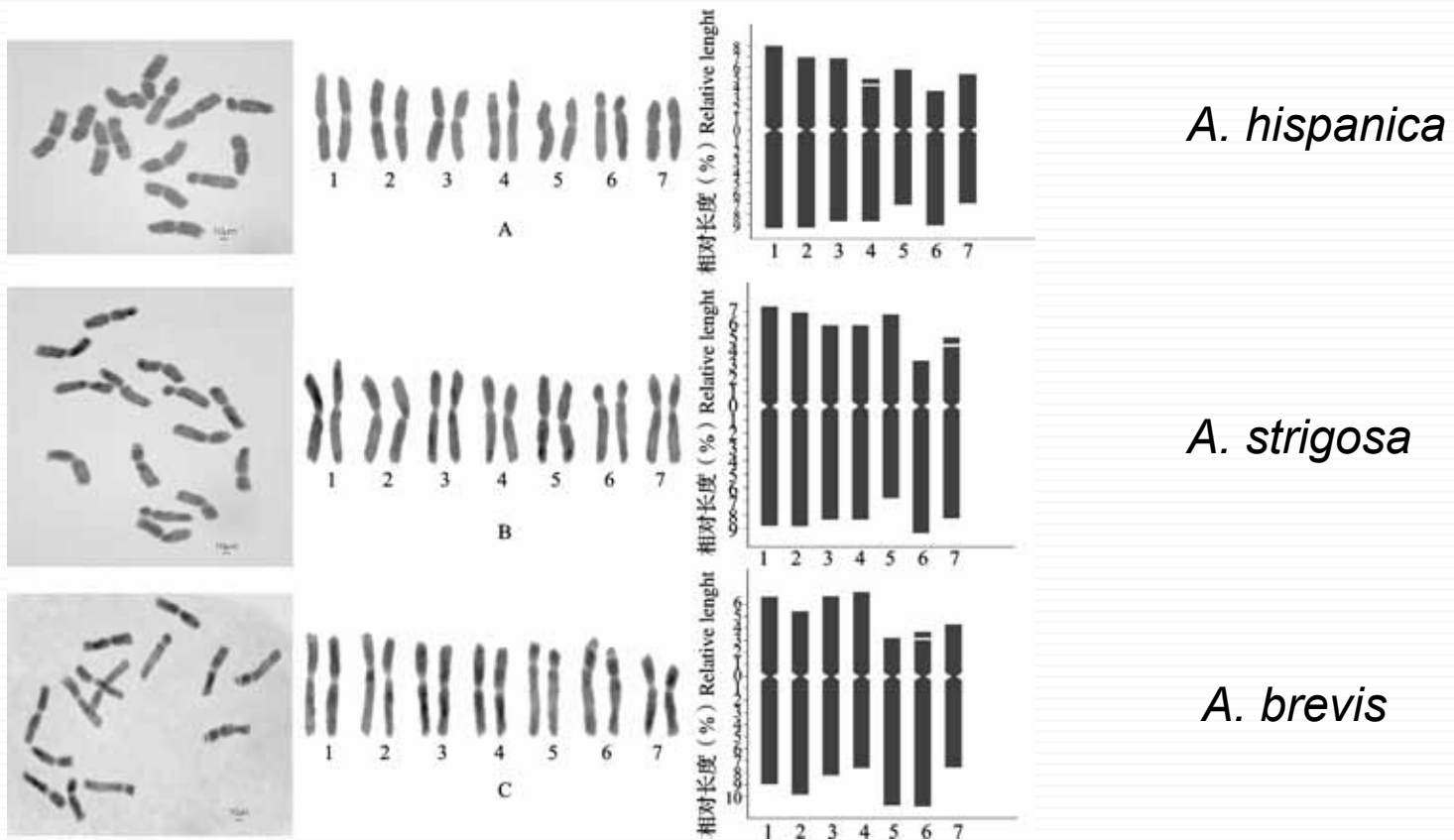6. Future concerns

Cytological identification
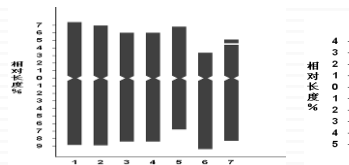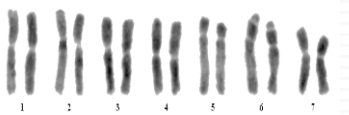
Diploid **Tetraploid** **Hexaploid**
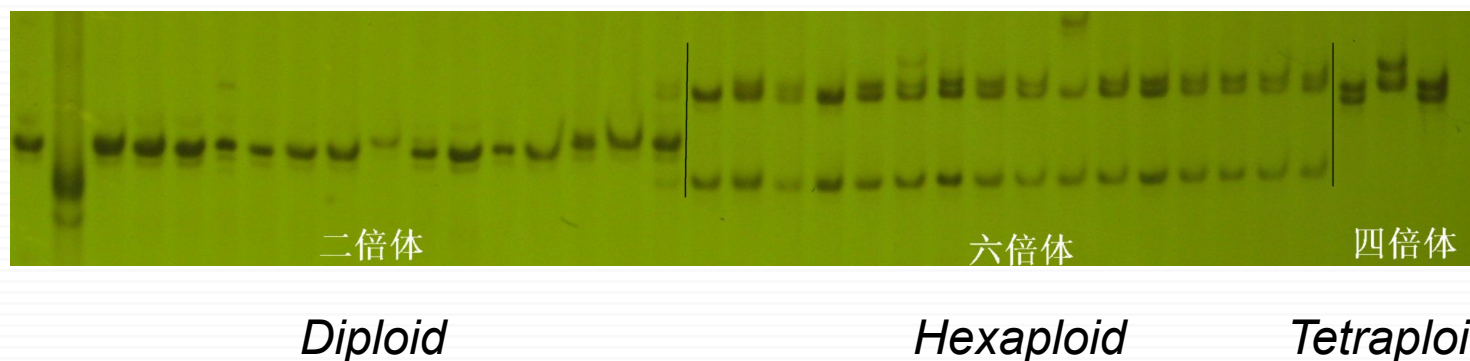
A. hispanica

