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QTL mapping in cattle: theoretical and empirical approach

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In tabulated form the localization is presented of all QTLs for milk production traits in cattle known from publications till April 2006 with special reference to those responsible for mastitis, fertility and other traits important in marker-assisted selection. The distribution is analysed of QTLs in *Bos taurus* autosomes, as well as most probable localization of QTLs for milk production traits. Special attention is paid to autosomes 1, 2, 3, 5, 6, 7, 9, 14, 19, 20, 23, 26, 27 and sex chromosome X. An evidence is provided for the pleiotropy of QTLs as a widely extended phenomenon in dairy cattle.

KEY WORDS: dairy cattle / gene mapping / *mastitis* / milk production traits / quantitative trait *loci*

Over the last decade, after appearing of the pioneer paper by Georges *et al*. [1995], numerous data on QTLs mapping have been published. In the reviews published so far the data up to 2004 were considered only. With each year the number of papers considerably increases. The main purpose of this review was to collect together all data on QTLs responsible for milk production traits in cattle, to identify the locations of QTLs, and to withdraw the appropriate conclusions.

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Material and methods

Mapping QTLs in cattle

Up to date, numerous articles have been published concerning search of QTLs for milk yield (M), milk protein yield (P), milk fat yield (F), protein content (%P), fat content (%F), somatic cell score (SCS) and *mastitis* (MST)*

In Table 1 positions of all the QTLs published up to March 2006 are quoted. All positions were rescaled to the MARC 97 map, provided the marker positions were available. Earlier the QTLmaps for dairy cattle have been published by Bovenhuis and Schrooten [2002], Mosig *et al*. [2003] and Kathar *et al*. [2004].

Genetic evaluation of livestock has traditionally been carried out using an infinitesimal model, were the trait is assumed to be influenced by an infinite number of genes, each with an infinitesimally small effect. The arguments justifying the use of the infinitesimal model are, however, being weakened by the increasing knowledge about the genetic architecture of quantitative traits. Therefore, also the finite *locus* model has been used to estimate additive and breeding values for different distributions for the gene effects across the *loci*: (i) uniform with *loci* of different effects, (ii) uniform with all *loci* having equal effects, (iii) exponential, and (iv) normal [Pong-Wong *et al*. 2002]. Orr [1998] using own calculations, has made the theoretical predictions about distribution of phenotypic effects among factors fixed during adaptation. The calculated correlation curve has a pleasingly simple, exponential form.

Calculations made for cattle have shown that 90% of the phenotypic variance for each milk production trait are determined by 50 to 100 segregating QTLs (17% of them being major QTLs), and the phenotyping distribution of QTLs has the gamma form [Hayes and Goddard 2001]. It becomes clear, that due to such distribution of QTLs, a population has an opportunity to quickly and adequately answer to the selection pressure, and in case of removal of the pressure, quickly return to an initial state. Going through the data presented in Table 1 may give a rough estimation of a number of QTLs on each bovine autosome (Tab. 2). No more than three QTLs have been localized in each autosome. So, it may be possible to calculate a maximum number of QTLs for each production trait, which is equal to $29 \times 3 = 87$, provided that QTLs are distributed uniformly in chromosomes. This number would be a limit if no more sensible methods for QTLs detection arise. How many QTLs may affect a trait? Taking into account that now a large granddaughter design may reveal no more than 7% QTLs [Bovenhuis and Schrooten 2002] the expected number will be 500-800. A theoretical approximation of QTL distribution based on the assumption that $\Delta\sigma_{phenotype} \rightarrow 0$ is rather problematic and open to criticism. In other words, the problem is the behaviour of a curved line of distribution in range less than 0.2 phenotype standard deviation. Solution of this problem depends on empirical data for each trait. This becomes evidently clear when the data contained in the paper of Hayes and Goddard

*These abbreviations apply to the further text of this article.

