IJPS INTERNATIONAL JOURNAL OF PLANT SCIENCES
e ISSN-0976-593X Volume **11** | Issue 2 | July, 2016 | 291-298

DOI: 10.15740/HAS/IJPS/11.2/291-298
Visit us - *www.researchjournal.co.in*

RESEARCH ARTICLE

Identification of candidate markers associated with frying colour trait of potato

■ **PUNAM GHARGE AND I.R.H.J. (HERMAN) VAN ECK**

SUMMARY

The demand for potato products like chips and French fries is steadily increasing all over the world. Consumers and potato processing industries have become more stringent for quality along with higher demand of products. Hence, potato breeders are stimulated to develop new potato cultivars with more emphasis on quality traits. Potato breeding is mainly based on crossing two heterozygous parents or complementary parental clones and multi-year clonal selection to identify candidate cultivars with excellent quality. Hence, modern breeders like to use DNA/molecular markers to speed up the selection process by screening large numbers of genotypes at a time. To end up with a shortlist of candidate markers, three criteria; consistency, redundancy and multiple testing corrections were used for removal of false positive and redundant associations. In total, 62 marker-trait associations for frying colour were found to be informative after consistency over several sub traits with threshold level >3.3 in at least three sub traits. Finally, replacement analysis was performed to replace unmapped markers with mapped markers. 22 markers for frying colour trait were selected as a set of marker which could be used in Marker assisted breeding. It is clear that statistical approach provides a quick way of analyzing vast amounts of marker-trait associations to end up with short list of candidate markers. However, conformation is still needed to validate the markers.

Key Words : Potato, Candidate markers, Marker assisted selection, Marker-trait associations, Frying colour etc.

How to cite this article : Gharge, Punam and Van Eck, I.R.H.J. (Herman) (2016). Identification of candidate markers associated with frying colour trait of potato. *Internat. J. Plant Sci.*, **11** (2): 291-298, **DOI: 10.15740/HAS/IJPS/11.2/291-298**.

Article chronicle : Received : 13.03.2016; **Revised :** 10.05.2016; **Accepted :** 16.06.2016

Potato is an autotetraploid (2n=4x=48), displaying tetrasomic inheritance (Bradshaw *et al.*, 2008). As a result, genetic analysis is more complex as compared to diploid species and potato breeding is genetically not easy. The selection of improved cultivars with DNA-based markers will become more easy with the knowledge of genes that control the inheritance of agronomically important traits (Li *et al.*, 2008). In commercial breeding companies, time to market is a key factor. Depending on plant type and traditional breeding methods, it takes about 16-18 years from pre-breeding to commercializing a new variety and 12-15 years from original cross to commercializing a new variety (Dejong, 1983). Therefore, modern breeders like to use DNA/ molecular markers to speed up the selection process by screening large numbers of genotypes at a time. Since,

MEMBERS OF THE RESEARCH FORUM

Author to be contacted :
PUNAM GHARGE, Department of Agricultural Botany, College of Agriculture (M.P.K.V.) BARAMATI (M.S.) INDIA

Address of the Co-authors:
I.R. H.J. (HERMAN) VAN ECK, Laboratory of Plant Breeding, Plant Sciences Group, Wageningen University and Research Center, NETHERLANDS

DNA can be harvested early in the year from crop. Genotypes can be assessed for frying quality before harvest based on DNA markers, which saves a lot of time because the alternative is that potatoes have to be stored for 2 to 6 months in order to determine frying quality.

At present, there are numerous cost effective methods to generate huge amount of molecular marker data due to development in DNA technology and genetics. As a consequence, constructions of dense linkage maps or genome wide marker scans are cheaper per data point. Therefore, breeders look forward to identify candidate markers for interesting traits and thereby adopt marker assisted breeding (MAS) in introgression breeding, progenitor development and also for speeding up the selection process during the breeding programme. Apart from the application of marker assisted selection, the identification of candidate genes and characterization of the allelic variation for genes involved in interesting traits is the basic prerequisite for enhancement of potato varietal development (Visser *et al.*, 2009). In recent years, association mapping is the most widely used technique to identify marker-trait associations in various crops, for example in rice for agronomic traits (Zhang *et al.*, 2005). Identification of marker-trait associations is the first step towards the identification of candidate genes and the study of allelic variation associated with the traits of interest.

Quality is also one of the important aspects related to a crop as it determines the value in terms of price and consumer acceptance of final product. Quality parameters are different according to the end use of products. Potatoes are used for direct consumption, processed food products like chips and French fries, for industrial starch production and for animal feed (Gebhardt *et al.*, 2007). During the breeding of new potato cultivars, the breeding goals differ for these three main areas. According to these goals, there are different agronomic and quality characteristics that are considered in the selection process during breeding. In this section, more effort will be put into the description of the background of important traits to be analysed in this research for candidate marker identification. Moreover, an attempt is made to describe other crucial traits which also express the quality of tuber and are interlinked with our interested traits *i.e.*, frying colour.

Frying colour of potato chips or French fries mainly depends on the amount of reducing sugars (glucose and fructose) in the tuber. There are various factors which influence reducing sugar contents and frying colour such as: genotype of potato (Coffin *et al.*, 1987), duration of potatoes in cold storage (Stevenson and Cunningham, 1961), minimization of storage temperature (Gould *et al.*, 1979) and tuber maturity at harvest (Hope *et al.*, 1960). For the production of potato chips and French fries, high frying temperature is used which activatesthe non-enzymatic Maillard reaction between free aldehyde groups of reducing sugars (glucose and fructose) and free á-amino groups of amino acids and proteins (Li *et al.*, 2005). Due to this Maillard reaction, acrylamide is formed which causes unattractive chips with a bitter flavour. Darker frying colour of chips or fries is positively correlated with higher reducing sugar content. Storage of tubers at low temperature below 4-8 °C, delays the sprouting and leads to a breakdown of starch into reducing sugars (cold sweetening) in response to cold stress (Burton, 1969). Accumulation of sugars starts when there is an imbalance between starch degradation, synthesis and respiration of carbohydrates. Breeding for improved frying colour can be effective because frying colour is found to be a heritable trait. Heritability values for chip colour are reasonably high: 0.81 to 0.87 following cold storage (Cunningham and Stevenson, 1963) and 0.47 to 0.63 for sugar contents (Pereira *et al.*, 1994). Consequently, knowing the genes responsible for reducing sugar contents and frying colour and developing markers near the gene possibly will make potato breeding more efficient.

