

REPORTING RESULTS AND ASSOCIATED STATISTICS IN QUANTITATIVE GENETIC STUDIES

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Abstract: The aim of the research was to investigate the statistical methods used in reporting quantitative genetic models in flower, vegetable, fruit, grape, and shrub and tree studies. A systematic literature review was performed in June 2008 on Oxford Journals database. The search methodology was developed, the inclusion criteria of the titles in the study were imposed, and the variable of interest were defined. A number of four-hundred and thirty-five titles were identified by applying the search string. Thirty-five titles accomplished the inclusion criteria and were included into the study. The analysis of results revealed that almost one-third of paper did not have any keywords and the most frequent one was quantitative trait loci. More than fifty percent of the papers included into the results descriptive statistic parameters and frequencies. Less than half of the investigated papers used any method of statistical inference in analysis of the results. A comprehensive analysis is needed in order to investigate the trends of statistical methods reported by quantitative genetic studies on studied fields by inclusion into the study a wide range of available databases.

INTRODUCTION

The study of inheritance of those differences between individuals that are quantitative rather than qualitative is the objective of quantitative genetics (Falconer and Mackay, 1996). The concept was established by the work of Ronald Aylmer Fisher (1890 - 1962, statistician, biologist, geneticist) (Fisher, 1930; Haldane, 1932), Sewall Wright (1889 - 1988, geneticist) (Wright, 1921; Wright, 1931) and John Burdon Sanderson Haldane (1892 - 1964, geneticist) and has as goal the study of the contribution of genetic and environmental factors to observed variance (either within or between population) of particular traits (Walsh, 2001).

The top three fields (Weir et al., 2006; O'Hara et al., 2008) where quantitative genetic is applied are human genetics (Langefeld and Fingerlin, 2007), evolution (Noor and Feder, 2006) and breeding (Morgante and Salamini, 2003; Shook, 2006).

The quantitative genetics is used in breeding as method for development cultivars with better performance for the primary traits of interest (Hallauer, 2007). Three main steps are used on breeding (Dydley and Moll, 1969): 1. Experimental quantitative genetics study of population done in order to study the properties of the genes associated with quantitative variation; 2. Experimental breeding for testing the validity of the theory from 1; 3. Experimental breeding for identifying those consequences of breeding that cannot be predicted from the theory. A series of statistical estimators of the relative importance of the type of genetic variation and heritability has been developed and are used in making decisions

for all plant breeding stages. The main methods and/or parameters and their application in plant breeding could be classified as:

- ÷ Heritability (Lush, 1945; Holland et al., 2003; Nyquist, 1991);
- ÷ Genetic gain prediction (Eberhart, 1970; Empig et al., 1972);
- ÷ Epistasis estimation: inclusion of epistatic effects in the covariance of relatives (Cockerham, 1954; Cockerham, 1956; Cockerham, 1961), factorial analysis (Fasoulas and Allard, 1962; Russell, 1971; Russell and Eberhart, 1970) and generation mean analysis (Hayman, 1960);
- ÷ Selection indices: multiplicative index (Elston, 1963), rank summation index (Mulamba and Mock, 1978), multiplicative index (Compton and Lonquist, 1982), and retrospective index weight (Bernardo, 1991a);
- ÷ Testcross selection as early testing method (Bernardo, 1991b; Bernardo, 1992; Rodriguez and Hallauer, 1991);
- ÷ Recurrent methods for selection (Hull, 1945; Comstock et al., 1949);
- ÷ Assessment of diallel mating design (Baker, 1978; Marquez-Sanchez and Hallauer, 1970).

The quantitative genetics theory is the basic topic when the plant breeding methods are discussed (Baker, 1984; Betran et al., 2004; Mayo, 1987). The usefulness and importance of quantitative genetic in plant breeding, inclusive in horticulture, is undoubtedly (Lamkey and Lee, 1993; Acquah, 2006).

The aim of the research was to investigate the statistical methods used in reporting quantitative genetic models in flower, vegetable, fruit, grape, and shrub and tree studies published in the Oxford Journals database.

MATERIALS AND METHODS

A systematic literature review was performed in June 2008 in order to identify the papers of quantitative genetic in flower, vegetable, fruit, grape, and shrub and tree studies. The Oxford Journals database (Oxford University Press; <http://www.oxfordjournals.org/>) was search.