A. strigosa

A. brevis

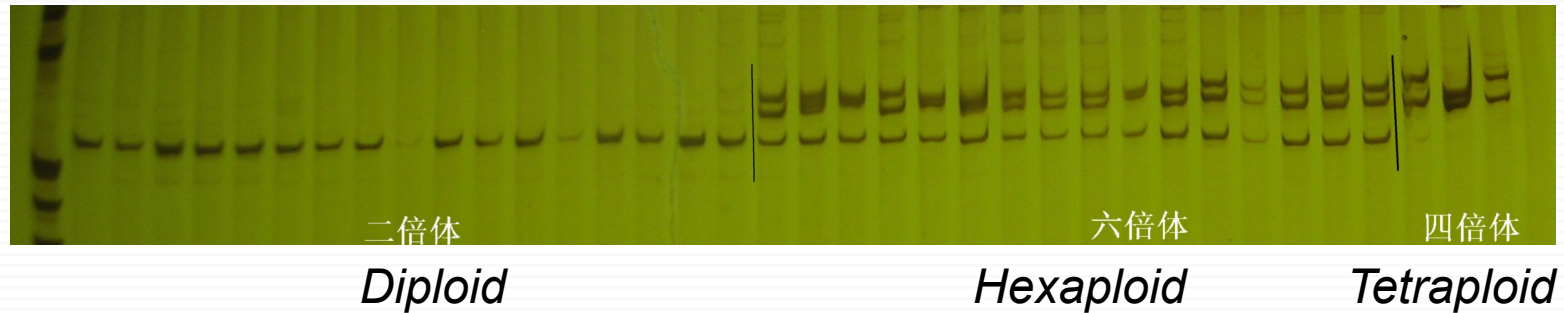Chromosomes shape(left),karyotype and karyotype pattern(right) of 3 diploid oat species

Molecular identification

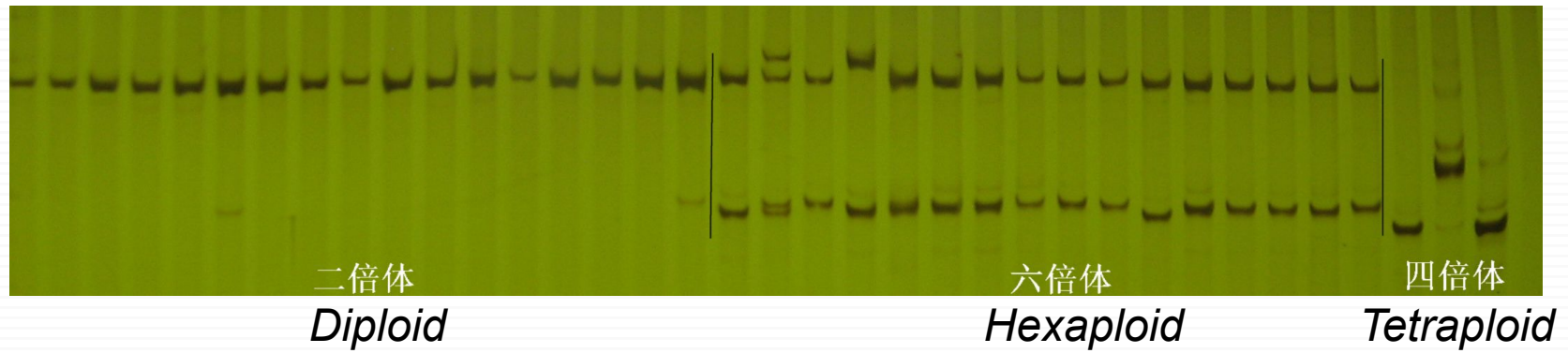- Identified 3 SSR markers associated with ploidy of oat species

Band pattern of Primer AM63 on different ploidy of oat

二倍体 Diploid   六倍体 Hexaploid   四倍体 Tetraploid

Band pattern of Primer AM447 on different ploidy of oat

二倍体 Diploid
六倍体 Hexaploid
四倍体 Tetraploid

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 ！