Table 1. Locations of dairy trait QTLs (cM) on *Bos taurus* (BTA) autosomes

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
1	0-20	**10** – Nadesalingam *et al*. [2001] **15** – Georges *et al*. [1995]	**21** – Nadesalingam *et al*. [2001] **20** – Georges *et al*. [1995]			**8** – Nadesalingam *et al*. [2001] **16** –Liu *et al*. [2004]	
1	20-40		**25** – Zhang *et al*. [1998]	**26** – Nadesalingam *et al*. [2001]	**26** – Nadesalingam *et al*. [2001] **27** – Liu *et al*. [2004] **38** – Nadesalingam *et al*. [2001]	**28** – Nadesalingam *et al*. [2001]	**39** – Schulman *et al*. [2004]
1	40-80	**56** – Nadesalingam *et al*. [2001] **70** – Nadesalingam *et al*. [2001]	**46** – Liu *et al*. 2004; Rodriguez-Zas *et al*. [2002a] **50** – Nadesalingam *et al*. [2001] **61** – Nadesalingam *et al*. [2001; Rodriguez-Zas *et al*. [2002a]	**65** – Mosig *et al*. [2003]	**46** – Heyen *et al*. [2005]; Olsen *et al*. [2002]		
1	80-142	**115** – Viitala *et al*. 1999] **142** – De Koning *et al*. [2001]; Maki-Tanila *et al*. [1998]; Rodriguez-Zas *et al*. [2002a]	**106** – Nadesalingam *et al*. [2001]; **109** – Rodriguez-Zas *et al*. 2002a] **142** – Heyen *et al*. [1999]	**110** – Georges *et al*. [1995] **119** – Mosig *et al*. [2003] **142** – Heyen *et al*. [2005]; Mosig *et al*. [2003]	**142** – Harder *et al*. [2006]$^{+}$		**115** – Rodriguez-Zas *et al*. [2002a] **132** – Reinsch *et al*. [1998] **146** – Rodriguez-Zas *et al*. 2002a]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
2	0-120	**34** – Viitala *et al.* [2003] **100** – Ron *et al.* [2004]	**45** – Ashwell *et al.* [2005] **108** – Ron *et al.* [2004]	**16** – Ashwell *et al* [2004] **27** – Heyen *et al.* [1999]; **57** – Mosig *et al.* [2003]; **69** – Ron *et al.* [2004]	**8** – Rodriguez-Zas *et al.* [2002a] **34** – Heyen *et al.* [2005] **37** – Ashwell *et al.* [2005] **110** – Harder *et al.* [2006]$^{+}$	**30** – Zhang *et al.* [1998] **34** – Ashwell *et al.* [2004] **107** – Ron *et al.* [2004]	**70** – Kuhn *et al.* [2004] **75** – Bennewitz *et al.* [2003]
3	0-30	**30** – Heyen *et al.* [1999]	**28** – Rodriguez-Zas *et al.* [2002b] **30** – Heyen *et al.* [1999]	**5** – Heyen *et al.* [1999] **20** – Viitala *et al.* [2003] **21** – Plante *et al.* [2001] **26** – Ashwell *et al.* [2004] **30** – Boichard *et al.* [2003]; Heyen *et al.* [2005]	**20** – Olsen *et al.* [2002] **26** – Ashwell *et al.* [2004] **30** – Heyen *et al.* [1999]	**5** – Heyen *et al.* [1999] **20** – Viitala *et al.* [2003] **30** – Heyen *et al.* [1999]	
3	30-70	**45** – Rodriguez-Zas *et al.* 2002b] **56** – Heyen *et al.* [1999]; Ron *et al.* [1998]; Zhang *et al.* [1998] **57** – Liu *et al.* [2004] **59** – Plante *et al.* [2001] **60** – Ashwell *et al.* [2004] **66** – Heyen *et al.* [2005]; Viitala *et al.* [2003]	**45** – Rodriguez-Zas *et al.* [2002a] **53** – Rodriguez-Zas *et al.* 2002a] **56** – Zhang *et al.* [1998] **64** – Ashwell *et al.* [2004] **66** – Heyen *et al.* [2005]	**36** – Ashwell *et al.* [2001]; Liu *et al.* [2004] **45** – Heyen *et al.* [1999] **56** – Heyen *et al.* [1999]; Zhang *et al.* 1998] **57** – Ashwell *et al.* [2004] **58** – Plante *et al.* [2001] **60** – Mosig *et al.* [2003] **66** – Heyen *et al.* [2005]	**45** – Heyen *et al.* [2005]; Rodriguez-Zas *et al.* [2002b] **56** – Heyen *et al* [1999] **58** – Rodriguez-Zas *et al.* [2002a] **69** – [Rodriguez-Zas *et al.* [2002a]	**41** – Liu *et al.* [2004] **45** – Heyen *et al.* 1999] **56** – Heyen *et al* [1999; Ron *et al.* [1998] **58** – Plante *et al.* [2001] **62** – Ashwell *et al.* [2004]	**35** – Klungland *et al.* [2001]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
3	70-125	**80** – Heyen *et al*. [2005] **104** – Heyen *et al*. [2005]; Rodriguez-Zas *et al*. [2002b]	**94** – Rodriguez-Zas *et al*. [2002b] **104** – Heyen *et al*. [2005] **110** – Rodriguez-Zas *et al*. [2002a]; Heyen *et al*. [2005]	**87** – Heyen *et al*. [1999]; Rodriguez-Zas *et al*. [2002b] **88** – Mosig *et al*. [2003] **104** – Heyen *et al*. [2005] **115** – Mosig *et al*. [2003] **116** – Ashwell *et al*. [2004]	**74** – Rodriguez-Zas *et al*. [2002a]	**116** – Heyen *et al*. [2005]	**87** – Schulman *et al*. [2004] **104** – Klungland *et al*. [2001]* **123** – Schrooten *et al*. [2000]
4	0-100	**10** – Heyen *et al*. [2005] **68** – Heyen *et al*. [2005]; Lindersson *et al*. [1998] **100** – Heyen *et al*. [2005]	**48** – Heyen *et al*. [2005] **68** – Heyen *et al*. [2005]	**25** – Mosig *et al*. [2003] **9** – Mosig *et al*. [2003] **95** – Lindersson *et al*. [1998] **100** – Heyen *et al*. [2005]	**24** – Rodriguez-Zas *et al*. [2002a] **87** – Lindersson *et al*. [1998]	**75** – Lindersson *et al*. [1998]	**43** – Zhang *et al*. [1998] **71** – Klungland *et al*. [2001]* **100** – Klungland *et al*. [2001]*
5	0-133	**64** – Rodriguez-Zas *et al*. [2002a] **74** – Heyen *et al*. [2005] **86** – Bennewitz *et al*. [2003]; Viitala *et al*. [2003] **98** – Bennewitz *et al*. [2004a] **100** – De Koning *et al*. [2001] **118** – Bennewitz *et al*. [2003]	**7** – Plante *et al*. [2001] **69** – Viitala *et al*. [2003] **90** – Bennewitz [*et al*. [2004a] **97** – Rodriguez-Zas *et al*. [2002a]	**7** – Plante *et al*. [2001] **43** – Bennewitz *et al*. [2003] **55** – Mosig *et al*. [2003] **76** – Heyen *et al*. 2005]; Mosig *et al*. [2003] **80** – Schrooten *et al*. [2004] **120** – Bennewitz *et al*. [2004a]	**60** – Plante *et al*. [2001] **99** – Bennewitz *et al*. [2003]; Heyen *et al*. [2005] **100** – Olsen *et al*. [2002] **115** – Schrooten *et al*. [2004]	**87** – Ashwell *et al*. [2004; Heyen *et al*. [2005] **99** – Bennewitz [2004a], Heyen *et al*. [1999] **105** – Bennewitz *et al*. [2003] **112** – Olsen *et al*. [2002]	**7** – Holmberg and Andersson-Eklund [2004] **46** – Rodriguez-Zas *et al*. [2002a] **54** – Ashwell *et al*. [2004] **99** – Heyen *et al*. [1999] **105** – Boichard and Bishop [1997]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