The following methodology was applied:

- ÷ Search string (keywords): Quantitative genetic* (Abstract | Title; words: all)
- ÷ Journals fields: Life Sciences, Mathematics & Physical Science
- ÷ Publication time: from November 1849 through September 2008
- ÷ Limitations of results: include all articles.
- ÷ Results format: standard & sort by best match.

A number of four-hundred and thirty-five titles were identified by applying the above methodology. The inclusion criteria of an article into the study were as follows:

- ÷ Method: quantitative genetic;
- ÷ Subject: flower, vegetable, fruit, grape, and shrub and tree studies;
- ÷ Type of article: original research;
- ÷ Type of access: access to the full paper.

The following variables were investigated: keywords (the first five ones when the article had more than five), descriptive statistic parameters (mean, standard deviation, range, maximum, minimum), frequency (absolute, relative, frequency distribution), heritability, analysis of variance, mapping quantitative trait locus, correlation analysis (correlation and

determination coefficient), coefficient of variation, inference statistic methods, and software used for analysing data and presenting results.

The data were summarized by using Microsoft Excel. The confidence interval associated to frequencies was calculated by using a method based on binomial distribution (Drugan et al., 2003; Bolboacă and Achimaş Cadariu, 2003).

RESULTS AND DISCUSSIONS

A number of thirty-five studies (8.05%, 95% CI [5.75 – 11.03], where 95% CI = 95% confidence interval for relative frequency) accomplished the inclusion criteria.

Three of the identified manuscript for the search string classified as original research proved to present software application used in quantitative genetics analysis: QTLNetwork 2.0 (Yang et al., 2007), mapping genome-genome epistasis (Cui and Wu, 2005), and QU-GENE (Podlich and Cooper, 1998).

The distribution on the fields and species of quantitative genetic models on the investigated sources accompanied by the reference is presented in Table I. Note that, even if the search string was applied for all publications since 1849, the “oldest” article that accomplished the inclusion criteria was published in 1994 and almost 34% of them were published in 2007. This trends could be explained by the limited access to the earlier publications included into Oxford Journals database and the access of the institution to the manuscripts published starting with 2005.

The analysis of the most frequent used keywords showed that ten out of thirty-five articles (28.57%, 95% CI [14.37 – 45.63]) did not contains any keyword even if there were considered original researches. The absence of the keywords could be explained by the policy of the journal regarding the instructions to authors and/or the methodology of indexing the articles.

Eleven keywords appear to more than one paper when first five keyword were investigated. The top-three most frequent keywords were: *quantitative trait loci* (twelve articles), *amplified fragment length polymorphism* (4 articles), *development* and *principal component analysis* (both with 3 apparitions). A series of seven keywords appear by two times as keywords in the investigated articles: *apple*, *Arabidopsis*, *domestication*, *flowering time*, *genetic variation*, *Phaseolus vulgaris*, and *Solanum lycopersicum*. The distribution of keywords follows the expectations, the most frequent one include one of the work used in search “quantitative”. The wide diversity of the research fields explains the absence of higher frequencies on keywords investigation. The most frequent keyword in investigated articles was the QTL (quantitative trait loci/locus) and the trend of these researches increase in the last years. This method seems to be used by many researchers even if its limits are known. Three problems are associated to the QTL analysis. First problem: the heritability associated with individual QTL is a small fraction of the heritability of the trait of interest, which is generally less than 50% (Kearsey, 1998). Second problem: when the environment and its interaction with genotype affect considerably the phenotypic of the trait, the efficiency of QTL could be small. Third problem: the accuracy of the QTL analysis is influenced by (Asíns, 2002): experimental design (e.g. type of segregation, population size, heritability of the trait, level of polymorphism of DNA markers, statistical methodology related to building the linkage map and to perform the QTL analysis (Carbonell and Asíns, 1996)), number of contributors of each quantitative trait locus to the total genotypic variance, percent of codominant markers, reliability of the order of markers in the linkage map, evaluation of the trait.