MATERIAL AND METHODS

Plant material :

Five phenotypic datasets (FT2006, FT2008, FT2009, MYML and a joint dataset FT2008_2009) recorded on 430 potato genotypes were used for identification of markers. These 430 cultivars were a representative set of the worldwide available potato germplasm and collected from five breeding companies and several gene banks. The core set contained 221 tetraploid potato cultivars and progenitor clones. The remaining 209 genotypes comprising parents of SH x RH mapping population, 17 extra tetraploid potato cultivars and 190 advanced breeding clones (approximately 40 of each company: Agrico research, Averis seeds, C Meijer, HZPC Research and Van Rijn). All five datasets contained different subsets of those 430 potato genotypes. All 430 genotypes were genotyped with AFLP markers.

Additionally a 384 SNP set was scored on the core set of 220 potato cultivars by (D'hoop *et al.*, 2010). In this research, the both marker sets were used.

Marker-trait associations :

For the removal of false positive and redundant associations, 99,225 marker-trait associations were analyzed. These associations were resulted from 27 phenotypic sub traits (27 frying colour) and 3675 (3364 AFLP + 311 SNP) markers [27*3675 = 99,225 data points]. The marker-trait association data was used from an analysis performed by D'Hhoop (2009). The *P*-values obtained for marker-trait associations were very small (as small as 10^{-13}) and, therefore, were transformed into -$\log_{10}$*p-value*s for better visibility of the significance level. Frying colour were measured several times per dataset. The combinations of year and time points are hereafter referred to as sub traits.

Removal of false positive and redundant associations :

In order to create a short list of candidate markers, marker- trait association were evaluated for removal of possible false positive and redundant associations. False positive associations create ambiguity to identify real associations as well as it increases time and cost of analysis. Therefore, three filtering steps were used to remove possible false positive associations of markers.

Consistency :

A marker is considered to be a false positive when it is significant (*p*- value < 0.05) in only one dataset. Consistency was assumed when a marker was significant in at least two dataset with -$\log_{10}p \geq 1.301$

Redundancy :

Redundancy refers to pairwise relationships between all pairs of markers in a given predictor dataset (Ooi *et al.*, 2006). Redundancy was assumed when two markers displayed an identical band pattern, mapped to the same position in mapping population and linked to the same gene in a QTL governing trait of interest. In that case, from both selected markers, one good marker will be used for analysis instead of both. Consequently, removal of redundant marker resulted in smaller number of markers, which reduces cost and also save time for further analysis. The redundancy of marker-trait associations were analysed by calculating marker-marker correlations. Intensity values of AFLP and theta values of SNP markers were used to calculate Pearson's correlation co-efficient (r) between a pair of markers (M-M). For this purpose, the bicorrelate function in Genstat (software) was used. However, high correlations do not always be a sign of true linkage between markers because sometimes high correlations between marker pair resulted from markers that were mapped on different chromosomes. Therefore, an additional criterion was applied to remove redundant markers *i.e.*, map position of markers.

Multiple testing correction :

A multiple testing correction was performed on remaining candidate marker-trait associations to reduce the number of false positive significant associations. The threshold for significance considering multiple testing (0.0005) was obtained by Bonferroni type of multiple testing correction threshold. Selections of informative markers were performed by using consistency and multiple testing analysis together to reduce the number of marker and retain only highly consistent markers across sub traits. Finally Replacement of unmapped selected markers with highly correlated mapped markers based on a marker which has larger fragment size, a map position, consistent -$\log_{10}p$-value and high correlation with selected marker. To identify highly correlated and mapped makers with these selected markers (top 30 markers), all significant (at ~=0.05) markers resulted from filtering false positive associations were paired. A table was produced by using marker-marker correlations between all significant ($p<0.05$) and selected markers. Map positions for these marker pairs were also given. If the marker pairs had a Pearson correlation co-efficient >0.3 they were selected for further analysis. If a marker has a small fragment size, then it is present at the bottom of the gel. Hence, cutting of the band is very complex. In addition, such small sized fragments have less sequence information. The -$\log_{10}p$-value from ChipCol_Oct8c_2008 and FrCol_Dec8c_2008 were used for better judgement of these selected markers because these two sub trait contain more significant markers. Only unmapped markers were replaced with mapped ones, which have good fragment size, good – log10*p*- value, high correlation (r).

RESULTS AND DISCUSSION

The present study was carried out to identify candidate marker-trait association for frying colour of

potato. Therefore, several filtering steps were used to remove false positive and redundant marker-trait associations to come up with a short list of candidate markers. In addition, finally selected markers were analyzed for a possible replacement with better markers which have a large fragment size, good *p*-value, map position, and high marker-marker correlation.

Removal of false positive associations :

From our finding the number of markers was decreased after each filtering step. A too stringent significance level for marker-trait associations might obscure false positives association. The first filtering step used to remove false positive marker-trait associations was consistency of markers across the datasets. The consistency criterion did not consider the markers significant at a *p*-value of 0.05 if it occurred in only one dataset. Less than half of the total markers were observed as significant in at least two datasets (consistent) with a p-value <0.05. The frying colour sub trait February 8C has the highest number of consistent markers while the frying colour sub trait April 8C has less consistent markers. The number of significant consistent markers per trait ranged from 666 to 1400 (Table 1).

Another criterion used to remove redundant marker-trait associations is redundancy. Redundancy involves two criterions: one is correlation between markers, so that redundant markers mapped to the same haplotype can be removed. The other is map position to remove redundant markers mapped to different haplotypes. We assumed that true linkage always give high correlation. Literature studies reported that the linkage yielded high correlation. Therefore, removal of one marker resulted in no loss of information (Cho and Dupuis, 2009). A high positive correlation between two markers means both markers present on same haplotype (coupling phase) and they are not segregating in another parent. Likewise, negative correlation between markers indicated that the marker-QTL associations present on different haplotypes (repulsion phase). If both highly correlated markers were found to be located within 1cM region of QTL of interest then removal of one of a set of linked markers would cause no loss of information. The correlation analysis yielded several highly correlated markers which were mapped at different chromosomes. These were called 'mismatches' by us. These mismatches suggested that something went wrong, either in the map position of one of the markers or in the correlation calculation. Therefore, map position information was used to detect first a possible mismatch of a marker pair. The first mismatch of a marker pair was observed at a Pearson's correlation co-efficient (r) = 0.85. This analysis was also resulted in identification of conflicting map position for 21 markers with high correlation co-efficient value. It is concluded that higher correlation was not always the result of true linkage. This conclusion was supported by studies of Nielsen *et al*. (2008) on how well linkage disequilibrium between markers predicts redundant associations. He also concluded that, the high linkage disequilibrium between markers does not indicate that the one marker is a direct substitute for another marker.