6	0-70	**2** – Schnabel *et al.* [2005a] **8** – Schnabel *et al.* [2005a] **7** – Heyen *et al.* [2005]; Ron *et al.* [1998] **28** – Velmala *et al.* [1999]; Wiener *et al.* [2000] **40** – Freyer *et al.* [2002] **44** – Ron *et al.* [2001] **47** – Georges *et al.* [1995] **48** – Viitala *et al.* [2003] **49** – Cohen *et al.* [2002]; Olsen *et al.* [2002]; Schnabel *et al.* [2005a]; Velmala *et al.* [1999]; Zhang *et al.* [1998] **53** – Ron *et al.* [1998] **58** – De Koning *et al.* [2001] **59** – Freyer *et al.* [2003] **60** – Harder *et al.* [2006]$^{+}$	**7** – Ron *et al.* [2001]; Schnabel *et al.* [2005a] **24** – Ashwell *et al.* [2004]; Schnabel *et al.* [2005a] **35** – Freyer *et al.* [2002]; Rodriguez-Zas *et al.* [2002a] **49** – Cohen *et al.* [2002]; Olsen *et al.* [2004]; Rodriguez-Zas *et al.* [2002b]; Ron *et al.* [2001]; Schnabel *et al.* [2005a]; Spelman *et al.* [2003] **57** – Heyen *et al.* [2005; Kuhn *et al.* [1999]	**5** – Schnabel *et al.* [2005a]; **7** – Heyen *et al.* [2005] **15** – Schnabel *et al.* [2005a] ; **23** – Schrooten *et al.* [2004] **34** – Schnabel *et al.* [2005a] **36** – Freyer *et al.* [2002]; Mosig *et al.* [2003]; Velmala *et al.* [1999] **43** – Bennewitz *et al.* [2004a]; Schnabel *et al.* [2005a] **46** – Olsen *et al.* [2004] **47** – Viitala *et al.* [2003] **48** – Ashwell *et al.* [2004]; Schnabel *et al.* [2005a] **49** – Liu *et al.* [2004]; Velmala *et al.* [1999]	**5** – Rodriguez-Zas *et al.* [2002a]; Ron *et al.* [2001]; Schnabel *et al.* [2005a] **15** – Schnabel *et al.* 2005a] **35** – Freyer *et al.* [2002] **46** – Ron *et al.* [2001] **49** – Cohen *et al.* [2002] **51** – Olsen *et al.* [2004; Ron *et al.* [2001] **52** – Freyer *et al.* [2003]; Spelman *et al.* [1996]; Zhang *et al.* [1998] **53** – Schnabel *et al.* [2005a] **57** – Kuhn *et al.* [1999]	**5** – Schnabel *et al.* [2005a] **8** – Schnabel *et al.* [2005a] **15** – Schnabel *et al.* [2005a] **33** – Schnabel *et al.* [2005a] **35** – Nadesalingam *et al.* [2000]; Schrooten *et al.* [2004] **37** – Freyer *et al.* [2004] **46** – Ashwell *et al.* [2004]; Olsen *et al.* [2004] **47** – Ron *et al.* [2001]; Schnabel *et al.* [2005a] **49** – Spelman *et al.* [1996]; Zhang *et al.* [1998] **51** – Ggeorges *et al.* [1995]	**50** – Klungland *et al.* [2001]* **55** – Heyen *et al.* [2005]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
6	0-70	**64** – Olsen *et al.* [2004]; Schnabel *et al.* [2005a] **67** – Heyen *et al.* [2005]	**59** – Freyer *et al.* [2003] **63** – Schnabel *et al.* [2005a] **67** – Freyer *et al.* [2002]; Heyen *et al.* [2005]; Rodriguez-Zas *et al.* [2002a]; Schnabel *et al.* [2005a]	**50** – Georges *et al.* [1995]; Mosig *et al.* [2003]; Ron *et al.* [2001]; Zhang *et al.* [1998] **56** – Schnabel *et al.* [2005a] **58** – Heyen *et al.* [2005]; Olsen *et al.* [2002] **66** – Schnabel *et al.* [2005a]; Nadesalingam *et al.* [2001]	**58** – Freyer *et al.* [2003] **62** – Szyda *et al.* [2005] **64** – Schnabel *et al.* [2005a] **67** – Heyen *et al.* [2005]	**52** – Schnabel *et al.* [2005a] **58** – Heyen *et al.* [2005]; Olsen *et al.* [2002] **64** – Schnabel *et al.* [2005a]	
6	70-125	**70** – Freyer *et al.* [2004]; Szyda *et al.* [2005] **74** – Nadesalingam *et al.* [2001] **76** – Liu *et al.* [2004] **80** – Velmala *et al.* [1999] **84** – Szyda *et al.* [2005] **90** – Schnabel *et al.* [2005a]; Thomsen *et al.* [2001]	**70** – Szyda *et al.* [2005] **75** – Schnabel *et al.* [2005a] **77** – Freyer *et al.* [2003]; Spelman *et al.* [1996] **83** – Nadesalingam *et al.* [2001]; Velmala *et al.* [1999]	**76** – Ashwell *et al.* [2001]; Mosig *et al.* [2003] **78** – Freyer *et al.* [2004] **83** – Ashwell *et al.* [2001]; Mosig *et al.* [2003]; Schnabel *et al.* [005a]; Velmala *et al.* [1999] **91** – Heyen *et al.* [2005]; Schnabel *et al.* [2005a]	**74** – Szyda *et al.* [2005] **80** – Freyer *et al.* [2003]; Velmala *et al.* [1999] **91** – Wiener *et al.* [2000] **112** – Harder *et al.* [2006][+] **113** – Schnabel *et al.* [2005a]	**70** – Freyer *et al.* [2004] **78** – Viitala *et al.* [2003] **89** – Schnabel *et al.* [2005a] **90** – Spelman *et al.* [1996] **113** – Heyen *et al.* [2005]; Ron *et al.* [2004]	**84** – Boichard and Bishop [1997] **86** – Bennewitz *et al.* [2004a]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
6	70-125	**91** –Spelman *et al.* [1996]; Wiener *et al.* 2000] **100** – Ron *et al.* [2001] **107** – Schnabel *et al.* [2005a] **113** – Heyen *et al.* [2005]	**84** – Szyda *et al.* [2005] **91** – Spelman *et al.* [1996]; Wiener *et al.* [2000] **100** – Freyer *et al.* [2003]; Schrooten *et al.* [2000] **113** – Heyen *et al.* [2005]; Rodriguez-Zas *et al.* [2002b]; Schnabel *et al.* [2005a] **114** – Ron *et al.* [1998]	**92** – Ashwell *et al.* [2004]; Boichard and Bishop [1997] **94** – Ron *et al.* [2001]			