Table 1

Quantitative genetic models: distribution on fields and/or species		
No.	Field	Species (reference)
1	Flower	<i>Stylosanthes scabra</i> (Thumma et al., 2001) <i>Arabidopsis thaliana</i> (Menga et al., 2008) <i>Silene latifolia</i> (Jolivet, and Bernasconi. 2007; Meagher et al., 2005) <i>Ranunculus nodiflorus</i> (Noel et al., 2007) <i>Arabidopsis</i> (Pouteau et al., 2006) <i>Anemones</i> (Zamer et al., 1999) <i>Silene vulgaris</i> (Bratteler et al., 2006) <i>Convolvulus arvensis</i> L. (Westwood et al., 1997) <i>Scenico vulgaris</i> L. (Comes, 1998) <i>Primula sieboldii</i> (Yoshioka et al., 2004) <i>Capsella bursa-pastoris</i> L. (Linde et al., 2001) <i>Arabidopsis thaliana</i> (Jönsson et al., 2005)
2	Vegetable	Potato <i>Solanum tuberosum</i> L. (Ortiz and Peloquin, 1994; Fernández-del-Carmen et al., 2007) Tomato Unspecified (Seymour et al., 2002) <i>Lycopersicon</i> (Moyle, 2007) <i>Solanum lycopersicum</i> (Brewer et al., 2007) <i>Solanum pimpinellifolium</i> (Chaïb et al., 2007) <i>Lycopersicon esculentum</i> (Causse et al., 2002; Bertin et al., 2003) <i>Solanum lycopersicum</i> , <i>Solanum pennelli</i> (Bermúdez et al., 2008) Lettuce <i>Lactuca sativa</i> & <i>Lactuca serriola</i> acc. (Zhang et al., 2007) <i>Lactucosonchus webbii</i> and <i>Sonchus radicans</i> (Kim, 2007) Pea <i>Pisum sativum</i> (Weeden, 2007) Bean <i>Phaseolus vulgaris</i> (Papa et al., 2007) <i>Brassica rapa</i> (Lou1 et al., 2007)
3	Fruit	Peach (<i>Prunus davidiana</i> & <i>P. persica</i> (L.) Batsch) (Quilot et al., 2005) Apple (Unspecified) (Foster et al., 2003) Strawberries (<i>Fragaria</i>) (Sargent et al., 2004)
4	Grape	<i>Vitis vinifera</i> (Abbal et al., 2007)
5	Tree and shrub	<i>Metroxylon sagu</i> (Kjár et al., 2004) <i>Pteridium aquilinum</i> L. (Wynn et al., 2000) <i>Quercus laevis</i> (Klaper et al., 2001) <i>Manihot esculenta</i> (Cach et al., 2005)

The analysis of the statistics used in reporting quantitative genetic models on investigated sample revealed the followings:

- ÷ The distribution of the data, expressed as absolute or relative frequency (cumulative relative frequency) and graphical representations were used by almost 69% of the articles (95% CI [51.51 – 82.78]).
- ÷ The results are described by using descriptive statistic parameters as mean (arithmetic or harmonic), standard error of the mean, minimum and maximum by almost 66% of the articles (95% CI [48.65 – 79.92]).
- ÷ Correlation and/or determination (squared correlation coefficient) coefficients are used in order to quantify the relationship between traits. Fifty-four percent of the articles used one of this statistical parameters but the method (Pearson, Spearman, Kendall, Gamma) used for calculations is presented just in six cases (~ 32%, 95% CI [10.80 – 57.62]).
- ÷ Different methods on mapping quantitative trait loci were used in sixteen cases out of thirty-five (~ 46%, 95% CI [28.65 – 62.78]).
- ÷ The analysis of variance was applied in thirteen cases out of thirty-five (37%, 95% CI [20.08 – 54.20]).

- ÷ The heritability index was reported in 8 out of thirty-five cases (~ 23%, 95% CI [11.51 – 39.92]).
- ÷ The coefficient of variation was reported in 4 out of thirty-five cases (11%, 95% CI [2.94 – 25.63]).

Note that, a single paper reported from one to up to five of the above-mentioned statistics (four out of thirty-five papers).

The report of the descriptive statistics parameters is directly related to the quantitative trait locus analysis and mapping which is based on the association of different marker genotypes with their trait mean values (Sofi and Rather, 2007).

