Quantitative trait loci and the study of plant domestication

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Abstract

Plant domestication ranks as one of the most important developments in human history, giving human populations the potential to harness unprecedented quantities of the earth's resources. But domestication has also played a more subtle historical role as the foundation of the modern study of evolution and adaptation. Until recently, however, researchers interested in domestication were limited to studying phenotypic changes or the genetics of simple Mendelian traits, when often the characters of most interest – fruit size, yield, height, flowering time, etc. – are quantitative in nature. The goals of this paper are to review some of the recent work on the quantitative genetics of plant domestication, identify some of the common trends found in this literature, and offer some novel interpretations of the data that is currently available.

Abbreviations: DRT – domestication related trait; QTL – quantitative trait locus.

Introduction

Plant domestication ranks as one of the most important developments in human history, giving human populations the potential to harness unprecedented quantities of the earth's resources. But domestication has also played a more subtle historical role as the foundation of the modern study of evolution and adaptation. Darwin explicitly identified domestication as the basis for his ideas of natural selection and evolution (Darwin, 1899), and many of his ideas about how natural selection might function are based on keen observations of the human-mediated selection of domesticated plants and animals. In fact, Darwin had good reason to look to domestication for an understanding of adaptation in nature. Unlike most natural cases of adaptation, studies of plant domestication have the potential to identify what selection pressures populations have responded to and infer how selection may have acted. Moreover, it has often been possible to pinpoint the geographic and phylogenetic origin of domesticates, thus allowing direct comparisons of descendents with their (usually extant) ancestors.

With only rare exceptions (e.g. Anderson et al., 1991; Dudley & Lambert, 1992; Cowie & Jones, 1998; Visser et al., 1998; Grant & Grant, 2002), studies of adaptation are restricted by the inability to observe selection in action over a meaningful period of time; the resulting changes are frequently the only clues biologists have with which to infer the processes involved in adaptation. Though focusing on domesticates alleviates many of the difficulties inherent in the study of adaptation, until recently researches interested in domestication were limited to studying phenotypic changes or the genetics of simple Mendelian traits, when often the characters of most interest – fruit size, yield, height, flowering time, etc. – are quantitative in nature.

The last 15 years, however, have seen an outpouring of data on the genetic basis of quantitative traits. Dozens, if not hundreds, of articles have investigated the number, location,

and effects of the chromosomal regions responsible for the phenotypic variation observed among organisms in the natural world. Whether for expediency or scientific curiosity, much of this research has focused on quantitative variation in crop plants, and a number of studies have specifically investigated traits thought to have been important in domestication. Two recent reviews highlight several of the major patterns that have emerged from the growing body of quantitative mapping studies in domesticated plants (Paterson, 2002; Frary & Doganlar, 2003) including the number, effect, and distribution of the quantitative trait loci (QTL) underlying domestication related traits (DRT), as well as similarities across species in the QTL involved in the domestication process. In the last two years, however, several new studies have helped to flesh out the patterns recognized by these reviews. These data reinforce many of the conclusions of earlier reviewers, but also allow us to extrapolate beyond the patterns recognized by those authors.

I will begin with a brief discussion of the major patterns present in QTL mapping studies of domesticated plants. Many of these trends have been recognized previously (Paterson, 2002; Frary & Doganlar, 2003), and I will instead focus on extending the analysis of these trends, adding information from the recent literature and suggesting some novel interpretations of the data currently available.

Major patterns

Distribution of QTL

Perhaps the most widely cited pattern to emerge from QTL mapping studies in domesticated plants has been the clustering of QTL. Most mapping studies have found that QTL are not randomly or even uniformly distributed throughout the genome, but occur in apparently linked clusters in certain regions of the chromosome (Cai & Morishima, 2002; Paterson, 2002). The few studies that fail to find extensive clustering (e.g. Hashizume, Shimamoto & Hirai, 2003) tend to suffer from methodological problems that severely constrain the power of these studies to detect QTL. In spite of the strong empirical support for this pattern, its genetic basis (i.e. tight physical linkage or pleiotropic

effects) and its significance in terms of adaptation remain open to debate.