7	0-134	**24** – Heyen *et al.* [2005] **30** – Ashwell *et al.* [2004] **77** – Ron *et al.* [2004] **84** – Boichard and Bishop [1997] **111** – Ashwell *et al.* [2004] **117** – Heyen *et al.* [1999]; Rodriguez-Zas *et al.* [2002a]	**18** – Ron *et al.* [2004] **30** – Ashwell *et al.* [2004] **75** – Rodriguez-Zas *et al.* [2002b] **82** – Boichard and Bishop [1997] **111** – Ashwell *et al.* [2004]	**01** – Mosig *et al.* [2003] **14** – Ron *et al.* [2004] **60** – Mosig *et al.* [2003] **75** – Heyen *et al.* [2005] **90** – Mosig *et al.* [2003] **117** – Mosig *et al.* [2003]	**15** – Ron *et al.* 2004] **60** – Heyen *et al.* [2005] **84** – Boichard *et al.* [2003] **116** – Heyen *et al.* [2005]	**15** – Ron *et al.* [2004] **24** – Heyen *et al.* [2005] **76** – Boichard *et al.* [2003]	**39** – Ron *et al.* [2004] **61** – Ashwell *et al.* [2004] **60** – Rodriguez-Zas *et al.* [2002a] **67** – Ashwell *et al.* [2004] **90** – Kuhn *et al.* [2003] **124** – Heyen *et al.* [1999]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
7	0-134	**124** – Heyen *et al*. [1999]	**117** – Heyen *et al.* [1999] **124** – Heyen *et al.* [1999]				
8	0-116		**53** – Heyen *et al.* [2005] **84** – Ashwell *et al.* [1997]	**19** – Mosig *et al*. [2003] **38** – Mosig *et al*. [2003] **59** – Mosig *et al*. [2003] **84** – Ashwell *et al*. [1997]		**70** – Zhang *et al*. [1998] **84** – Ashwell *et al.* [1997]	**16** – Reinsch *et al*. 1998] **31** – Klungland *et al.* [2001]* **38** – Heyen *et al*. [2005] **55** – Klungland *et al.* [2001] **61** – Heyen *et al*. [2005] **85** – Schnabel *et al.* [2005]
9	0-109	**45** – Heyen *et al.* [2005]; Vilkki *et al.* 1997] **51** – Plante *et al.* [2001] **70** – Zhang *et al*. [1998] **72** – Wiener *et al.* [2000] **84** – Wiener *et al*. [2000]	**45** – Heyen *et al.* [2005]; Wiener *et al*. [2000] **50** – Schnabel *et al.* [2005] **58** – Georges *et al*. [1995] **59** – Wiener *et al*. [2000];	**41** – Plante *et al.* [2001] **45** – Mosig *et al*. [2003] **59** – Mosig *et al*. [2003] **84** – Mosig *et al*. [2003]	**37** – Wiener *et al.* [2000] **48** – Georges *et al.* [1995] **61** – [Wiener *et al*. [2000] **70** – Zhang *et al*. [1998] **84** – Wiener *et al.*	**98** – Heyen *et al.* [2005]	**72** – Holmberg *et al.* [2004* **74** – Heyen *et al*. [2005] **95** – Holmberg *et al*. [2004] **98** – Heyen *et al.* [2005]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
9	0-109	**85** – Heyen *et al.*[2005]; Rodriguez-Zas *et al.* [2002a]	Harder *et al.* [2006]$^{+}$ **70** – Zhang *et al.* [1998] **84** – Wiener *et al.* [2000]		[2000; Harder *et al.* [2006]$^{+}$ **98** – Heyen *et al.* [2005]; Schnabel *et al.* [2005]		**103** – Boichard *et al.* [2003]
10	0-100	**12** – Thomsen *et al.* [2001] **44** – Plante *et al.* [2001] **98** – Ashwell *et al.* [2004]		**19** – Mosig *et al.* [2003] **29** – Mosig *et al.* [2003] **50** – Georges *et al.* [1995] **55** – Mosig *et al.* [2003] **73** – Mosig *et al.* [2003]; Plante *et al.* [2001]	**30** – Schrooten *et al.* 2004] **43** – Georges *et al.* [1995]		**7** – Schulman *et al.* [2004]* **46** – Boichard and Bishop [1997] **49** – Kuhn *et al.* [2003] **74** – Heyen *et al.* [2005] **75** – Schnabel *et al.* [2005] **77** – Schrooten *et al.* [2000]
11	0-123	**105** – Boichard *et al.* [2003]	**83** – Ashwell *et al.* [2004] **115** – Rodriguez-Zas *et al.* [2002a]	**10** – Mosig *et al.* [2003] **48** – Mosig *et al.* [2003] **85** – Mosig *et al.* [2003]	**86** – Olsen *et al.* [2004] **90** – Ashwell *et al.* [2004]		**10** – Schulman *et* [*al.* 2004] **26** – Holmberg and Andersson-Eklund [2004]* **33** – Schnabel *et al.* [2005] **38** – Schulman *et al.* [2004*]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
11	0-123						**41** – Holmberg, Andersson-Eklund [2004] **46** – Boichard and Bishop [1997] **52** – Schulman *et al*. [2004] **58** – Rodriguez-Zas *et al*. [2002] **67** – Zhang *et al*. [1998] **93** – Schnabel *et al*. [2005]
12	0-105	**27** – De Koning *et al*. [2001] **42** – Viitala *et al*. [2003]	**18** – Rodriguez-Zas *et al*. [2002a] **46** – Viitala *et al*. [2003]	**21** – Mosig *et al*. [2003] **40** – Viitala *et al*. [2003] **49** – Mosig *et al*. [2003] **80** – Mosig *et al*. [2003] **99** – Mosig *et al*. [2003]	**57** – Viitala *et al*. [2003] **80** – Heyen *et al*. [2005]; Rodriguez-Zas *et al*. [2002a] **98** – Heyen *et al*. [2005]		**62** – Rodriguez-Zas *et al*. [2002a] **80** – Heyen *et al*. [2005]
13	0-87	**19** – Heyen *et al*. [2005] **84** – Ashwell *et al*. [2004]; Heyen *et al*. [2005]	**19** – Heyen *et al*. [2005] **58** – Rodriguez-Zas *et al*. [2002b] **77** – Ashwell *et al*. [2004]	**15** – Mosig *et al*. [2003] **20** – Mosig *et al*. [2003] **25** – Olsen *et al*. [2002] **34** – Ashwell *et al*. [2004], Heyen *et al*. [2005] **44** – Mosig *et al*. [2003] **56** – Mosig *et al*. [2003]	**38** – Plante *et al*. [2001]	**62** – [Heyen *et al*. 2005]	**0** – Rodriguez-Zas *et al*. [2002a] **65** – Zhang *et al*. [1998]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