Almost forty-nine percent of the investigated articles reported results using one to up to four inferential statistics methods. The ANOVA and ANCOVA, Bonferroni, chi-square, Student t-test, linear and logistic regressions, Kruskal-Wallis test, Wilcoxon test, Tukey test, Mantel test, Mann-Whitney test, Duncan test were used as inference statistics instruments. Factorial analysis and principal component analysis methods have also been applied in data analysis. As expected, the inference statistics method reported in the investigated manuscripts are directly linked to the methods used in analysis of the quantitative traits. The statistical methods used for QTL analysis include Student t-test, analysis of variance (ANOVA), linear regression (the coefficient of determination from the marker explains the phenotypic variation arisen from the QTL linked to the marker), probability values, percent of phenotypic variation explained by QTL, etc. (Collard et al., 2005). The heritability, the ration of the additive genetic variance to the phenotypic variance (Nyquist, 1991; Holland et al., 2003), lost its importance due to its limits of generality (Hallauer, 2007).

Most of the paper reported results on the primary experimental data but a series of papers reported results on data collected from available databases. The following resources were used: Genoscope (http://www.cns.fr/cgi-bin/blast_server/projet_ML/blast.pl); National Center for Biotechnology Information databases (<http://www.ncbi.nlm.nih.gov/>); ExPaSy (<http://www.expasy.org/>); Unigene (<http://www.sgn.cornell.edu>); Solanaceae Genomic Network (<http://www.sgn.cornell.edu/>); WU-BLAST (<http://blast.wustl.edu>); KEGG (<http://www.genome.jp/kegg/>); SGN (<http://www.sgn.cornell.edu>); and Brassica rapa (<http://www.Brassica-rapa.org>).

Three statistical software were reported as being used for data analysis: JMP V 5.1 (<http://www.jmp.com/>), SPSS (<http://www.spss.com/>), and MVSP 3.1. (<http://www.kovcomp.co.uk/mvsp/>).

Fourteen dedicated software (two image processing and twelve quantitative genetic software) were used in data analysis: Scion Image (<http://rsb.info.nih.gov/nih-image>), Irfanview (<http://www.irfanview.com>), BLASTX (<https://pdc.usace.army.mil/software/blastx>), BLASTN 2.0 MPWashU (<http://blast.wustl.edu>), MAPMAKER (<http://www.mapmaker.com/>), Joinmap (<http://www.kyazma.nl/index.php/mc.JoinMap/>), APQTL (<http://www.kyazma.nl/index.php/mc.MapQTL/>), MapChart (<http://www.biometris.wur.nl/uk/Software/MapChart/>), Genescan (<http://genes.mit.edu/GENSCAN.html>), Genotyper, Genstat (<http://www.vsnl.co.uk/products/genstat/>), FDIST2 (<http://www.rubic.rdg.ac.uk/~mab/software.html>), Tomato Analyser (<http://www.oardc.ohio-state.edu/vanderknaap/>), and QTL Cartographer (<http://statgen.ncsu.edu/qtlcart/WQTLCart.htm>).

The present analysis on models and statistics reported in quantitative genetic papers showed that the approach is applied on all investigated fields with a high frequency on vegetable and flowers analysis on the investigated resource. The limits of the present research did not allow extrapolating the results to all published original research on quantitative genetics reported on fields of interest. The investigation of articles published just in Oxford Journals database, which could not be consider representative for all original articles on

quantitative genetics in investigated fields, is the first limit of the study. There was choosing to investigate just the proposed database due to limitation in terms of time, and resources and full text journals availability. The second limit refers the impossibility of inclusion into the study of some articles due to the access to full text (some articles needed a subscription or pay-per-article). The investigation just of the data presented in the abstract could be a solution but this was not our aim due to lack of detailed information given contained by an abstract. A similar analysis on other databases could be performing in order to obtain a comprehensive overview on statistical methods used to present the results of quantitative genetic analysis. This will be investigating in future researches.

CONCLUSIONS

The main method applied on investigated original article was quantitative trait loci analysis even if its limits are well known.

More than a half of the investigated sources did not include an inferential statistical analysis when the results of a quantitative genetic study are reported.

The results of the present study did not indicate the trends in reporting quantitative genetic on investigated fields due to investigation of a single journals database. A comprehensive analysis is intended to be perform in order to investigate the statistical methods in reporting quantitative genetic in fields of interest by analysing all available databases.

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