Size and number of QTL

To many biologists, one of the most surprising finds of QTL studies has been the number of loci controlling many quantitative traits. QTL analysis allows the determination of a lower bound on the number of genes that control a given trait. And while classical quantitative genetic theory attributes continuous variation in nature to the small, additive effects of a nearly infinite number of genes, many studies of traits associated with domestication have found that much of the phenotypic variation can be explained by a few loci of relatively large effect. Though methodological problems – marker density, sample size, crossing scheme, etc. – can cloud the interpretation of these data (Beavis, 1994; Mauricio, 2001), the claim that most DRT are controlled by few loci of large effect seems to hold true for many studies across a variety of taxa. Counterexamples (Burke et al., 2002) do exist however, and the reasons for differences in effect size across studies or taxa are not completely clear. One difficulty in comparing QTL across studies has been the definition of 'major effect,' since transgressive variation among the progeny can decouple absolute morphological change from percent of phenotypic variance explained by a QTL.

QTL homology

The central theme of Frary and Doganlar's (2003) review is the similarity of QTL location and identity across taxa. Extensive synteny among QTL of major effect for DRT has been well established in the grass family (Paterson et al., 1995), and recent work has extended these findings to the Solanaceae, revealing similarities in QTL number and location across several genera of the family (Doganlar et al., 2002, Frary et al., 2003b). This similarity of genic and phenotypic character variation across a wide array of taxa seems to corroborate Vavilov's (1922) 'law of homologous series in variation,' – the assertion that character variation found in one taxa should exist in related or similar taxa.

Interpretations

Genetic basis of DRT

Loci of major effect are commonly found in mapping studies of DRT. The size of effect of a QTL is usually determined by the amount of phenotypic variation it explains. The percent variation explained by a QTL, however, does not necessarily correlate with the heritability of a given trait, nor with the absolute amount of change a gene effects (Burke et al., 2002). While there is good reason to interpret results evidencing QTL of major effect with some caution (Beavis, 1994; Mauricio, 2001; Paterson, 2002), the overall pattern is too common to ignore. Classic theory suggests that quantitative traits should be controlled by many genes of small effect, and that, more often than not, mutations of large effect would be deleterious in nature (Lande, 1983). This contrasts with reviews of phenotypic evolution in plants, which offer results similar to those reported in mapping studies: Hilu (1983) and Gottlieb (1984) both point to the important role of mutations of large effect. Similarly, recent theoretical advances find fault with the Neo-Darwinian dogma, suggesting an adaptive role for mutations of large phenotypic effect (Orr & Coyne, 1992; Orr, 1998a, 2003). On finding no QTL of large effect for DRT in crosses between wild and domesticated sunflower, Burke et al. (2002) make the argument that 'domestication may have occurred more readily without requiring the fortuitous occurrence of multiple major mutations.' While this may be true if adaptation under artificial selection depends solely on novel mutations, theory suggests that the opposite could occur if selection acts on standing genetic variation: selection will fix single alleles of large effect much faster than it could fix a multitude of small alleles (Barton & Keightley, 2002). Loci of large effect can then be later modified by selection acting on other genes (Hillman & Davies, 1990), which could well lead to distributions of allele effects quite similar to those seen in empirical mapping studies.