14	0-20	**0,1** – Schrooten *et al.* [2004] **1** – Harder *et al.* [2006]$^{+}$ **5** – Bennewitz *et al.* [2003]; Boichard *et al.* [2003]; Chamberlain *et al.* [2002]; Coppieters *et al.* [1998]; Rodriguez-Zas *et al.* [2002b] **20** – Fisher *et al.* [2004]	**0,1** – Bennewitz *et al.* 2003; Schrooten *et al.* [2004] **5** – Chamberlain *et al.* [2002] **20** – Fisher *et al.* [2004]	**0,1** – Bennewitz *et al.* [2003]; Heyen *et al.* [1999] **5** – Boichard *et al.* [2003; Chamberlain *et al.* [2002]; Coppieters *et al.* [1998]; Schrooten *et al.* [2004] **9** – Ashwell *et al.* [2004] **20** – Bennewitz *et al.* [2003]	**0,1** – Rodriguez-Zas *et al.* [2002a]; Schrooten *et al.* 2004] **5** – Ashwell *et al.* [2004]; Bennewitz *et al.* [2003]; Boichard *et al.* [2003]; Chamberlain *et al.* [2002]; Heyen *et al.* [1999]; Viitala *et al.* [2003] **14** – Ashwell *et al.* [2001] **17** – Rodriguez-Zas *et al.* [2002a]	**0,1** – Schrooten *et al.* [2004]; Viitala *et al.* [2003] **2** – Farnir *et al.* [2002] **3** – Ashwell *et al.* [2004] **5** – Bennewitz *et al.* [2003]; Boichard *et al.* [2003]; Chamberlain *et al.* [2002]; Coppieters *et al.* [1998]; Heyen *et al.* [1999] **11** – Heyen *et al.* [2005] **14** – Ashwell *et al.* [2001] **18** – Heyen *et al.* [1999]	
14	20-86	**25** – Rodriguez-Zas *et al.* [2002a] **37** – Ashwell *et al.* [1997] **61** – Schnabel *et al.* [2005]	**58** – Rodriguez-Zas *et al.* [2002a] **63** – Rodriguez-Zas *et al.* 2002b] **66** – Heyen *et al.* [2005]	**28** – Viitala *et al.* [2003] **37** – Heyen *et al.* [2005] **54** – Schnabel *et al.* [2005] **66** – Heyen *et al.* [2005] **80** – Mosig *et al.* [2003]	**33** – Ashwell *et al.* [2004]; Zhang *et al.* [1998] **79** – Harder *et al.* [2006]$^{+}$	**33** – Ashwell *et al.* [1997]; Zhang *et al.* [1998]	**28** – Schulman *et al.* [2004]* **25** – Zhang *et al.* [1998] **37** - Ashwell *et al.* [1997]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
14	20-86	**67** – Heyen *et al.* [1999]	**74 –** Ashwell *et al.* [2004] **81** – Rodriguez-Zas *et al*. [2002a] **86 –**Heyen *et al*. [2005]	**88** – Ashwell *et al.* [2001]	**86** – Heyen *et al*. 1999]		**40 –** Schulman *et al.* [2004] **80** – Bennewitz *et al.* [2004a] **86** – Rodriguez-Zas *et al.* [2002b]; Schulman *et al.* [2004] **86 –** Klungland *et al.* [2001*]
15	0-94		**26** – Harder *et al.* [2006]$^{+}$	**35** – Boichard *et al*. [2003]	**0** – Harder *et al.* [2006]$^{+}$ **20** – Harder *et al.* [2006]$^{+}$	**3 –** Heyen *et al*. [2005] **35** – Boichard *et al.* [2003]	**3** – Boichard *et al.* [2003] **30** – Reinsch *et al.* [1998 **35** – Boichard *et al.* [2003]; Ashwell *et al.* [2004]]
16	0-93	**83** – Rodriguez-Zas *et al.* [2002a]	**10 –** Rodriguez-Zas *et al*. [2002a] **26** – [Rodriguez-Zas *et al*. 2002a] **89** – [Rodriguez-Zas *et al*. 2002a]	**12** – Mosig *et al.* [2003] **53** – Mosig *et al*. [2003]	**41** – Rodriguez-Zas *et al*. [2002a]		**30** – Boichard and Bishop [1997] **56** – Rodriguez-Zas *et al.* [2002a] **78** – Ashwell *et al.* [1997]
17	0-99	**70 –** Rodriguez-Zas *et al.* [2002a]; Zhang *et al*. [1998] **95** – Plante *et al.* [2001]	**6 –** Heyen *et al.* [2005], Rodriguez-Zas *et al*. [2002a];	**5** – Heyen *et al.* [2005] **90** – Heyen *et al.* [2005]	**5** - Heyen *et al.* [2005]	**62** – Plante *et al.* [2001] **74**- Heyen *et al.* [2005]	**74** – Heyen *et al.* [2005]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
17	0-99		Zhang *et al.* [1998] **87** – Boichard *et al.* [2003] **90** – Plante *et al.* [2001] **96** –Ashwell *et al.* [2004]		**70** – Rodriguez-Zas *et al.* [2002a]; Harder *et al.* [2006]$^{+}$ **74** – Heyen *et al.* [2005]		
18	0-81	**39** – Olsen *et al.* [2002] **78** – Ashwell *et al.* [1997]; Harder *et al.* [2006^{+}]	**70** – Olsen *et al.* [2002] **78** – Ashwell *et al.* [1997]	**10** – Boichard *et al.* [2003] **55** – Mosig *et al.* [2003] **80** – Schrooten *et al.* [2004]	**78** – Ashwell *et al.* [1997] **81** – Ashwell *et al.* [2004]; Bennewitz *et al.* [2004a]; Harder *et al.* [2006]	**78** – Ashwell *et al.* [1997]	**53** – Schrooten *et al.* [2000] **65** – Rodriguez-Zas *et al.* [2002a] **78** – Ashwell *et al.* [1997] **82** – Schulman *et al.* [2004*] **81** – Bennewitz *et al.* [2003]; Kuhn *et al.* [1999]; Schulman *et al.* [2004]
19	0-100	**16** – Heyen *et al.* [2005] **98** – Boichard *et al.* [2003]	**81** – Boichard *et al.* [2003]	**67** – Bennewitz *et al.* [2004a]	**47** – Bennewitz *et al.* [2004a] **53** – Bennewitz *et al.* [2003] **98** – Boichard *et al.* [2003]	**66** – Bennewitz *et al.* [2003]; Bennewitz *et al.* [2004a] **72** – Viitala *et al.* [2003]; Boichard *et al.* [2003]	**28** – Bennewitz *et al.* [2003] **42** – Bennewitz *et al.* [2003] **48** – Bennewitz *et al.* [2004a] **64** – Boichard and Bishop [1997]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
20	0-75	**5** –Chamberlain *et al*. [200] **20** – Liu *et al*. [2004] **23** – Arranz *et al*. [2004]; De Koning [2001] **38** – De Koning [2001]; Plante *et al*. [2001] **40** – Liu *et al*. [2004]; Arranz *et al*. [2004]; Blott *et al*. [2003] **54** – Ashwell *et al*. [2004]; Viitala *et al*. [2003] **68** – Ashwell *et al*. [2004]	**5** – Arranz *et al*. [2004]; Heyen *et al*. [2005] **19** – Liu *et al*. [2004] **24** – Plante *et al*. [2001] **35** – Plante *et al*. [2001] **40** – Blott *et al*. [2003]; Rodriguez-Zas *et al*. [2002b] **66** – Olsen *et al*. [2002]	**5** – Heyen *et al*. [2005] **5** – Georges *et al*. [1995] **31** – Arranz *et al*. [2004]; Boichard *et al*. [2003]; Mosig *et al*. [2003]; Ron *et al*. [1998] **36** – Chamberlain *et al*. [2002] **40** – Ashwell *et al*. [2004]; Blott *et al*. [2003]; Georges *et al*. [1995]; Zhang *et al*. [1998] **45** – Ashwell *et al*. [2001] **52** – Bennewitz *et al*. [2004a] **53** – Mosig *et