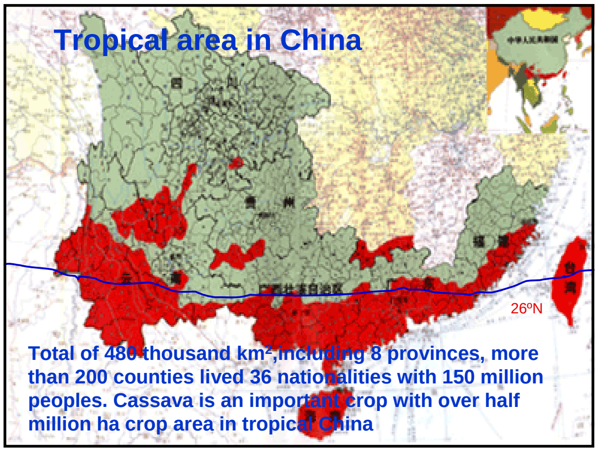
Development of QTLs for starch content and storage root productivity based on two F_1 populations of non-inbred parents in Cassava (*Manihot esculenta* Crantz)

Wenquan Wang

Institute of Tropical Biosciences
& Biotechnology, CATAS, CHINA

2006.11.22

Tropical area in China



Total of 480 thousand km², including 8 provinces, more than 200 counties lived 36 nationalities with 150 million peoples. Cassava is an important crop with over half million ha crop area in tropical China

---

Cassava, characteristics and value-added products

The fourth of the most important tropical food crop globally. More than half billion people living with cassava a dietary staple

One of the potential bio-energy crop in the very near future, and will play very important roles in bio-ethanol supplication

Higher photosynthesis rate and starchy root output, tolerance to abiotic stresses and better starch quality

---

Cultivation:
Intercropping with water melon used plastic cover in Guangxi, China 2006

Cultivation: 2-years cassava planted in Guangxi, China 2006

Breeding objectives in China

High starch content and high yield

Tolerance to lower temperature: fast early growth to build shape and root system; hold a higher grow rate in 18-25 ; tolerance to cold

Waxy starch with different percent of amylose 0-12%

Industral quanlity better for produce bio-ethanol

Cultivation: cropped in sand soil lower land in Hainan island, China 2005

Conventional breeding is not successful usually

All clones are heterotic

Genetic load (bad genes deposed in each genotypes)

Less chance to recombine & segregate in genetics for somatic propagation reason

The problem is:

How to use molecular markers find good genes distributed in different individuals and combine them into one elite cultivar

Biotechnology would be used in breeding extensively but never instead of it

- Grouping and selection of parents based on molecular diversity analysis
- Test of heterosis based on markers
- Molecular assist selection (MAS)
- Somatic and microspore culture help enlarge the population to accelerate the breeding
- Genetic Modification (GM) added or knock out a special gene to dissolve a single-gene genetic defect
- Other more effective tools developed by genomics.

Construct a mapping population

Population I

SC6 × **Mianbao**
(female) ↓ **(male)**
F1
(211 individuals)

Population II

SC6 × **WH**
(female) ↓ **(male)**
F1
(184 individuals)

Developing the useful molecular markers linked with important traits

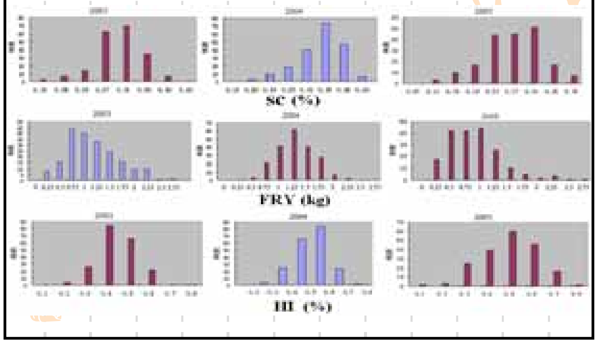
Selected diversity parents to construct a mapping population

Phenotyping the traits in the field or experimental condition

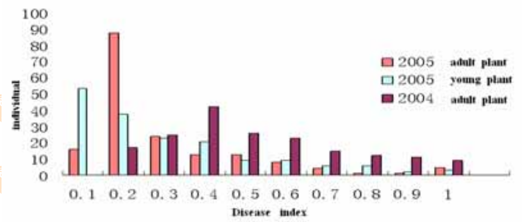
Population screening by SSR markers in lab

Combining the above data, where and what QTLs of these traits have been detected by software that could be used in MAS breeding.