In addition to measuring the size of effect of QTL, mapping studies can elucidate the mode of action of the loci. Given that random mutation is more likely to inactivate a functional gene than to modify it or create a new function, it has been argued that the majority of DRT should be recessive. Many domesticated characters are in fact recessive (Ladizinsky, 1985; Lester, 1989), and both of the so-called 'domestication genes' which have been successfully cloned are essentially recessive (Doebley, Stec & Hubbard, 1997; Frary et al., 2000). Data from Burke et al. (2002) contradict this idea, showing no evidence for a predominance of recessive types among the alleles from domesticated sunflower. Other mapping studies show mixed results. Some show few or no recessive alleles in the domesticates (Paterson et al., 1991; Peng et al., 2003), yet other crosses find recessive alleles to be frequent (Doganlar et al., 2002; Xiong et al., 1999). Burke et al. (2002) actually argue that a lack of recessive alleles should have made the domestication of sunflower simpler. Again, however, if adaptation depends predominantly on standing variation rather than novel mutations, theory suggests that recessive alleles for DRT would be more likely to be fixed than nonrecessive ones (Orr & Betancourt, 2001). Until more data – especially on the relative importance of novel mutations and existing genetic variation – is available, however, it does not seem possible to make any general conclusions about the significance of the mode of action of QTL involved in crop domestication.

Tempo of domestication

Several lines of evidence suggest that the traditional Neo-Darwinian view of gradual change under domestication is no longer a tenable hypothesis. Paterson (2002) discusses the issue in some detail, arguing that the size of QTL, the existence of QTL clusters that could act as coadapted gene complexes, the coincidence of QTL across taxa, and the relative ease with which domesticates can lose DRT and become feral or weedy all support a relatively fast or punctuational tempo of domestication. Mathematical models of domestication based on empirical estimates of selection coefficients support his conclusion, estimating that domestication could take as little as 20–100 years (Hillman & Davies, 1990). Analysis of nucleotide variation in maize corroborates this conclusion, concluding that the current patterns of diversity are consistent with domestication having taken as little as ten years in very small populations (Eyre-Walker et al., 1998). Population bottlenecks, such as those suggested by the data in

Eyre-Walker et al., have long been thought to play an important role in plant domestication (Ladizinsky, 1985), and recent work (Ross-Ibarra, 2004) is consistent with the prediction that elevated levels of drift in such small populations would select for increased recombination (Otto & Barton, 2001). Finally, work in maize has provided a molecular model for rapid evolutionary change in domesticates, linking changes in the regulation of a single gene to major shifts in branching and inflorescence structure (Wang et al., 1999).

QTL distribution and adaptation

As mentioned above, nonrandom distribution of QTL has been a nearly ubiquitous finding in mapping studies of DRT. Most authors are careful to note that these clusters can be interpreted in at least two ways: either multiple genes are actually clustered together in linked groups, or the same genes are identified as QTL for several different traits (pleiotropy). The latter explanation seems probable for many of the reports of QTL for similar or correlated traits such as fruit weight and yield in peppers (Rao et al., 2003) or color shade and intensity in eggplant (Doganlar et al., 2002). Yet many studies have nonetheless found clustering of QTL for traits that do not seem likely to be pleiotropic effects of a single gene: Cai and Morishima (2002) mapped QTL relating to mineral tolerance, heading behavior, germination speed, and anther length all to a very short interval on one of the 12 chromosomes of rice, and similar clusters of seemingly unrelated QTL have been reported in a variety of species (Koinange et al., 1996; Poncet et al., 2000; Bres-Patry et al., 2001; Baum et al., 2003; Huang et al., 2003). As crossing strategies and mapping technologies improve, continued efforts at fine-scale mapping of QTL clusters (e.g. Takeuchi et al., 2003) combined with the development of new statistical analyses (e.g. Varona et al., 2004) should enable researchers to better distinguish between pleiotropy and linkage.

Many authors have made some variation of an adaptive argument for the observed presence of QTL clusters. Koinange et al. (1996) adopt the explanation of Pernes (1983) that, in allogamous plants, selection against recombinant hybrids between wild and cultivated plants will lead to the clustering of QTL for DRT in tightly linked groups, and computer simulations (Le Thierry D'Ennequin et al., 1999) of wild to crop gene flow during domestication seem to support this argument. Theoretical work has similarly shown that maladaptive gene flow creates positive associations among beneficial alleles in the reference population, thus selecting for increased linkage or decreased recombination (Lenormand & Otto, 2000). Cai and Morishima (2002) ascribe clustering of QTLs to Grant's (1981) concept of 'multifactorial linkages,' or weak linkages brought about by the random distribution of multiple factors throughout the genome. These linkages are then somehow preserved by selection for coadapted gene complexes, perhaps via a process similar to that of Pernes (1983). Poncet et al. (1998) proposed that linked clusters of QTL for DRT would become fixed more rapidly in a population than unlinked genes, through a type of 'reciprocal' hitchhiking effect.