al*. [2003] **56** – Viitala *et al*. [2003] **60** – Arranz *et al*. [2004]; Plante *et al*. [2001] **63** – Ashwell *et al*. [2004] **70** – Mosig *et al*. [2003] **75** – Blott *et al*. [2003]	**8** – Heyen *et al*. [2005]; Plante *et al*. [2001] **20** – Arranz *et al*. [2004] **37** – Kim *et al*. [2002] **42** – Blott *et al*. [2003] **53** – Arranz *et al*. [2004]	**21** – Chamberlain *et al*. [2002] **23** – Arranz *et al*. [2004] **32** – Arranz *et al*. [2004] **40** – Blott *et al*. [2003]; Zhang *et al*. [1998] **43** – Georges *et al*. [1995] **53** – Bennewitz *et al*. [2004a] **75** – Blott *et al*. [2003]	**0,1** – Rodriguez-Zas *et al*. [2002a] **29** – Ashwell *et al*. [2004; Heyen *et al*. [2005] **64** – Heyen *et al*. [2005]; Rodriguez-Zas *et al*. [2002a]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
21	0-89	**0** – Harder *et al*. [2006]$^{+}$ **10** – Rodriguez-Zas *et al.* [2002a] **15** – Ashwell *et al.* [1997] **34** – De Koning *et al.* [2001]; Viitala *et al.* [2003] **43** –Rodriguez-Zas *et al.* [2002b] **44** –Heyen *et al.* [1999]	**15** – Ashwell *et al.* [1997] **44** – Heyen *et al.* [1999]; Rodriguez-Zas *et al.* [2002a] **72** – Rodriguez-Zas *et al.* [2002b]	**13** – Heyen *et al*. [2005]; Mosig *et al*. [2003] **30** – Ashwell *et al.* [1997] **32** – Heyen *et al*. [2005]; Mosig *et al*. [2003] **67** – Heyen *et al*. [2005]; Mosig *et al*. [2003]	**0** – Heyen *et al.* [2005]; Rodriguez-Zas *et al*. [2002b] **15** – Ashwell *et al.* [1997] **43** – Heyen *et al.* [2005]; Rodriguez-Zas *et al*. [2002b] **57** – Rodriguez-Zas *et al*. [2002a] **67** – Heyen *et al.* [2005]; Rodriguez-Zas *et al.* [2002b]	**0** – Heyen *et al.* [2005] **30** – Ashwell *et al.* [1997] **67** – Heyen *et al.* [2005]	**16** – Schnabel *et al.* [2005b] **25** – Schulman *et al.* [2004]* **32** – Heyen *et al*. [1999]; Rodriguez-Zas *et al.* [2002a] **51** – Schulman *et al*. [2004] **67** – Boichard *et al.* [2003]; Heyen *et al.* [2005] **72** – Rodriguez-Zas *et al.* [2002a]
22	0-80	**46** – Heyen *et al.* [2005]	**0** – Boichard *et al.* [2003]; Rodriguez-Zas *et al.* [2002a] **30** – Ashwell *et al*. [2004 **46** – Heyen *et al.* [2005]; Rodriguez-Zas *et al.* [2002b]	**45** – Heyen *et al*. [2005] **76** – Mosig *et al*. [2003] **77** – Ashwell *et al*. [2004]	**18** – Rodriguez-Zas *et al*. [2002a] **46** – Heyen *et al.* [2005] **80** – Harder *et al.* [2006]$^{+}$	**80** – Boichard *et al*. [2003]	**0** – Heyen *et al.* [1999] **45** – Heyen *et al.* [1999] **51** – Ron *et al.* [1998] **80** – Ashwell *et al.* [2004]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
23	0-67	**10** – Viitala *et al*. [2003] **15** – Plante *et al*. [2001] **20** – De Koning *et al*. [2001] **30** – Bennewitz *et al*. [2003] **35** – Ashwell *et al*. [1997] **36** – Bennewitz *et al*. [2004a]	**24** – Schrooten *et al*. [2004] **36** – Bennewitz *et al*. [2004a] **37** – Bennewitz *et al*. [2003] **67** – Ashwell *et al*. [1997]	**4** – Bennewitz *et al*. [2003] **7** – Mosig *et al*. [2003] **17** – Mosig *et al*. [2003] **24** –Viitala *et al*. [2003] **31** –Elo *et al*. [1999]; Maki-Tanila *et al*. [1998] **34** – Heyen *et al*. [2005] **64** – Bennewitz *et al*. [2004a] **67** – Ashwell *et al*. [1997]	**22** – Plante *et al*. [2001] **24** – Ashwell *et al*. [1997] **35** – Ashwell *et al*. [1997] **36** – Bennewitz *et al*. [2004a] **41** – Zhang *et al*. [1998] **42** – Plante *et al*. [2001]	**36** – Ashwell *et al*. [1997]; Heyen *et al*. [2005] **64** – Ashwell *et al*. [1997]	**10** – Ron *et al*. [1998]; Schulman *et al*. [2004] **17** – Ashwell *et al*. [1997]; Boichard *et al*. [2003] **20** – Reinsch *et al*. [1998] **35** – Ahhwell *et al*. [1997]; Heyen *et al*. [2005] **48** – Heyen *et al*. [1999] **50** – Ashwell *et al*. [2004] **51** – Heyen *et al*. [2005] **64** – Ashwell *et al*. [1997] **67** – Ashwell *et al*. [1997]; Holmberg and Andersson-Eklund [2004]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
24	0-62		**36** – Rodriguez-Zas *et al*. [2002a] **68** – Heyen *et al.* [2005]	**34** – Mosig *et al*. [2003]	**68** – Heyen *et al.* [2005]		**28** – Schulman *et al*. [2004]
25	0-64	**60** – Viitala *et al*. [2003] ; Harder *et al*. [2006]$^{+}$	**54** – Viitala *et al*. [2003]	**0** – Viitala *et al*. [2003] **(0-44)** – Mosig *et al.* [2003]			**10** – Holmberg and Andersson-Eklund [2004]*
26	0-73	**15 –** Plante *et al.* [2001] **25** – Bennewitz *et al.* [2003]; Bennewitz *et al.* [2004a] **50** – Bennewitz *et al*. [2003]; Boichard *et al.* [2003]	**15** – Plante *et al*. [2001] **23** – Bennewitz *et al*. [2003] **29** – Bennewitz *et al.* [2004a] **50** – Bennewitz *et al.* [2003] Boichard *et al*. [2003]; Gautier *et al*. [2005] **77** – Gautier *et al.* [2005]	**25** – Bennewitz *et al* [2003]; Bennewitz *et al.* [2004a]; Mosig *et al.* [2003] **72** – Mosig *et al.* [2003]	**11** – Gautier *et al.* [2005; Plante *et al.* [2001] **21** – Bennewitz *et al.* [2003] **25** – Bennewitz *et al.* [2003] **35 –** Gautier *et al.* [2005] **38 –** Plante *et al.* [2001] **40** – Ashwell *et al.* [1997] **50** – Bennewitz *et al*. [2003]; Boichard *et al.* [2003]	**11** – Zhang *et al*. [1998] **38** – Plante *et al*. [2001] **40** – Ashwell *et al*. [1997] **51 –** Viitala *et al.* [2003]	**10** – Ashwell *et al*. [2004] **25 –** Heyen *et al*. [1999] **40** – Ashwell *et al.* [1997] **54** – Zhang *et al.* [1998] **78** – Boichard and Bishop [1997]