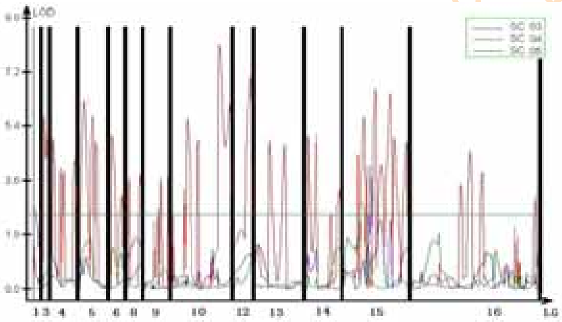
Evaluated data of the traits in the field test

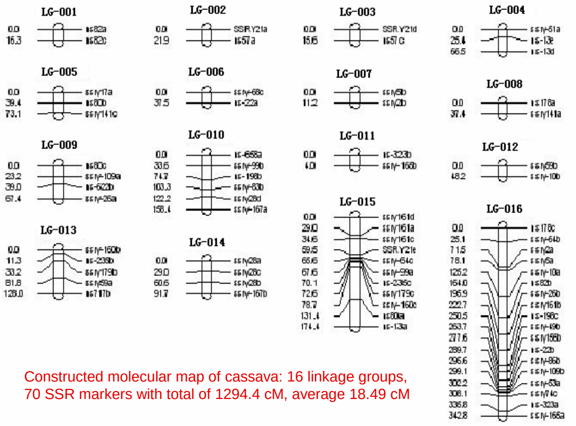


Disease index of BLS in different environments in cassava



QTLs for Starch content (SC)





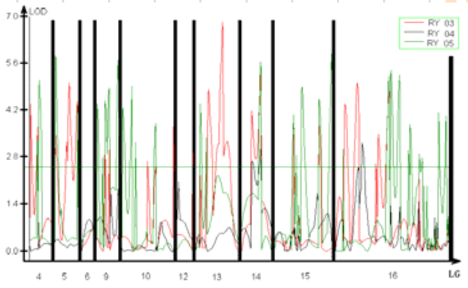
Constructed molecular map of cassava: 16 linkage groups, 70 SSR markers with total of 1294.4 cM, average 18.49 cM

QTLs for starch content (SC)

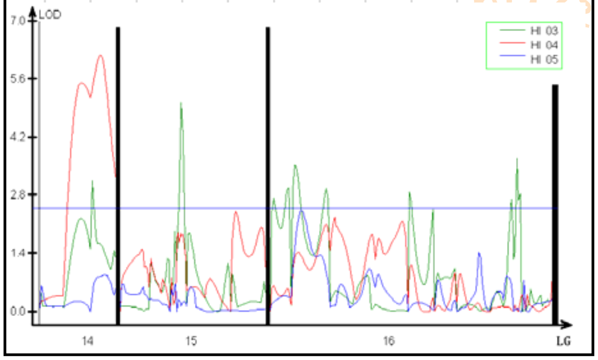
19 QTLs with PVE 21.77 to 45.13% have been discovered in three conditions (2003-2005) with distribution in LG4, LG8, LG9, LG10, LG12, LG14,LG15 and LG16.

QTL	LG	Marker Interval	Position cM	LOD Score	Additive effect	R2(%)
qSCb14-1	14	SSRY28a-SSRY28c	2.01	5.0983	0.0002	26.53
qSCb14-2	14	SSRY28a-SSRY28c	26.01	5.1375	0.0006	28.97
qSCF-15-1	15	ssry161c-SSRY21e	38.61	4.4404	0.0002	31.82
qSCF-15-2	15	ssry161c-SSRY21e	46.61	2.8819	1.7486	25.04
qSCF-15-3	15	SSRY21e-ssy64c	63.51	4.0584	0.0016	21.77

QTLs for Fresh root yield (RY)



QTLs for Harvest Index (HI)



QTLs for fresh root yield (FY)