There is, however, no a priori reason to believe that the clustering of genes is caused or maintained by strong selection. Westerbergh and Doebley (2002) analyzed the genetic basis of quantitative traits between two wild species of maize. Applying Orr's (1998b) QTL sign test, they conclude that phenotypic differences between the species can be best explained by neutral drift or temporal fluctuation in the direction of selection. Yet, in spite of an apparent lack of strong directional selection for any of the traits studied, Westerbergh and Doebley's linkage map shows the familiar pattern of clustered QTL. Furthermore, Pernes' (1983) hypothesis predicts a lack of clustering in selfing species, a result that is not supported by data gathered for common bean (Koinange et al., 1996), eggplant (Doganlar et al., 2002), rice (Thomson et al., 2003), soybean (Wang et al., 2004) or wheat (Peng et al., 2003), all predominantly selfing species.

Different interpretations of the pattern are entirely possible, however. It is well known that genes are not uniformly distributed throughout the genome, but that chromosomes usually contain both gene-rich and gene-poor regions (Gill et al., 1996; Ware & Stein, 2003; Aert et al., in press) I argue that QTL for DRT are found more often than not in tight clusters simply because all genes, more often than not, are found clustered together – the pattern does not require any adaptive explanation peculiar to domestication. Peng et al. (2003), for example, note that each of their seven

domestication syndrome factors (clusters of QTL for DRT) land squarely in one of these gene-rich regions of the wheat genome. Gene rich regions have also been shown to be 'hot spots' of recombination – Gill et al. (1996) found that 1 cM of genetic distance on a barley linkage map corresponds to approximately 120 kb in gene rich regions but to more than 22 Mb of DNA in areas of low gene density. While increased recombination might make linkage seem less likely in gene-dense regions, the comparatively small size of these regions means that genes within clusters could nonetheless be fairly tightly linked – genes in part of the *bz* gene cluster in maize are separated by less than 0.1 cM (Fu, Zheng & Dooner, 2001). If tight linkage were selected for during domestication, one might expect to find genes for DRT in regions of low density and low recombination. Furthermore, a recent comparison of the literature on recombination rates in domesticated plants suggests that domestication actually selects for an increase in recombination rate (Ross-Ibarra, 2004), a finding that is in good concordance with theory on the evolution of recombination (Otto & Barton, 1997, 2001). It is even conceivable that genes are clustered together for precisely the opposite reason that Pernes (1983) and others suspected – there might well be a selective advantage for genes that occur in regions of high recombination.

The argument could even be taken a step further, turning the logic of Pernes (1983) and Le Thierry D'Ennequin et al. (1999) on its head: both theory and simulation show that maladaptive gene flow should select for decreased recombination, yet revision of the empirical data available reveals that recombination has actually increased, suggesting that maladaptive gene flow was not of great impact during the domestication of most crop plants. Indeed, Poncet et al. (1998) claim that the relatively high levels of gene flow currently observed between wild and cultivated pearl millet have not adversely affected cultivation.

Direction of effects

Given the strong directional selection associated with domestication and the presumed genetic basis of morphological variation, it is not surprising to find QTL whose effect are in the direction of the domesticated trait. In fact one would expect the domesticated allele to increase seed size, fruit sweetness, quantity of seed produced, or whatever other DRT was under investigation. This is in fact what is generally found: in a review of QTL effects in domesticated taxa, Rieseberg et al. (2002) found that the vast majority of QTL for DRT are in the direction expected, suggesting a central role for directional selection in their differentiation.