The third filtering step to remove false positive marker-trait associations is a multiple testing correction threshold. Our study ended with 16-220 markers per trait after applying the multiple testing correction thresholds. The highest number of markers was retained for the trait frying colour February 8c. This may be due to frying colour has enormous number of significant marker-trait associations (Table 1). Tatonetti *et al*. (2010) used multiple testing correction to score the candidate gene from association studies for warfarin doses. He

Table 1 : Overview of markers retained after Consistency (at least in two datasets with $-\log_{10}p \geq 1.301$) and multiple testing correction threshold analysis for frying color traits.

Filtering criteria	Consistent markers (at least in 2 datasets with p<0.05 or $-\log_{10} p \geq 1.3$)			Multiple testing correction (at least in 2 dataset with p< 0.0005 or $-\log_{10} p \geq 3.3$)		
Trait	AFLP	SNP	Total	AFLP	SNP	Total
Frying colour						
Oct_FrCol_8c	605	69	674	7	9	16
Dec_FrCol_8c	908	80	988	38	8	46
Feb_FrCol_8c	1291	109	1400	160	10	170
Apr_FrCol_8c	629	37	666	22	1	23
May_FrCol_8c	674	64	738	34	2	36
May_FrCol_4c	755	65	820	19	1	36

Table 2a: Results of selection of informative markers based on multiple testing and consistency using associations resulted from AFLP markers for combined frying color and chipping colour trait. Each column represents frying colour sub traits. Sum_all represents the summation of significant + non-significant $-\log_{10}(p)$ values. The column "significant P/27" shows the consistency of a marker over 27 sub traits. Values greater than 3.301 are highlighted.

Mnr	Marker name	FT2008 FryingCol_DecBc	FT2008 FryingCol_FEBRc	FT2008 FryingCol_APRRc	FT2008 FryingCol_MayAc	FT2008 FryingCol_DecBc	FT2008 FryingCol_FEBRc	FT2008 ChipCol_OctBc	FT2008 ChipCol_MayAcG	FT2008 ChipCol_FebSc	FT2008 ChipCol_MayBc	FT2008 ChipCol_MayAcR	FT2009 FryingCol_DecBc
M001344	E35_M50_133_19_GST	-3.858	-5.974	-5.506	-4.807	6.948	2.638	6.376	6.497	5.015	4.358	5.284	-0.940
M002850	P13_M42_127_12_GST	3.493	3.707	4.823	1.857	4.127	3.774	5.329	2.959	2.171	3.203	1.296	0.872
M000782	E33_M48_230_99_GST	-2.043	-3.718	-3.180	-2.958	3.472	0.968	5.476	4.558	5.441	5.004	3.448	0.464
M001017	E35_M49_183_87_GST	-2.795	-4.375	-4.746	-4.246	5.546	2.350	6.738	4.861	4.789	3.507	4.182	-0.731
M000444	E32_M54_430_74_GST	-1.754	-3.893	-3.499	-4.013	5.227	1.458	5.340	4.104	4.731	3.683	3.392	-0.440
M001610	E39_M36_557_16	-2.785	-5.394	-4.425	-3.651	4.321	1.400	5.313	5.330	7.689	5.174	4.721	0.229
M001267	E35_M42_230_57_GST	-2.554	-4.595	-5.189	-5.087	4.379	1.402	5.862	3.860	4.403	5.079	3.354	0.078
M002197	P13_M38_132_36_GST	-2.439	-3.305	-3.838	-3.504	3.802	1.863	3.751	4.402	3.349	4.055	2.969	-1.080
M001640	E39_M60_353_48_GST	-4.883	-4.626	-4.008	-2.631	5.058	4.815	4.383	4.782	3.387	3.961	2.359	-2.557
M002135	P13_M38_218_94_GST	2.088	3.706	4.224	4.759	3.814	4.711	4.157	3.601	4.034	2.591	4.194	1.393
M000370	E32_M54_070_60_GST	4.094	2.644	3.279	2.164	2.740	1.011	4.467	2.434	2.137	3.465	1.601	-0.471
M001417	E35_M62_163_40_GST	-2.030	-3.180	-4.660	-2.927	3.903	1.593	4.275	3.396	2.401	3.467	3.020	-1.399
M000354	E32_M51_377_17_GST	-2.926	-3.551	-6.258	-3.943	2.951	2.108	3.362	3.597	5.544	4.440	3.888	-0.075
M003286	P18_M41_117_02_GST	1.179	3.899	4.899	1.909	2.885	1.169	5.019	1.567	1.625	4.829	2.220	0.140
M002573	P13_M33_120_94_GST	4.697	4.628	1.538	1.838	4.128	4.798	4.563	4.468	2.768	5.042	3.501	0.055
M003015	P14_M41_139_15_GST	-3.526	-2.329	-3.746	-2.541	3.394	2.182	4.227	3.254	4.344	6.427	7.073	0.130