QTL	LG	Marker Interval	Position	LOD Score	Additive Value	PVE(%)	Test
qFYT4-1	4	ssry51a-ns13e	2.01	4.387	0.0666	0.2023	03
qFYT4-2	4	ssry51a-ns13e	24.01	3.3027	0.04	0.2576	05
qFYT5-2	5	ns80b-ssry141c	43.41	5.0236	0.0544	0.3083	03
qFYT5-3	5	ns80b-ssry141c	69.41	4.4559	0.0229	0.291	03
qFYT5-4	5	ns80b-ssry141c	69.41	4.3262	0.0553	0.2918	05
qFYT13-1	13	ns235b-ssry179b	13.31	4.4083	0.0691	0.263	05
qFYT13-2	13	ns235b-ssry179b	31.31	2.517	0.0378	0.1567	03
qFYT13-3	13	ns235b-ssry179b	31.31	3.3873	0.0509	0.2521	05
qFYT14-1	14	ssry28c-ssry28b	31.01	4.1871	0.0208	0.2161	03
qFYT14-2	14	ssry28c-ssry28b	33.01	2.6953	0.0314	0.2078	04
qFYT14-3	14	ssry28c-ssry28b	59.01	3.124	0.0486	0.1826	04
qFYT14-4	14	ssry28c-ssry28b	59.01	5.4048	0.0943	0.2209	03

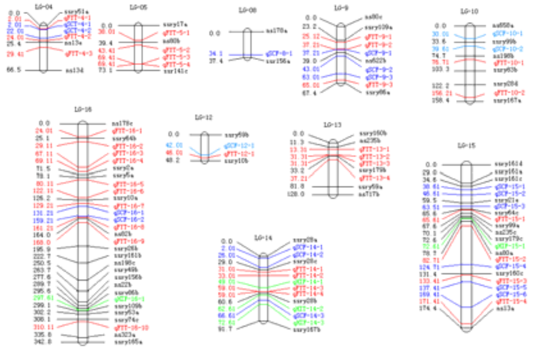
Total of 34 QTLs has been mapped on LG4, LG5, LG9, LG10, LG12, LG13, LG14, LG15 and LG16. The PVE of QTL are ranged from 15.67 to 34.16%

QTL for harvest index (HI)

4 QTL with PVE 11.1 to 20.46% have been located on LG14 and LG15. *qHI15* between ssry179c to ssry160c in LG15 with left distance 0.01cM and right distance 6.09cM is an important QTL

QTL	LG	Marker Interval	Position	LOD Score	Additive Value	PVE (%)	Test
qHIT14-2	14	ssry28b-ssry167b	62.61	3.1498	0.0195	0.2046	03
qHIF15-1	15	ssry179c-ssry160c	72.61	5.0384	0.0653	0.1112	03

Establishment of the linkage map



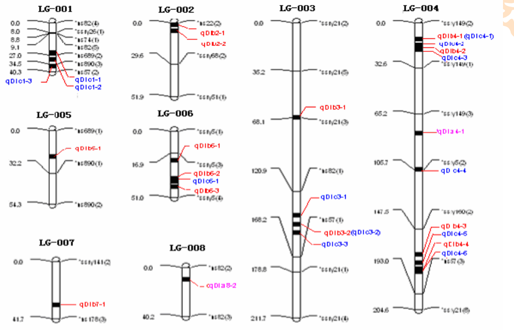
Using the software Mapmaker/Exp 3.0b to construct the linkage map, (LOD=3.0, mix distance=50.0)

QTL for Brown leaf spot (BLS)

29 QTLs conferring resistance to BLS were detected, including 15 main effective QTLs with over 30% of percent of phenotypic variance explained.