Not all QTL for DRT show this trend, however. Burke et al. (2002) discovered a large number of QTL of the opposite direction expected in a mapping study of domesticated sunflower. They suggest that negative QTL could become established in domesticates via hitchhiking selecting on other linked QTL, and they interpret the existence of multiple positive QTL in the wild species as evidence consistent with the idea of multiple domestications of sunflower. Evidence from studies of other purported multiple domesticates is not entirely convincing: bean (Koinange et al., 1996), pearl millet (Poncet et al., 1998), barley (Pillen, Zacharias & Leon, 2004) and rice (Xiao et al., 1998; Xiong et al., 1999) show similar evidence of beneficial alleles in their wild progenitors, but a mapping study in peppers finds only very few of these alleles (Rao et al., 2003). Moreover, numerous studies of crops not thought to be of recurrent origin report alleles of varying direction in both the wild and domesticated parents (Doebley et al., 1990; Fulton et al., 1997; Johnson et al., 2000; Doganlar et al., 2002; Peng et al., 2003).

Unless the genetic basis of DRT is thought to have originated completely by novel mutations that arose during the process of domestication, the genetic variation present in the wild progenitor of a cultivated plant would have to include some agriculturally beneficial alleles. Given the equivocal evidence available and the improbability of successful domestication relying entirely on novel mutations, the most likely conclusion is that the pattern of cryptic allelic variation observed by Burke et al. (2002) is probably not a result of multiple domestications but instead quite possibly a common feature of domestication in general.

Conclusions

We have clearly come a long way towards a more concrete understanding of the genetic basis of domestication, and current data allow for

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many intriguing speculations as well. Equally clear, however, is the fact that we still have a long way to go. The patterns that we have thus far observed suggest questions that we do not yet have the data to answer, and future studies are sure to raise as many new questions as they answer old ones. Much is still lacking in the way of basic data: one has only to compare a list of the most important agricultural crops to the (much shorter) list of domesticated plants for which we have some idea of the genetic basis of quantitative DRT to get an idea of how much work is still ahead. Students of domestication should see this not as a disheartening lack of data but instead as a great opportunity to more fully understand a process that has not only been key in our own history, but key to our conceptualization of evolution as well.

Acknowledgements

References

Aert, R., L. Sági & G. Volckaert, in press. Gene content and density in banana (*Musa acuminata*) as revealed by genomic sequencing of BAC clones. Theor. Appl. Genet.

Anderson, W.W., J. Arnold, D.G. Baldwin, A.T. Beckenbach, C.J. Brown, S.H. Bryant, J.A. Coyne, L.G. Harshman & W.B. Heed, 1991. Four decades of inversion polymorphism in *Drosophila pseudoobscura*. Proc. Natl. Acad. Sci. USA 88: 10367–10371.

Barton, N.H. & P.D. Keightley, 2002. Understanding quantitative genetic variation. Nat. Rev. Genet. 3: 11–21.

Baum, M., S. Grando, G. Backes, A. Jahoor, A. Sabbagh & S. Ceccarelli, 2003. QTLs for agronomic traits in the Mediterranean environment identified in recombinant inbred lines of the cross 'Arta' × *H. spontaneum* 41-1. Theor. Appl. Genet. 107: 1215–1225.

Bres-Patry, C., M. Lorieux, G. Clement, M. Bangratz & A. Ghesquiere, 2001. Heredity and genetic mapping of domestication-related traits in a temperate japonica weedy rice. Theor. Appl. Genet. 102: 118–126.

Burke, J.M., S. Tang, S.J. Knapp & L.H. Rieseberg, 2002. Genetic analysis of sunflower domestication. Genetics 161: 1257–1267.

Cai, H.W. & H. Morishima, 2002. QTL clusters reflect character associations in wild and cultivated rice. Theor. Appl. Genet. 104: 1217–1228.