M000292	E32_M51_028_91_GST	-0.777	-3.197	-3.578	-2.869	2.901	1.222	3.989	3.818	5.828	2.377	2.501	-0.188
M001483	E38_M60_115_92_GST	3.642	3.355	1.888	2.559	4.735	2.461	4.116	3.963	2.354	2.820	2.628	-0.099
M001284	E38_M42_313_98_GST	4.339	2.036	2.705	1.254	2.579	2.051	4.733	1.917	0.943	4.306	0.883	-1.354
M002298	P13_M40_237_01_GST	2.024	2.521	3.953	4.316	2.948	3.485	2.780	3.137	6.183	2.435	3.308	0.397
M000028	E32_M41_141_16_GST	-1.978	-2.642	-2.681	-2.266	4.066	1.070	3.483	1.843	3.136	2.750	2.380	-0.017
M001410	E35_M62_165_10_GST	-1.018	-2.087	-4.253	-1.475	2.859	1.256	3.819	3.171	3.381	4.561	1.464	0.125
M000716	E33_M40_315_00_GST	-1.267	-3.377	-2.131	-3.016	4.628	0.712	2.465	3.708	3.862	2.609	0.998	0.179
M000695	E33_M40_175_84_GST	-2.748	-4.494	-3.041	-1.838	4.818	1.630	3.309	3.288	2.056	4.520	1.324	0.059
M001384	E35_M62_032_29_GST	-1.974	-3.550	-3.267	-1.799	4.552	2.480	3.332	2.163	2.432	2.196	1.240	-0.548
M001289	E35_M42_310_75_GST	2.779	2.889	2.654	1.546	3.287	2.109	3.878	3.241	1.501	3.638	1.541	-0.314
M002791	P13_M40_272_14_GST	0.243	0.191	-0.282	0.026	0.104	0.048	0.007	0.024	0.435	0.102	0.025	-0.202
M001197	E35_M61_283_20_GST	0.231	0.993	0.918	1.087	0.928	0.538	0.898	0.723	0.868	0.613	0.925	0.159
M001003	E35_M49_147_28_GST	-2.960	-4.278	-2.444	-3.148	3.780	3.030	3.961	4.829	1.872	3.696	2.938	-0.289
M002809	P13_M40_319_56_GST	5.569	4.340	0.888	1.284	3.228	2.864	4.595	2.286	1.437	1.621	1.633	0.578
M003020	P14_M41_210_29_GST	-1.574	-2.447	-1.429	-0.482	3.919	3.079	3.463	2.083	0.943	3.669	1.069	-0.022
M002081	E45_M60_149_41_GST	-1.951	-3.052	-3.212	-2.977	3.128	1.395	3.698	5.623	4.214	4.326	2.720	0.098
M001397	E38_M62_091_23_GST	2.259	2.827	2.518	3.131	2.636	2.623	3.665	3.528	1.807	4.498	1.862	-0.754
M000498	E33_M60_232_18_GST	3.327	2.853	2.638	2.277	3.028	2.269	3.779	3.613	2.519	4.297	2.337	-1.011
M002700	P13_M36_316_51_GST	-2.703	-0.669	-1.135	-0.949	1.732	1.670	1.052	0.306	0.561	2.250	0.601	-0.371
M002141	P13_M33_243_01_GST	2.948	2.080	1.324	0.320	2.228	2.554	2.349	1.108	1.033	1.000	1.498	0.973
M000414	E32_M54_222_15_GST	1.280	2.381	1.032	2.998	4.398	2.049	1.749	3.513	3.752	1.588	0.832	0.723
M000287	E32_M51_088_89_GST	-1.837	-2.552	-1.978	-1.301	2.328	3.594	2.969	1.721	2.596	1.939	2.153	-0.850
M000525	E32_M61_083_43_GST	-2.175	-2.787	-2.547	-2.128	5.981	2.403	3.146	3.057	5.502	4.526	3.127	-1.595
M000130	E32_M48_339_88	-0.090	-0.021	-0.892	-0.339	0.586	0.251	0.019	0.308	0.111	0.121	0.553	-0.779
M000144	E32_M48_393_12_GST	0.573	0.119	0.422	0.433	0.582	0.232	0.205	0.278	0.132	0.328	0.220	0.122
M002066	E45_M60_177_92_GST	-1.105	-1.199	-0.110	-0.048	0.031	0.119	0.033	0.419	0.304	0.858	0.456	-0.912
M001638	E38_M48_136_99_GST	1.000	0.248	0.848	0.041	0.012	0.208	0.371	0.071	0.298	0.320	0.083	-0.038
M001321	E38_M50_111_72_GST	0.351	0.539	0.248	0.570	1.717	0.540	0.700	0.559	1.445	0.815	0.934	-0.082
M000388	E32_M54_134_41_GST	-0.907	-1.498	-2.569	-0.481	2.274	1.552	3.903	3.453	2.158	5.957	1.426	0.550
M001976	E45_M59_173_97_GST	0.254	0.062	0.855	0.184	0.998	0.392	1.517	0.725	1.368	1.343	0.738	0.159
M001627	E38_M48_096_14_GST	0.129	1.479	0.385	0.323	1.424	2.901	1.526	0.768	1.298	1.454	0.396	-0.065
M000087	E32_M48_168_83_GST	-2.608	-5.044	-4.310	-2.307	2.777	1.825	3.177	3.996	1.729	2.735	1.843	0.464
M000894	E33_M40_167_04_GST	-4.035	-4.229	-1.844	-1.345	5.977	2.191	1.131	2.897	1.986	1.429	1.885	-0.884
M002965	P14_M41_079_61_GST	-1.147	-3.777	-1.544	-0.955	4.648	2.332	1.316	2.705	0.785	1.343	1.610	-0.547
M002024	P13_M40_070_50_GST	1.094	2.780	0.937	1.362	2.047	2.701	2.544	1.331	1.813	1.750	2.702	0.519
M003335	P13_M41_308_81	4.208	2.754	2.643	1.492	1.921	0.736	3.063	1.408	3.115	3.130	1.725	0.449