Table 1 continued

BTA	Range (cM)	Location of quantitative trait *loci* (cM)					
		of milk yield	of protein yield	of protein content	of fat yield	of fat content	of somatic cell score (with no mark) and *mastitis* (marked with asterisk)
27	0-64	**1** – Rodriguez-Zas *et al.* [2002a] **17** – Van Tassell *et al.* [2004] **45** – Viitala *et al.* [2003] **64** – Ashwell *et al.* [1997]	**0** – Rodriguez-Zas *et al.* [2002a] **17** – Rodriguez-Zas *et al.* [2002a]; Van Tassell *et al.* [2004] **34** – Ron *et al.* [2004] **45** – Viitala *et al.* [2003] **64** – Ashwell *et al.* [1997]	**0** – Mosig *et al.* [2003] **2.5** – Ron *et al.* [2004] **15** –Mosig *et al.* [2003] **64** – Ashwell *et al.* [1997]	**5** – Ashwell *et al.* [2004] **15** – Rodriguez-Zas *et al.* [2002a] **17** – Van Tassell *et al.* [2004] **36** – Ron *et al.* [2004] **64** – Zhang *et al.* [1998]	**0** – Ron *et al.* [2004] **41** – Van Tassell *et al.* [2004]; Zhang *et al.* [1998] **64** – Ashwell *et al.* [1997]	**3** – Kuhn *et al.* [2003] **15** – Rodriguez-Zas *et al.* [2002a]; Schulman *et al.* [2004] **42** - Van Tassell *et al.* [2004] **48** – Klungland *et al.* [2001]*
28	0-52	**18** – Rodriguez-Zas *et al.* [2002a] **25** – Ashwell *et al.* [2004]	**43** –Rodriguez-Zas *et al.* [2002a]	**20** – Zhang *et al.* [1998] **51** – Ashwell *et al.* [2001]		**21** – Zhang *et al.* [1998]	
29	0-65	**10** – Ashwell *et al.* [2004] **11** – Heyen *et al.* [1999]; Rodriguez-Zas *et al.* 2002a] **30** – Viitala *et al.* [2003] **44** – De Koning *et al.* [2001]	**11** – Heyen *et al.* [1999] **12** – Ashwell *et al.* [2004] **25** – Viitala *et al.* [2003]	**1** – Mosig *et al.* [2003] **20** – Mosig *et al.* [2003]	**5** – Ashwell *et al.* [2004] **58** – Rodriguez-Zas *et al.* [2002a]		**9** – Schulman *et al.* [2004] **59** – Ashwell *et al.* [2004]; Heyen *et al.* [2005]
X	0-150	**147** – Harder *et al.* [2006]+	**147** – Harder *et al.* [2006]+		**112** – Sandor et al. [2006 – in press]		

+Persistency of appropriate traits.

Table 2. Expected number of QTLs on *Bos taurus* autosomes

Trait	Autosome				Maximum number of QTLs
	with no QTL	with one QTL	with two QTLs	with three QTLs	
Milk yield	8,15,24	11,12,16,22,25,28	2,5,9,13,17,18,19, 21,23,26,29	1,3,4,6,7,10, 14,20,27	55
Protein yield	10,15	2,4,11,18,19, 25,28,29	7,8,9,12,13,16,17, 22,23,24,26	1,3,5,6,7,14, 20,21,27	57
Protein content		15,19,24,25,28	2,9,10,13,16,17, 22,23,26,29	1,3,4,5,6,7,8,11, 12,14,18,20,21,27	67
Fat yield	8,15,25,28	1,10,11,13,16, 18,22,24	2,4,5,9,12,17,19, 20,21,23,26,29	3,6,7,14,27	47
Fat content	10,11,12,16,24, 25,29	4,5,8,9,13,17, 18,19,22,28	1,2,7,15,20,23,26,27	3,6,14,21	38
Somatic cell score	25,28	2,6,9,11,19,24	1,3,4,7,8,10,12,13,14, 15,16,17,18,21,22,27,29	5,20,23,26	52
Mastitis	1,2,5,7,12,13,15, 16,17,19,20,22, 23,24,26,28,29	3,4,6,8,9,10, 11,18,21,25,27	14		13

[2001] are compared with those of Weller *et al*. [2005].