Cowie, R.H. & J.S. Jones, 1998. Gene frequency changes in *Cepaea* snails on the Marlborough Downs over 25 years. Biol. J. Linn. Soc. 65: 233–255.

Darwin, C., 1899. The Origin of Species. H.M. Caldwell Co., New York, NY., USA.

Doebley, J., A. Stec & L. Hubbard, 1997. The evolution of apical dominance in maize. Nature 386: 485–488.

Doebley, J., A. Stec, J. Wendel & M. Edwards, 1990. Genetic and morphological analysis of a maize-teosinte F-2 population implications for the origin of maize. Proc. Natl. Acad. Sci. USA 87: 9888–9892.

Doganlar, S., A. Frary, M.C. Daunay, R.N. Lester & S.D. Tanksley, 2002. Conservation of gene function in the Solanaceae as revealed by comparative mapping of domestication traits in eggplant. Genetics 161: 1713–1726.

Dudley, J.W. and R.J. Lambert, 1992. Ninety generations of selection for oil and protein in maize. Maydica 37:1–7

Eyre-Walker, A., R.L. Gaut, H. Hilton, D.L. Feldman & B.S. Gaut, 1998. Investigation of the bottleneck leading to the domestication of maize. Proc. Natl. Acad. Sci. USA 95: 4441–4446.

Frary, A. & S. Doganlar, 2003. Comparative genetics of crop plant domestication and evolution. Turkish J. Agr. For. 27: 59–69.

Frary, A., S. Doganlar, M.C. Daunay & S.D. Tanksley, 2003. QTL analysis of morphological traits in eggplant and implications for conservation of gene function during evolution of solanaceous species. Theor. Appl. Genet. 107: 359–370.

Frary, A., T.C. Nesbitt, A. Frary, S. Grandillo, E. van der Knaap, B. Cong, J. Liu, J. Meller, R. Elber, K.B. Alpert & S.D. Tanksley, 2000. fw2.2: A quantitative trait locus key to the evolution of tomato fruit size. Science 289: 85–88.

Fu, H., Z. Zheng & H.K. Dooner, 2001. Recombination rates between adjacent genic and retrotransposon regions in maize vary by 2 orders of magnitude. Proc. Natl. Acad. Sci. USA 99: 1082–1087.

Fulton, T.M., B.T. Beck, D. Emmatty, Y. Eshed, J. Lopez, V. Petiard, J. Uhlig, D. Zamir & S.D. Tanksley, 1997. QTL analysis of an advanced backcross of *Lycopersicon peruvianum* to the cultivated tomato and comparisons with QTLs found in other wild species. Theor. Appl. Genet. 95: 881–894.

Gill, K.S., B.S. Gill, T.R. Endo & E.V. Boyko, 1996. Identification and high-density mapping of gene-rich regions in chromosome group 5 of wheat. Genetics 143: 1001–1012.

Gottlieb, L.D., 1984. Genetics and morphological evolution in plants. Am. Nat. 123: 681–709.

Grant, P.R. & B.R. Grant, 2002. Unpredictable evolution in a 30-year study of Darwin's finches. Science 296: 707–711.

Grant, V., 1981. Plant Speciation. Columbia University Press, New York, NY., USA.

Harlan, J.R., 1992. Crops and Man. American Society of Agronomy: Crop Science Society of America, Madison WI, USA.

Hashizume, T., I. Shimamoto & M. Hirai, 2003. Construction of a linkage map and QTL analysis of horticultural traits for watermelon [*Citrullus lanatus* (Thunb.) Mastsum and Nakai] using RAPD, RFLP and ISSR markers. Theor. Appl. Genet. 106: 779–785.

Hillman, G.C. & M.S. Davies, 1990. Domestication rates in wild-type wheats and barley under primitive cultivation. Biol. J. Linn. Soc. 39: 39–78.

Hilu, K.W., 1983. The role of single-gene mutations in the evolution of flowering plants. Evol. Biol. 16: 97–128.