Mnr	FT2009 ChipCol_OctBc	FT2009 ChipCol_FebBc	FT0809 FryingCol_DecBc	FT0809 ChipCol_OctBc	FT0809 ChipCol_FebBc	[illegible] FryingCol_DecBc	[illegible] FryingCol_FEBRc	[illegible] FryingCol_APRRc	[illegible] FryingCol_MayAc	[illegible] FryingCol_MayBc	[illegible] ChipCol_OctBc	[illegible] ChipCol_FebBc	[illegible] ChipCol_AprSc	[illegible] ChipCol_MayBc	[illegible] ChipCol_MayAcR	Sum_All
M001344	-0.703	-0.588	-0.490	-0.832	-0.647	7.597	6.559	5.569	2.304	3.601	2.020	0.460	1.473	1.881	1.714	85.
M002850	1.182	0.180	1.909	3.231	2.305	5.991	5.721	4.231	4.083	3.618	2.093	0.314	1.578	3.935	3.552	81.
M000782	0.288	0.739	0.231	-0.172	0.281	5.659	5.804	7.952	3.349	5.150	3.752	0.284	2.888	3.112	3.103	83.
M001017	-0.778	-0.470	-0.595	-1.042	-0.887	8.326	5.624	5.529	3.174	4.220	1.382	0.437	1.152	2.225	1.779	88.
M000444	-0.491	-0.388	-0.434	-0.993	-0.887	6.624	4.407	4.656	2.696	3.346	1.080	0.598	0.758	2.146	1.349	71.
M001610	0.459	0.532	0.262	0.597	0.457	4.633	3.097	2.050	1.390	4.619	1.518	0.267	1.577	3.308	2.879	73
M001267	0.063	0.059	0.192	-0.141	0.081	8.132	5.912	4.918	1.549	2.542	1.942	0.020	1.837	2.742	2.804	79
M002197	-0.825	-0.439	-0.722	-1.052	-0.495	3.080	3.407	4.540	3.552	2.793	1.268	0.882	1.173	2.508	1.788	66
M001640	-2.603	-2.406	-1.572	-1.015	-1.699	3.986	3.954	1.654	1.861	1.574	0.229	0.442	0.007	2.094	0.647	73
M002135	1.053	0.557	0.835	0.117	0.050	4.233	2.980	1.422	1.047	1.013	1.644	0.278	1.191	2.704	2.550	63
M000370	-0.118	0.014	-0.287	0.020	0.063	3.897	3.814	3.979	3.041	4.667	5.071	6.463	4.142	2.087	2.828	71
M001417	-1.303	-0.713	-0.903	-1.588	-0.921	7.920	10.026	9.573	5.632	3.707	2.020	1.294	0.593	0.878	1.072	64
M000354	0.283	-0.105	0.006	0.282	0.074	0.573	1.328	0.314	0.219	0.860	0.412	0.109	0.082	0.500	0.216	42.
M003286	0.082	0.186	-0.128	0.419	0.044	3.734	4.122	3.625	2.837	3.543	0.883	0.491	0.915	0.611	0.534	52.
M002573	0.105	0.084	-0.336	-0.189	-0.338	1.720	0.929	0.779	0.282	1.508	2.282	0.256	0.333	1.051	1.260	53.
M003015	0.429	0.580	-0.205	0.193	0.133	0.250	0.950	0.377	0.867	0.952	0.882	0.803	2.325	2.277	2.343	58.
M000292	0.313	0.208	-0.224	-0.337	-0.182	5.875	5.850	4.895	1.744	2.812	0.601	0.797	0.395	0.686	0.459	57.
M001483	0.270	0.413	-0.513	-0.360	-0.400	4.081	2.638	2.490	0.715	2.285	4.426	0.807	0.435	2.703	1.888	58.
M001284	-0.438	-1.028	-0.378	-0.078	-0.245	2.509	3.498	5.290	2.477	3.328	1.720	4.338	2.403	0.893	2.083	60.
M002298	0.388	0.619	0.380	0.193	0.181	1.407	1.617	2.215	6.321	1.860	2.657	0.504	2.584	2.056	3.525	63
M000028	-0.155	0.021	-0.147	-1.174	-0.434	9.128	7.424	7.961	4.227	4.335	3.235	2.197	1.340	2.728	2.533	75
M001410	0.120	0.130	0.489	-0.068	0.251	3.678	3.364	0.654	4.220	1.406	0.154	0.227	0.415	0.016	0.246	41
M000716	0.243	0.397	0.528	0.118	0.253	4.985	5.105	2.463	0.818	1.311	0.434	0.827	0.334	0.625	0.726	43
M000695	-0.391	0.057	0.095	-0.474	-0.049	3.408	4.573	2.012	0.451	1.603	0.686	2.191	0.362	1.373	0.432	51
M001384	-0.134	-0.146	-0.521	-1.425	-1.042	5.524	4.665	4.186	0.189	1.725	2.755	1.447	0.225	0.605	0.389	57
M001289	0.007	0.035	0.043	0.232	0.291	4.388	4.394	3.541	1.328	3.900	3.187	2.329	1.995	1.954	2.402	50
M002791	-1.039	-0.087	-1.431	-1.957	-0.983	1.516	0.978	1.492	1.827	1.184	4.007	4.364	4.525	3.550	4.745	35.
M001197	-0.204	0.822	-0.457	-0.159	-0.077	1.793	0.535	0.271	0.720	1.783	4.199	3.494	5.404	4.844	4.803	32.
M001003	-0.148	-0.208	0.152	0.621	0.844	0.092	0.138	0.073	0.307	0.080	0.342	2.980	1.078	0.189	0.327	44.
M002809	0.375	0.322	0.003	-0.081	-0.309	4.558	3.516	2.215	1.176	1.122	0.155	0.965	0.025	0.745	0.911	47.
M003020	-0.284	0.213	-0.512	-0.637	-0.229	2.789	4.397	3.774	2.353	3.027	3.209	1.984	3.104	1.374	2.549	54.
M002081	0.138	0.388	0.156	0.678	0.485	3.301	1.509	1.409	0.885	1.807	1.705	0.091	1.725	3.228	2.881	55.
M001397	-0.040	0.112	0.032	0.308	0.238	3.191	2.925	3.155	1.690	3.353	2.882	2.414	2.215	3.093	3.550	61.
M000498	-0.469	-0.358	-0.026	0.209	-0.099	1.790	1.865	1.130	0.647	0.355	0.154	2.108	0.239	0.117	0.081	43
M002700	-0.286	-0.698	-0.565	-0.520	-0.515	2.205	1.479	1.615	3.515	2.305	1.952	1.867	4.075	4.520	3.397	44
M002141	0.262	-0.032	-0.259	-0.348	-0.251	3.090	1.902	4.144	1.694	0.616	4.626	0.581	4.377	1.020	3.332	45
M000414	1.375	0.998	1.687	1.580	2.024	0.799	1.571	0.284	1.292	0.305	0.939	7.021	0.445	0.326	0.029	47
M000287	-0.523	-0.830	-0.456	-0.319	-0.449	3.908	5.087	2.877	2.540	3.310	2.436	0.540	0.942	1.243	1.484	51
M000525	-0.028	-0.953	-0.580	-0.875	-0.465	3.026	3.385	1.347	1.604	1.608	0.013	0.198	0.534	1.073	0.026	55
M000130	-0.484	-0.396	0.080	-0.170	-0.040	0.279	0.089	0.523	0.011	0.283	3.041	7.156	4.023	0.839	3.715	35
M000144	0.053	0.176	-0.081	-0.098	-0.253	2.014	2.463	3.615	1.376	0.133	4.528	0.644	4.149	0.206	2.484	28.
M002066	-1.248	-2.270	-1.004	-0.343	-0.619	1.459	0.672	0.402	0.672	1.181	3.587	0.051	1.807	3.626	3.744	27.
M001638	-0.257	0.117	-0.044	-0.101	0.089	0.558	1.680	2.172	4.209	0.783	2.780	4.163	4.725	1.313	2.425	29.
M001321	0.092	-0.318	-0.154	0.054	-0.303	2.544	0.605	2.413	1.795	2.112	3.310	1.390	2.435	4.320	3.762	33.
M000388	0.469	0.813	0.691	0.007	0.412	2.067	0.756	0.121	0.883	0.131	0.146	0.506	0.142	0.212	0.074	34.
M001976	0.287	0.143	0.903	1.028	0.420	3.740	5.201	4.763	2.238	0.861	0.573	1.479	0.888	0.859	2.868	34.
M001627	-0.248	-0.016	0.221	-0.024	0.073	3.799	2.876	3.735	5.055	2.280	1.574	0.446	0.392	1.895	1.490	38.
M000087	0.387	0.746	0.452	0.231	0.302	0.098	0.236	0.098	0.232	0.017	0.468	0.241	1.109	0.788	0.776	39
M000894	-1.077	-0.912	-0.216	-0.165	-0.242	0.878	1.969	1.918	0.945	0.087	1.420	0.087	1.555	0.030	0.054	41
M002965	-1.156	-0.511	-0.842	-1.349	-0.754	4.104	3.727	1.931	1.996	2.609	1.672	0.381	0.044	0.692	0.335	44
M002024	1.220	1.151	-0.230	-0.090	-0.125	5.115	5.329	2.924	3.964	1.295	0.728	0.288	0.555	0.692	0.382	46
M003335	0.247	0.798	-0.345	0.070	0.134	4.871	4.947	2.517	1.190	1.302	1.147	0.193	0.437	0.495	0.459	46

