

Population Structure of the Rice Composite Set

The population structure of the composite rice collection of 2757 accessions was investigated using 50 SSR markers through collaboration between IRRI, Agropolis-CIRAD, CIAT, EMBRAPA, CAAS, WARDA and Cornell University. To construct the composite rice set, nominations of materials were solicited from the genebank and other holdings among the partners and from within the breeding programs and INGER at IRRI. Accessions were chosen to balance coverage across 7 eco-regional gene pools that reflect centers of diversity and its dispersion throughout the world: South, East, SE, West Asia, Oceania, Africa plus Central and South America, and Europe plus North America. This set included special purpose sets of germplasm that have been extensively characterized, both phenotypically and by molecular markers, as well as reference lines for drought mapping populations and the Cornell panel for SSR analysis. The SSRs used are a subset of the Cornell panel developed by Coburn et al. (2002, *Crop Sci.* 42:2092-2099).

SSR Marker set

50 SSRs having repeat types:

- o 30 dinucleotide
- o 13 trinucleotide
- o 3 tetranucleotide
- o 4 complex

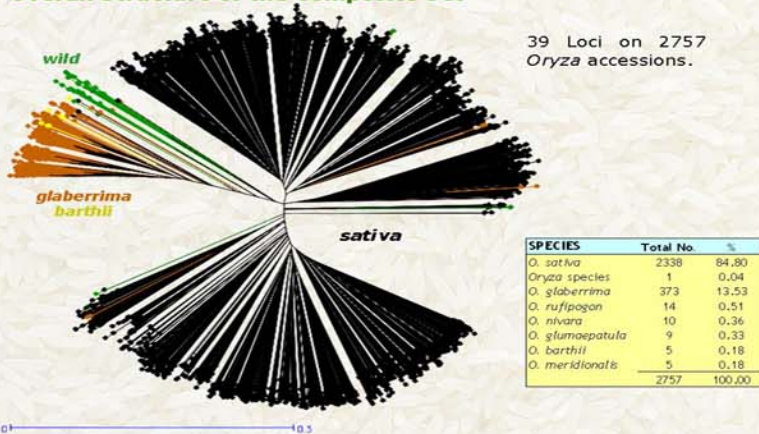
Split across the centers:

- o 24 at IRRI plus 6 (were CAAS)
- o 7 at CIRAD
- o 4 at CIAT and 3 at EMBRAPA
- o 6 at Cornell with WARDA

Statistical Analysis

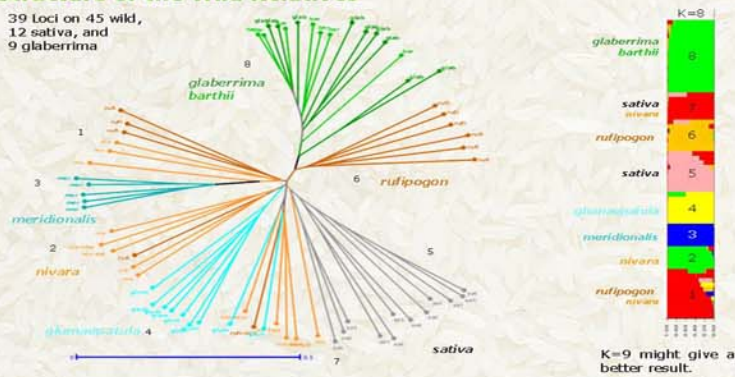
Statistics on the SSRs were computed using PowerMarker version 3.25. Clustering was accomplished using DARwin4 with the simple matching coefficient for distances followed by unweighted Neighbor Joining. Model-based inference of population structure was attempted using Structure 2.1 using a burn-in of 5,000 or 10,000, run lengths from 15,000 to 40,000, and a model allowing for admixture and correlated allele frequencies. Entries with <80% contribution from a single group are considered admixed.