Huang, X.Q., H. Coester, M.W. Ganal & M.S. Roeder, 2003. Advanced backcross QTL analysis for the identification of quantitative trait loci alleles from wild relatives of wheat (*Triticum aestivum* L.). Theor. Appl. Genet. 106: 1379–1389.

Johnson, W.C., L.E. Jackson, O. Ochoa, R. van Wijk, J. Peleman, D.A. St. Clair & R.W. Michelmore, 2000. Lettuce, a shallow-rooted crop, and *Lactuca serriola*, its wild progenitor, differ at QTL determining root architecture and deep soil water exploitation. Theor. Appl. Genet. 101: 1066–1073.

Koinange, E.M.K., S.P. Singh & P. Gepts, 1996. Genetic control of the domestication syndrome in common bean. Crop Sci. 36: 1037–1045.

Ladizinsky, G., 1985. Founder effect in crop-plant evolution. Econ. Bot. 39: 191–199.

Lande, R., 1983. The response to selection on major and minor mutations affecting a metrical trait. Heredity 50: 47–65.

Le Thierry D'Ennequin, M., B. Toupance, T. Robert, B. Godelle & P.H. Gouyon, 1999. Plant domestication: a model for studying the selection of linkage. J. Evol. Biol. 12: 1138–1147.

Lenormand, T. & S.P. Otto, 2000. The evolution of recombination in a heterogeneous environment. Genetics 156: 423–428.

Lester, R.N., 1989. Evolution under domestication involving disturbance of genic balance. Euphytica 44: 125–132.

Mauricio, R., 2001. Mapping quantitative trait loci in plants: uses and caveats for evolutionary biology. Nat. Rev. Genet. 2: 370–381.

Orr, H.A., 1998a. The population genetics of adaptation: the distribution of factors fixed during adaptive evolution. Evolution 52: 935–949.

Orr, H. A., 1998b. Testing natural selection vs. genetic drift in phenotypic evolution using quantitative trait locus data. Genetics 149: 2099–2104.

Orr, H.A., 2003. The distribution of fitness effects among beneficial mutations. Genetics 163: 1519–1526.

Orr, H.A. & A.J. Betancourt, 2001. Haldane's sieve and adaptation from the standing genetic variation. Genetics 157: 875–884.

Orr, H.A. & J.A. Coyne, 1992. The genetics of adaptation: a reassessment. Am. Nat. 140: 725–742.

Otto, S.P. & N.H. Barton, 1997. The evolution of recombination: removing the limits to natural selection. Genetics 147: 879–906.

Otto, S.P. & N.H. Barton, 2001. Selection for recombination in small populations. Evolution 55: 1921–1931.

Paterson, A.H., 2002. What has QTL mapping taught us about plant domestication? New Phytol. 154: 591–608.

Paterson, A.H., S. Damon, J.D. Hewitt, D. Zamir, H.D. Rabinowitch, S.E. Lincoln, E.S. Lander & S.D. Tanksley, 1991. Mendelian factors underlying quantitative traits in tomato – comparison across species, generations, and environments. Genetics 127: 181–197.

Paterson, A.H., Y.R. Lin, Z. Li, K.F. Schertz, J.F. Doebley, S.R.M. Pinson, S.C. Liu, J.W. Stansel & J.E. Irvine, 1995.

Convergent domestication of cereal crops by independent mutations at corresponding genetic loci. Science 269: 1714–1718.

Peng, J., Y. Ronin, T. Fahima, M.S. Roder, Y. Li, E. Nevo & A. Korol, 2003. Domestication quantitative trait loci in *Triticum dicoccoides*, the progenitor of wheat. Proc. Natl. Acad. Sci. USA 100: 2489–2494.

Pernes, J., 1983. The genetics of the domestication of cereals. Recherche 14: 910–919.