corrected *p*- values using conservative Bonferroni multiple hypothesis correction Another difference is that in Tatonetti *et al*. (2010) studies, the consistency across datasets was not considered.

Selection of informative markers :

In this study, -10 log transformed *p*-values resulting from marker-trait association analyses were used. With 3.3 cut off *p*-value in at least 3 datasets, 52 AFLP and 10 SNP markers consistent across 27 frying colour sub traits were identified (Table 2a and 2b). Consistency of markers varied from 3 to 14 for AFLP markers and 3 to 12 for SNP markers for frying colour traits. When the first 10 selected markers of frying colour (Table 2a) were traced to map positions, 6 markers were mapped on SH mapping parent at 16.6 cM, Bin 21 on chromosome 9. It is a centromeric region. Studies of Mendenze *et al*.(2002); Li *et al*.(2005) and Gebhardt *et al*. (2007)have reported that an 'apoplastic InvGE/GF locus is present on chromosome 9. This locus consists of duplicated

Table 2b: Selection of SNP markers based on multiple testing and consistency for combined frying colour and chipping colour trait. Each column represents frying color sub traits. Sum_all represents the summation of significant + non-significant –log$_{10}$ (*p*) values. The column "significant P/27" shows the consistency of a marker over 27 sub traits. Values higher than 3.301 are highlighted.

		FT2006				FT2008								FT2009				FT0809			MYML											
Mnr	Marker name	FryingCol_Dec8c	FRyingCol_FEB8c	FRyingCol_AFR8c	FRyingCol_May4c	FryingCol_Dec8c	FRyingCol_FEB8c	ChipCol_Oct8c	ChipCol_May8cG	ChipCol_Feb8c	ChipCol_May8c	ChipCol_May4cR	FryingCol_Dec8c	ChipCol_Oct8c	ChipCol_Feb8c	FryingCol_Dec8c	ChipCol_Oct8c	ChipCol_Feb8c	FryingCol_Dec8c	FRyingCol_FEB8c	FRyingCol_AFR8c	FRyingCol_May4c	FryingCol_May8c	ChipCol_Oct8c	ChipCol_Feb8c	ChipCol_Apr8c	ChipCol_May8c	ChipCol_May4cR	Sum_All	Significant P/27
M003371	Contig11267_741	-4.482	-5.389	-4.264	-3.058	-5.319	-3.377	-4.444	-2.651	-3.031	-2.084	-2.398	-5.002	-6.966	-4.903	-5.848	-6.677	-5.588	-2.381	-2.700	-0.989	-0.504	-0.465	-0.441	-0.329	-0.322	-0.677	-0.561	83.839	12
M003468	Contig11267_612	4.962	4.684	3.694	2.913	4.131	2.259	3.291	1.210	1.916	2.391	1.915	2.822	5.243	3.703	3.982	5.471	4.008	2.975	3.049	1.849	0.728	0.132	0.514	0.462	1.910	1.682	1.750	73.646	9
M003585	Contig10534_1698	3.573	4.384	1.319	0.787	2.129	3.433	4.199	2.060	0.982	2.478	0.617	4.737	4.285	2.863	4.424	5.100	2.885	0.575	1.992	1.594	0.121	0.147	0.861	0.114	0.390	0.111	0.875	57.034	8
M003477	Contig17320_576	4.101	2.903	4.137	3.560	2.253	2.670	3.202	1.259	0.973	3.036	2.070	3.878	3.147	2.947	3.934	4.387	3.168	1.278	1.819	1.941	1.233	0.186	0.600	0.375	0.463	0.437	1.369	61.327	6
M003448	Contig21066_584	1.344	3.080	2.123	2.451	2.173	2.788	2.436	1.823	1.073	1.143	1.599	3.632	3.119	3.892	3.943	3.727	4.114	1.801	1.256	1.009	0.464	-0.076	0.930	0.568	0.345	0.468	0.444	51.823	5
M003626	Contig10591_647	2.589	2.979	1.854	2.785	2.378	3.806	4.010	1.821	1.359	3.158	2.470	3.641	3.207	1.835	3.871	4.444	2.963	0.628	0.995	0.222	0.311	0.083	0.202	-0.013	0.364	-0.070	0.773	52.829	5
M003428	Contig10739_640	-3.062	-3.134	-1.926	-1.644	-1.497	-1.113	-4.969	-1.132	-2.621	-1.465	-1.898	-2.290	-3.174	-2.891	-2.228	-4.415	-3.382	-2.393	-1.946	-1.324	-0.766	-2.201	-1.538	-2.331	-3.571	-1.752	-1.097	60.228	4
M003405	Contig14342_319	0.084	-0.619	-1.688	-1.545	-1.922	-0.491	-3.573	-1.001	-2.643	-2.845	-1.298	-1.986	-4.594	-2.865	-2.210	-4.698	-3.532	-2.934	-1.676	-2.787	-1.652	-1.668	-1.171	-0.519	-1.147	-0.857	-1.833	50.533	4
M003367	Contig24388_293	-0.844	-1.669	-1.621	-1.427	-2.722	-0.966	-3.310	-1.237	-2.716	-1.391	-0.828	-3.704	-2.876	-1.798	-3.648	-3.659	-3.171	-1.195	-0.638	-0.520	-0.928	-0.222	-0.606	-1.785	-1.753	-0.272	-1.643	45.292	4
M003386	Contig11527_914	2.501	1.561	1.874	2.518	1.554	1.163	3.315	1.828	2.058	2.367	1.225	1.482	2.879	1.788	1.648	3.437	2.700	1.359	2.153	3.041	3.474	1.331	1.223	0.370	0.407	0.520	0.721	50.498	3

Mnr = Marker number, FT = Field trial, MYML = Multi year multi location, Chipcol = Chip colour

Table 3 : Final subset of markers associated with frying colour. Marker name (M1) represents the final selected markers after replacement analysis; likewise, marker name (M2) contains the rejected markers that are previously selected after consistency across sub traits and backward selection. Correlation is a correlation co-efficient between M1 and M2 used as a replacement criteria. Map position shows chromosome number of M1-M2. cM represents centimorgan distance of M1-M2; LG is a linkage group of M1 and bins is a bin position of M1 on linkage group. The size of marker fragment, presence/absence data availability, allele frequency and –log10P valueare replacement criterion and the values in these columns belonging to "M1". The markers in M1 column replaced or not are shown in last column by yes/No.Absence of information is indicated by N/A.