Overall Structure of the Composite Set

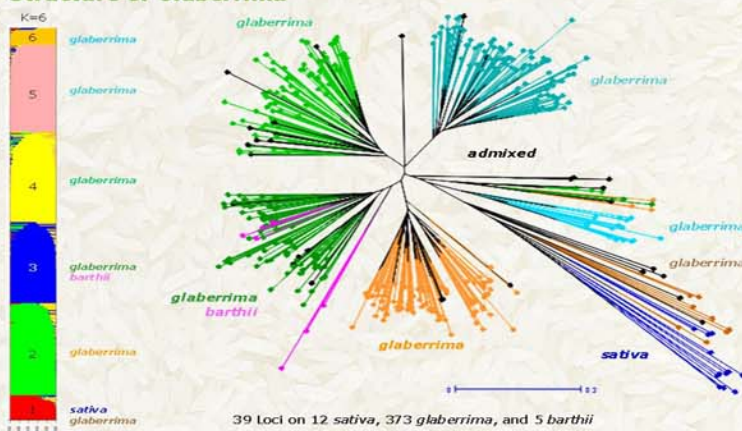


39 Loci on 2757 *Oryza* accessions.

Structure of the Wild Relatives



Structure of Glaberrima

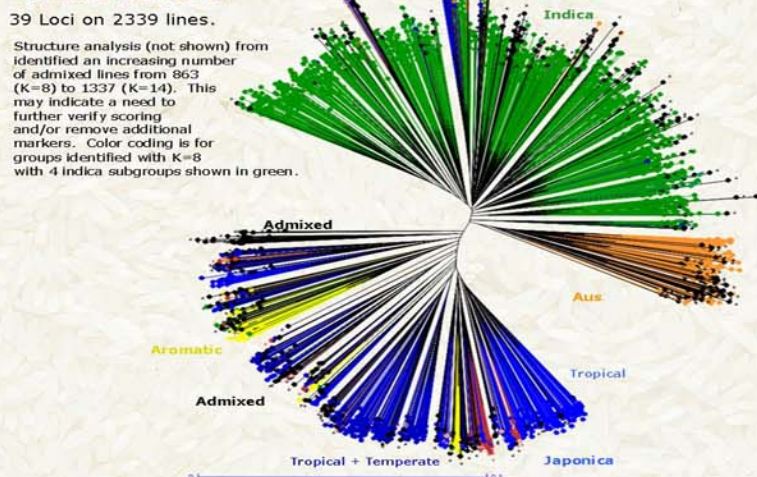


Summary statistics on SSRs:

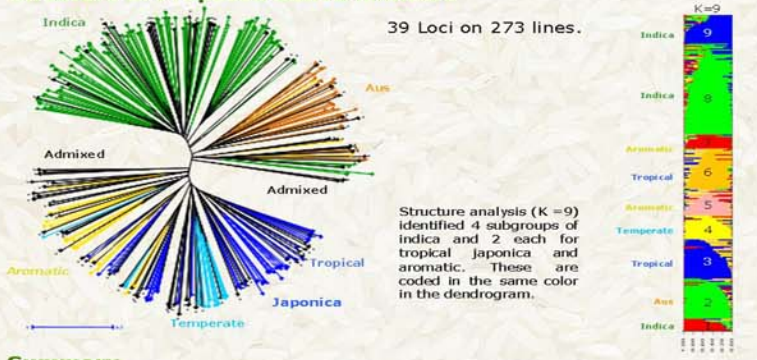
Marker	Major Allele Frequency	Genotype No.	Simple Size	No. of obs.	Allele No.	Availability	Gene Diversity	Heterozygosity	PK	F
RM101	0.337	150	2757	2282	43	0.854	0.834	0.135	0.821	0.839
RM358	0.413	49	2757	2443	19	0.888	0.731	0.150	0.693	0.794
RM1	0.171	150	2757	2155	32	0.782	0.914	0.078	0.908	0.915
RM125	0.383	37	2757	2488	14	0.908	0.717	0.053	0.689	0.928
RM154	0.125	105	2757	2313	38	0.839	0.926	0.052	0.920	0.944
RM284	0.635	19	2757	2529	7	0.917	0.552	0.025	0.515	0.955
RM24	0.352	44	2757	2219	21	0.809	0.784	0.034	0.771	0.857
RM65	0.317	53	2757	2212	22	0.802	0.803	0.085	0.779	0.895
RM1	0.160	160	2757	2615	33	0.948	0.916	0.223	0.911	0.756
RM14	0.361	26	2757	2532	19	0.855	0.732	0.039	0.705	0.988
OSR13	0.201	80	2757	2480	33	0.900	0.864	0.092	0.849	0.894
RM105	0.227	100	2757	2641	32	0.958	0.856	0.178	0.841	0.792
RM118	0.390	59	2757	2615	7	0.970	0.689	0.067	0.643	0.918
RM133	0.419	16	2757	2655	8	0.878	0.706	0.031	0.657	0.956
RM152	0.399	41	2757	2744	17	0.995	0.760	0.257	0.730	0.662
RM162	0.246	93	2757	2712	24	0.954	0.855	0.109	0.841	0.872
RM215	0.214	61	2757	2740	17	0.994	0.860	0.044	0.845	0.949
RM237	0.393	59	2757	2443	21	0.886	0.769	0.038	0.742	0.951
RM25	0.157	118	2757	2712	21	0.894	0.910	0.354	0.904	0.811
RM271	0.189	94	2757	2340	21	0.849	0.877	0.085	0.865	0.903
RM277	0.418	19	2757	2747	7	0.996	0.648	0.075	0.582	0.884
RM283	0.294	52	2757	2700	15	0.979	0.823	0.040	0.802	0.951
RM287	0.199	104	2757	2659	29	0.975	0.859	0.104	0.879	0.853
RM308	0.377	51	2757	2709	19	0.983	0.784	0.142	0.769	0.874
RM313	0.249	176	2757	2593	33	0.941	0.871	0.389	0.869	0.553
RM41	0.461	75	2757	2676	19	0.971	0.748	0.169	0.731	0.719
RM452	0.520	19	2757	2683	7	0.873	0.621	0.098	0.560	0.842
RM465	0.405	26	2757	2718	12	0.906	0.671	0.209	0.614	0.906
RM5	0.221	98	2757	2481	34	0.900	0.877	0.142	0.855	0.838
RM507	0.300	29	2757	2654	16	0.963	0.814	0.042	0.790	0.949
RM510	0.243	68	2757	2588	25	0.942	0.869	0.049	0.857	0.943
RM514	0.237	90	2757	2404	25	0.901	0.871	0.083	0.859	0.904
RM512	0.399	42	2757	2688	11	0.875	0.737	0.140	0.698	0.810
RM524	0.523	11	2757	2581	4	0.826	0.607	0.043	0.537	0.930
RM59	0.288	60	2757	2344	26	0.850	0.841	0.053	0.824	0.937
RM116	0.451	57	2757	2648	22	0.860	0.743	0.070	0.718	0.906
RM113	0.338	72	2757	2643	26	0.859	0.781	0.073	0.751	0.906
RM131	0.371	48	2757	2629	15	0.954	0.745	0.056	0.708	0.925
RM236	0.332	33	2757	2642	17	0.958	0.795	0.051	0.769	0.936
Mean_Pair	0.226	66	2757	2666,233333	20,667	0.931	0.790	0.096	0.763	0.866
Mean	0.310	74	2757	2508.9	23.3	0.9100	0.802	0.106	0.777	0.868

39 SSRs (yellow highlight) used for clustering and structure.

Structure of Sativa



Structure of Proposed Sativa minicore



Summary

These analyses of the structure within the composite rice collection are based on 39 of 44 scored markers. Six additional markers have been genotyped and are being scored (the markers assigned to CAAS were genotyped at IRRI). This additional data might help to clarify the relationships. The structures observed in these initial analyses are analogous to those for sativa (Garris et al, 2005, Genetics 169:1631-1638) and for glaberrima (Semon et al, 2005, Genetics 169:1639-1647). Allele calls should be checked for consistency, and the data re-analyzed to clarify the degree of admixture. Once publicly available, new tools developed specifically for modeling inbred population structure will be applied.

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