Pillen, K., A. Zacharias & J. Léon, 2004. Comparative AB-QTL analysis in barley using a single exotic donor of *Hordeum vulgare* ssp. *spontaneum*. Theor. Appl. Genet. 108: 1591–1601.

Poncet, V., F. Lamy, K.M. Devos, M.D. Gale, A. Sarr & T. Robert, 2000. Genetic control of domestication traits in pearl millet (*Pennisetum glaucum* L., Poaceae). Theor. Appl. Genet. 100: 147–159.

Poncet, V., F. Lamy, J. Enjalbert, H. Joly, A. Sarr & T. Robert, 1998. Genetic analysis of the domestication syndrome in pearl millet (*Pennisetum glaucum* L., Poaceae): Inheritance of the major characters. Heredity 81: 648–658.

Rao, G.U., C.A. Ben, Y. Borovsky & I. Paran, 2003. Mapping of yield-related QTLs in pepper in an interspecific cross of *Capsicum annuum* and *C. frutescens*. Theor. Appl. Genet. 106: 1457–1466.

Rieseberg, L.H., A. Widmer, A.M. Arntz & J.M. Burke, 2002. Directional selection is the primary cause of phenotypic diversification. Proc. Natl. Acad. Sci. USA 99: 12242–12245.

Ross-Ibarra, J., 2004. The evolution of recombination under domestication: a test of two hypotheses. Am. Nat. 163: 105–112.

Takeuchi, Y., S.Y. Lin, T. Sasaki & M.Yano, 2003. Fine linkage mapping enables dissection of closely linked quantitative trait loci for seed dormancy and heading in rice. Theor. Appl. Genet. 107: 1174–1180.

Thomson, M.J., T.H. Tai, A.M. McClung, X-H. Lai, M.E. Hinga, K.B. Lobos, Y. Xu, C.P. Martinez & S.R. McCouch, 2003. Mapping quantitative trait loci for yield, yield components and morphological traits in an advanced backcross population between *Oryza rufipogon* and the *Oryza sativa* cultivar Jefferson. Theor. Appl. Genet. 107: 479–493.

Varona, L., L. Gomez-Raya, W.M. Rauw, A. Clop, C. Ovilo & J.L. Noguera, 2004. Derivation of a Bayes factor to distinguish between linked or pleiotropic quantitative trait loci. Genetics 166: 1025–1035.

Vavilov, N., 1922. The law of homologous series in variation. J. Genet. 12: 47–89.

Visser, M.E., A.J. van Noordwijk, J.M. Tinbergen & C.M. Lessells, 1998. Warmer springs lead to mistimed reproduction in great tits (*Parus major*). Proc. R. Soc. Lond., Ser. B: Biol. Sci. 265: 1867–1870.

Wang, R.L., A. Stec, J. Hey, L. Lukens & J. Doebley, 1999. The limits of selection during maize domestication. Nature 398: 236–239.

Wang, D., G.L. Graef, A.M. Procopiuk, & B.W. Diers, 2004. Identification of putative QTL that underlie yield in interspecific soybean backcross populations. Theor. Appl. Genet. 108: 458–467.

Ware, D & L. Stein, 2003. Comparison of genes among cereals. Curr. Opin. Plant Biol. 6: 121–127.

Westerbergh, A. & J. Doebley, 2002. Morphological traits defining species differences in wild relatives of maize are controlled by multiple quantitative trait loci. Evolution 56: 273–283.

Xiao, J.H., J.M. Li, S. Grandillo, S.N. Ahn, L.P. Yuan, S.D. Tanksley & S.R. McCouch, 1998. Identification of trait-improving quantitative trait loci alleles from a wild rice relative, *Oryza rufipogon*. Genetics 150: 899–909.

Xiong, L.X., K.D. Liu, X.K. Dai, C.G. Xu & Q.F. Zhang, 1999. Identification of genetic factors controlling domestication-related traits of rice using an F-2 population of a cross between *Oryza sativa* and *O. rufipogon*. Theor. Appl. Genet. 98: 243–251.