Marker name (M1)	Marker name (M2)	Correlation	Map position (Chromo.No.)	cM	LG	Bins	Size of marker fragment	Presence/Absence Data	Allele frequency	$-\log_{10}$(P)_ ChipCol_Oct8c_2008	$-\log_{10}$(P)_FrCol_Dec8c_2008	M1 selected after replacement
E36_M62_091_23_GST	E32_M54_070_60_GST	0,72	9-unmapped	24.5-	RH09	B031	91,23	Y	34,51	3,665	2,636	Yes
E36_M50_242_42_GST	E32_M51_377_17_GST	0,63	5-unmapped	35.6-	RH05	B044-B046	242,42	N/A	N/A	1,580	2,262	Yes
E32_M54_430_74_GST	E32_M51_086_91_GST	0,62	9-unmapped	16.6-	SH09	B021	430,74	N/A	N/A	5,340	5,227	Yes
E45_M59_265_65_GST	E32_M51_377_17_GST	0,61	5-unmapped	31.3-	SH05	B043	265,65	N/A	N/A	0,427	0,724	Yes
P14_M41_199_15_GST	E32_M51_377_17_GST	0,54	5-unmapped	33.5-	SH05	B046	199,15	Y	79,11	4,227	3,394	Yes
E36_M42_230_57_GST	E33_M40_175_84_GST	0,53	9-unmapped	16.6-	SH09	B021	230,57	N/A	N/A	5,862	4,379	Yes
E33_M36_092_73_GST	E32_M54_070_60_GST	0,37	9-unmapped	24.5-	RH09	B031	92,7	Y	78,40	1,710	1,106	Yes
Contig16731_528	P18_M41_117_02_GST	0,34	3-unmapped	31.5-				N/A	N/A	-0,988	-1,073	Yes
Contig10343_128	E36_M62_082_29_GST	0,34	12-unmapped	43.1-				N/A	N/A	-1,334	-0,565	Yes
Contig10739_640	E39_M36_557_16	0,32	unmapped-unmapped	-				N/A	N/A	-4,969	-1,497	Yes
Contig22158_852	E39_M36_557_16	-0,31	10-unmapped	11.5-				N/A	N/A	2,542	2,913	Yes
Contig12261_37	Contig10534_1698	-0,37	2-unmapped	39.2-				N/A	N/A	-1,352	-0,384	Yes
Contig15682_565	E36_M62_082_29_GST	-0,39	12-unmapped	43.1-				N/A	N/A	1,778	0,723	Yes
Contig13004_844	E39_M36_557_16	-0,41	unmapped-unmapped	-				N/A	N/A	1,254	1,807	Yes
Contig11267_612	Contig11267_741	-0,65	2-2	0.8-2.3				N/A	N/A	3,291	4,131	Yes
E36_M62_165_10_GST			7	53,9	SH07	B070	165,1	N/A	N/A	3,819	2,859	No
P12_M40_237_01_GST			unmapped				237,01	Y	10,56	2,780	2,945	No
P13_M33_180_94_GST			unmapped				180,94	Y	23,94	4,563	4,128	No
P13_M42_187_12_GST			unmapped				187,12	Y	30,52	5,329	4,127	No
Contig11267_741			2	2,3				N/A	N/A	4,444	5,319	No
Contig17320_576			unmapped					N/A	N/A	3,202	2,253	No
Contig10534_1698			unmapped					N/A	N/A	4,199	2,129	No

invertase gene invGE and invGF which colocalizes with cold induced sweetening QTL sug9.This QTL present in between 3-8cM distance which is not a centromeric region. Another thing is that InvGE/GF gene is a berry specific gene and thus, cannot influence chip quality (Anne-marie Wolters, personal communication). Therefore, there may be other genes in centromeric region which might be associated with chip quality.

Final selection of markers :

The markers selected from consistency across sub trait analysis were analyzed for replacement by using several criterion like map position, high M-M correlation, good *p*-values, larger fragment size. Because these criteria saves lot of our further work like mapped marker easily find back, higher fragment size is easy to excise from gel and *p*-values provides assurance about quality of marker. Short size of a marker fragment resulted in short DNA sequence which can affect designing of PCR primers. Another reason to select large fragment size markers is less chances of multiple fragment extraction due to clear separation of band at the top of gel. In total, 22 markers are finally selected for frying colour. For example, marker E32_M51_086_91_GST was replaced with E32_M54_430_74_GST because marker E32_M54_430_74_GST was highly correlated (r = 0.62) and has a map position on chromosome 9 at 16.6 cM. The fragment size of 430 nucleotide of E32_M54_430_74_GST marker is much bigger as compared to marker E32_M51_086_91_GST. Hence, the marker fragment present on the top level on a gel which is easy to excise due to clear separation between different allelic bands of a marker. It reduces the chances of multiple fragment extraction during conversion of marker into simple easy to use marker. Another reason to select marker E32_M54_430_74_GST instead of E32_M51_086_91_GST was more significant association of E32_M54_430_74_GST with frying colour. Some markers were not replaced with other markers because of their good fragment size, allele frequency and good *p*-values. For example, Marker E36_M62_165_10_GST was not replaced with another markers because marker E36_M62_165_10_GST have map position 53.9cM on chromosome 7, fragment size of 165 nucleotides and good *p*-values (Table 3).

Mostly AFLP markers were replaced with SNP markers although SNP markers were unmapped. It might be due to theSNP markers have 50 nucleotides known sequence. During blasting, a very few matching segments with SNP marker sequence from genome sequence will be obtained as compared to AFLP marker. Therefore, it is easy to find back SNP marker on the potato genome sequence. For AFLP markers, only the primer sequences with 3 additional nucleotides were known. Therefore, too many matching segments of DNA sequence will be obtained from blasting to the potato genome sequence. Furthermore, AFLP markers are less suitable for marker-assisted selection, allele frequencies studies(Brugmans *et al.*, 2003). Also, AFLP markers are too expensive and laborious.