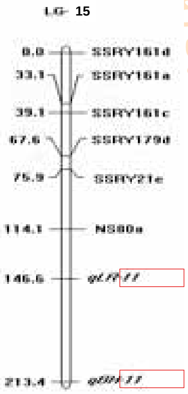
QTLs	LG	position	marker interval	nearby marker	LOD	Additive	Dominance	PVE
qDIc1-1	1	25.11	NS82（5）-NS689（2）	NS689	11.9685	-0.3007	-0.442	0.4732
qDIc1-2	1	31.01	NS689（2）-NS890（3）	NS689	10.4905	-0.338	-0.4515	0.422
qDIc1-3	1	36.51	NS890（3）-NS57（2）	NS890	8.8179	-0.3507	-0.451	0.4106
qDIc2-1	2	2.01	NS22（2）-SSRY68（2）	NS22	13.5682	-0.2741	-0.2197	0.5313
qDIb2-1	2	2.01	NS22（2）-SSRY68（2）	NS22	7.8091	-0.2744	-0.3097	0.3737
qDIb2-2	2	6.01	NS22（2）-SSRY68（2）	NS22	10.5138	-0.2498	-0.2725	0.5148
qDIb3-1	3	68.11	SSRY21（3）-NS82（1）	SSRY21	9.6357	0.0192	0.7125	0.1335
qDIc3-1	3	138.91	NS82（1）-NS57（1）	NS82	14.7523	-0.0282	0.4376	0.6481
qDIb3-2	3	144.91	NS57（1）-NS82（1）	NS57	5.3704	0.1154	-0.8916	0.2201
qDIc3-2	3	144.91	NS82（1）-NS57（1）	NS57	6.5436	0.0738	-0.8409	0.1079
qDIc3-3	3	150.91	NS82（1）-NS57（1）	NS57	15.3712	-0.0364	0.4459	0.653
αDIc4-1	4	12.01	SSRY149a（2）-SSRY149（1）	SSRY149	10.8485	0.2122	-0.5763	0.6052
qDIb4-1	4	12.01	SSRY149（2）-SSRY149（1）	SSRY149	3.0548	0.2003	-0.8204	0.521
qDIc4-2	4	16.01	SSRY149（2）-SSRY149（1）	SSRY149	10.2119	0.2192	0.9494	0.5355
qDIb4-2	4	18.01	SSRY149（2）-SSRY149（1）	SSRY149	4.5363	0.2036	-0.7894	0.5364
qDIc4-3	4	20.01	SSRY149（2）-SSRY149（1）	SSRY149	10.8289	0.2235	0.9322	0.536
qDIa4-1	4	79.21	SSRY149(3)-SSRY5(2)	SSRY149	5.7632	0.1944	-0.6048	0.5767
qDIc4-4	4	105.21	SSRY149（3）-SSRY5（2）	SSRY5	10.787	0.2929	-0.0723	0.3986
qDIb4-3	4	165.51	SSRY160（2）-NS57（3）	SSRY160	15.8282	-0.0806	-0.8988	0.0986
qDIc4-5	4	171.51	SSRY160（2）-NS57（3）	NS57	17.2017	-0.0685	-0.7379	0.0961
qDIb4-4	4	175.51	SSRY160（2）-NS57（3）	NS57	14.5642	-0.1032	1.6344	0.1759
qDIc4-6	4	177.51	SSRY160（2）-NS57（3）	NS57	12.4096	-0.0747	-0.7419	0.133
qDIb5-1	5	20.01	NS689（1）-NS890（1）	NS890	2.9596	-0.0981	1.5752	0.1228
qDIb6-1	6	22.91	SSRY5（3）-SSRY5（4）	SSRY5	5.1109	0.0939	-0.9053	0.1041
qDIb6-2	6	36.91	SSRY5（3）-SSRY5（4）	SSRY5	4.2964	-0.1149	1.732	0.1861
qDIc6-1	6	38.91	SSRY5（3）-SSRY5（4）	SSRY5	8.5273	0.0939	-0.7977	0.1731
qDIb6-3	6	42.91	SSRY5（3）-SSRY5（4）	SSRY5	5.6018	0.0766	1.6093	0.0989
qDIb7-1	7	32.01	SSRY141（2）-NS178（3）	NS178	3.2088	-0.1252	-0.7993	0.2465
qDIa8-2	8	10.01	NS82(2)-NS82(3)	NS82	2.5718	0.1116	-0.0527	0.1647

Population II



Branching height (BH) and leaf retention (LR)

BH and LR, as qualitative loci have been mapped on terminal of LG 15



Conclusion and ongoing work

A primary genetic map have been established in cassava used different population

QTls for SC FRY HI LR BH BLS have been developed, at least 16 QTLs is reliable and have main effects. 5 for SC, 7 for FY, 2 for HI and 2 for BLS. these QTLs have positive effect, higher PVE and nearby markers, Or the result can be repeated among 2-3 years , these QTLs could be used in MAS breeding

In this work , the map we constructed have not enough markers and it will affect the results. The PVE of QTL perhaps are higher than the real value. So the work we going to do is enrich the map dense use new molecular tools

Team

Yang Zixian, Wang Haiyan, Lu Cheng
Li Jie, Zhu Wenli, Fu Yuhua, Wang Huijun Zhao Chao, Xia zhiqiang, Lu Xiaojin, Zou Mielin, Ji Jiamin

Wenquan Wang

Co-operation partners:
Prof Kaimian Li and his group
Institute of Tropical Crop Genetic Resources, CATAS

Prof Peng Zhang
Institute of Plant Physiology and Ecology, Shanghai, CAS
Institute of Plant Sciences, ETH, Switzerland

What is the problems?

- The more effective marker tools?
  AFLP, DArT, EST,SNP etc.
- What can we do together combine biotechnology to conventional breeding
- Genomics and cassava breeding: from sequencing to EST, Mutants creating?

What kinds of collaborative project globally?

Thanks for your attention
and
welcome to visit China