Conclusion :

A statistical approach provided a quick way of analyzing marker-trait associations for candidate markers associated with frying colour traits. The consistency across sub traits combined with multiple testing correction threshold analysis is helped to identify markers with consistent associations of candidate markers for frying colour trait. As our result is only based on statistical analysis. Therefore, for assurance, there is need to sequence these markers and blast the sequencing result against potato genome to obtain the correct map position.

Acknowledgement :

Author are thankful to Dr. Bjorn Hoop, Peter Vos , Dr.Chris Maliepaard, Dr. Herman van Eck Professors, Department of Plant Sciences, Wageningen University and Research Center(WUR), The Netherlands, for there valuable guidance, advice and motivation for this work.

REFERENCES

Bradshaw, J., Hackett, C., Pande, B., Waugh, R. and Bryan, G. (2008). Qtl mapping of yield, agronomic and quality traits in tetraploid potato (*solanum tuberosum subsp tuberosum*). *TAG Theoretical & Appl. Genet.*, **116**(2): 193-211.

Brugmans, B., van der Hulst, R.G.M., Visser, R.G.F., Lindhout, P. and van Eck, H.J. (2003). A new and versatile method for the successful conversion of aflp™ markers into simple single locus markers. *Nucleic Acids Res.*, **31**(10) : e55.

Burton, W. (1969). The sugar balance in some british potato varieties during storage. Ii. The effects of tuber age, previous storage temperature, and intermittent refrigeration upon low-temperature sweetening. *Potato Res.*, **12**(2) : 81-95.

Cho, K. and Dupuis, J. (2009). Handling linkage disequilibrium in qualitative trait linkage analysis using dense snps: A two-step strategy. *BMC Genet.*, **10**(1): 44.

Coffin, R., Yada, R., Parkin, K., Grodzinski, B. and Stanley, D. (1987). Effect of low temperature storage on sugar concentrations and chip colour of certain processing potato cultivars and selections. *J. Food Sci.*, **52**(3): 639-645.

Cunningham, C. and Stevenson, F. (1963) Inheritance of factors affecting potato chip colour and their association with specific gravity. *American J. Potato Res.*, **40**(8): 253-265.

D'hoop, B.B. (2009). Marker-trait associations in potato. Association mapping in tetraploid potato, Ph.D. Thesis, Wageningen University, The Netherlands, 71-87pp.

D'hoop, B.B., Paulo, M., Kowitwanich, K., Sengers, M., Visser, R., van Eck, H. and van Eeuwijk, F. (2010). Population structure and linkage disequilibrium unravelled in tetraploid potato. *TAG Theoretical & Appl. Genet.*, **121**(6) : 1151-1170.

Dejong, H. (1983). Inheritance of sensitivity to the herbicide metribuzin in cultivated diploid potatoes. *Euphytica*, **32**(1) : 41-48.

Gebhardt, C., Li, L., Pajerowska-Mukthar, K., Achenbach, U., Sattarzadeh, A., Bormann, C., Ilarionova, E. and Ballvora, A. (2007). Candidate gene approach to identify genes underlying quantitative traits and develop diagnostic markers in potato.

Gould, W., Hair, B. and Baroudi, A. (1979). Evaluation of potato cultivars before and after storage regimes for chipping. *American J. Potato Res.*, **56**(3): 133-144.

Hope, G., MacKay, D. and Townsend, L. (1960). The effect of harvest date and rate of nitrogen fertilization on the maturity, yield and chipping quality of potatoes. *American J. Potato Res.*, **37**(1) : 28-33.

Li, L., Paulo, M.J., Strahwald, J., Lübeck, J., Hofferbert, H.-R., Tacke, E., Junghans, H., Wunder, J., Draffehn, A., van Eeuwijk, F. and Gebhardt, C. (2008). Natural DNA variation at candidate loci is associated with potato chip colour, tuber starch content, yield and starch yield. *TAG Theoretical & Appl. Genet.*, **116**(8): 1167-1181.

Li, L., Strahwald, J., Hofferbert, H.R., Lubeck, J., Tacke, E., Junghans, H., Wunder, J. and Gebhardt, C. (2005). DNA variation at the invertase locus invge/gf is associated with tuber quality traits in populations of potato breeding clones. *Genet.*, **170**(2) : 813-821.

Menendez, C.M., Ritter, E., Schafer-Pregl, R., Walkemeier, B., Kalde, A., Salamini, F. and Gebhardt, C. (2002). Cold sweetening in diploid potato: Mapping quantitative trait loci and candidate genes. *Genetics*, **162**(3) : 1423-1434.

Nielsen, D.M., Suchindran, S. and Smith, C.P. (2008). Does strong linkage disequilibrium guarantee redundant association results? *Genet. Epidemiol.*, **32**(6): 546-552.

Ooi, C., Chetty, M. and Teng, S. (2006). Differential prioritization between relevance and redundancy in correlation-based feature selection techniques for multiclass gene expression data. *BMC Bioinformat.*, **7**(1): 320.

Pereira, A.D.S., Tai, G.C.C., Yada, R.Y., Tarn, T.R., Souza-Machado, V. and Coffin, R.H. (1994). Effect of selection for chip colour on some economic traits of potatoes. *Plant Breed.*, **113**(4) : 312-317.

Stevenson, F. and Cunningham, C. (1961). Chip colour in relation to potato storage. *American J. Potato Res.*, **38**(4): 105-113.

Tatonetti, N., Dudley, J., Sagreiya, H., Butte, A. and Altman, R. (2010). An integrative method for scoring candidate genes from association studies: Application to warfarin dosing. *BMC Bioinformat.*, **11**(Suppl 9): S9.

Visser, R., Bachem, C., de Boer, J., Bryan, G., Chakrabati, S., Feingold, S., Gromadka, R., van Ham, R., Huang, S., Jacobs, J., Kuznetsov, B., de Melo, P., Milbourne, D., Orjeda, G., Sagredo, B. and Tang, X. (2009). Sequencing the potato genome: Outline and first results to come from the elucidation of the sequence of the world's third most important food crop. *American J. Potato Res.*, **86**(6): 417-429.

Zhang, N., Xu, Y., Akash, M., McCouch, S. and Oard, J.H. (2005). Identification of candidate markers associated with agronomic traits in rice using discriminant analysis. *TAG Theoretical & Appl. Genetics*, **110**(4): 721-729.