According to the data shown in Table 2, all major QTLs (which determine 7-50% of the phenotype variance) have already been discovered. The high number (67) of QTLs for %P is likely to be a result of interference of weak magnitude of QTLs M and P that could not overcome a threshold level, or weak-magnitude pleiotropic QTLs M and P (see analysis of BTA3). The least number of reports (38) for %F QTLs is probably a combined result of many factors: tendency towards to couple phase between M QTLs and F QTLs, negligible pressure of selection, high heritability (0.45-0.6), fixation of few major %F QTLs in populations and/or difficulties of the milk fat recording in cattle (peculiarities of genetic control of triglyceride synthesis in milk). For example, the DGAT1 gene determined in different Holstein cattle populations is responsible for 8% [Weller *et al*. 2003] up to 50% [Grisart *et al*. 2004] of the %F phenotypic variation. The high number (57) of SCS QTLs testifies the complex genetic control of this trait. Compared to SCS, the number of MST QTLs is fairly low (14), which may be only a result of few studies, but also emphasises the difficulty in recording this trait.

If a QTL affects several traits, a dilemma emerges: is there one pleiotropic QTL or several QTLs? In cattle, the pleiotropy of M, P and %P QTLs has to be clearly defined. Those QTLs that increase (decrease) milk yield and decrease (increase) %P and %F may be a consequence of the pleiotropy. Their influence on "osmo factors" – lactose, calcium ions *etc*., or membrane permeability factors might modify the osmotic pressure of milk and thus affect its composition. As shown by Viitala *et al*. [2003], such QTLs have been revealed in the Ayrshire breed. All subsequent data presented in this review testify for prevalence of pleiotropic QTLs for milk production traits.

It is also known that genes which are functionally related to each other may be located in close proximity to one another [Hurst *et al*. 2004]. These genes may create QTLs. Two and more such QTLs may mutually increase or decrease their effects on a trait. The extent of such effects may be enough to mask the effects of individual QTLs. Such regions of chromosomes may be named "QTL black holes", by analogy with astronomical "black holes". Key condition for their existence is little DNA recombination in these regions. So, QTL black holes may be of different size. The largest one might be of up to 1 cM if a haplotype fixation takes place. Candidates for such regions may be genes in repulsion[1], especially weak-magnitude QTLs with phenotypic standard deviation less than 0.3. Occurrence of QTLs black holes of intermediate size is possible, which might occupy some area of the active chromatin with a great number of different regulatory sequences. Tiny QTL black holes may also occur which are restricted to one gene only. Such QTL black holes may appear as result of the interference between intragenic nucleotide substitutions, which means intragenic

[1]For example, the QTL alleles for milk yield and fat yield appear to be in repulsion, *i.e*. the high milk yield QTL allele is in the same haplotype with allele determining the low fat yield QTL and *vice versa*. This produces a marked effect on fat content. Alleles may be from one gene or from two different genes.

suppression. As an example of the realisation of such possibility the DGAT1 gene on BTA14 can be used (see BTA14). As to black hole-like QTLs, only the precise mapping within the region or combining tagSNP–microarray analyses may allow their further identification. Owing to epistasis, a part of weak magnitude QTLs cannot be detected. Therefore, there is a strong need for special statistical methods [Carlborg and Haley 2004]. Evaluation of such hidden QTLs is a task for further investigations.

Analysis of location of QTLs on some autosomes of cattle

All calculations have been done assuming a normal distribution of QTLs along the autosomes. Standard deviation can be calculated for F-criteria as SD = 0.5 (Fmax) $^{-1/2}$ x L; where L = length of autosome.

SD = CI/3.9, if P≤ 0.05 (CI=confidence interval). In cases where other statistical criteria are applied, use of the mean SD for that trait is best. In all cases, the arithmetic mean is then calculated. Outlier QTLs can be calculated using the formula

$$\frac{x - \overline{x}}{\sigma} = T$$

and then calculated T mean has to be compared with table mean values for different P values. As far as possible, we take data from a within-family analysis. Sometimes we take QTL data that do not exceed threshold levels in each individual investigation, but were found to exceed threshold level in other works. Table 3 summarizes the results of our calculations. Individual chromosomes are discussed separately.

BTA 1. In this autosome clear evidence was found for three QTLs: M, P and %P (Tab. 3). Probably, they are pleiotropic QTLs. Nadesalingam *et al*. [2001] pointed to a strong P, F and %F QTLs in BTA1.

BTA 2. In BTA2 there are three regions where QTLs are concentrated: 30-40 cM, 60-70 cM and 100-110 cM (Tab. 1 and 3).

BTA 3. For this autosome a phenomenon can be observed, which is also found in other autosomes, namely, that a probability of registration of the %P QTLs is higher than that of QTLs M and P. This results either from an interference of weak magnitude QTLs M and P, which do not overcome the threshold levels (now and further we shall understand interference as a result of the physical interference between QTLs in genome) or from the pleiotropic M, P and %P QTLs with weak magnitude of M and P and strong magnitude of %P trait. This is outlined in the following example. Weak magnitude of M QTL at 30 cM (revealed in one case by Heyen *et al*. [1999]) and weak magnitude of P QTL at 29.0 cM (revealed by Heyen *et al.* [1999] and Rodriguez-Zas *et al*. [2002a]) give rise to a heavy magnitude %P QTL at 28.4 cM (revealed in seven different studies [Heyen *et al*. 1999, Ashwell *et al*. 2001, 2004, Plante *et al*. 2001, Boichard *et al*. 2003, Vitala *et al*. 2003, Liu *et al*. 2004] – Table 1 and 2. As a matter of fact we are dealing with the interaction between two QTLs, one M QTL and one P QTL, virtually leading to a third one – the %P QTL. Such inter-trait interference leads to increasing or decreasing values for the trait %P. Without

Table 3. Location (cM) of QTLs on *Bos taurus* autosomes (BTA) as based on data from Table 1

BTA	M QTL	P QTL	%P QTL	F QTL	%F QTL	Other QTLs
1	13.1±6	22±8			17±9	25±15 – Schulman *et al*. [2004]**
				30 ±8		39±25
	63±8	52.8±6.7				65±17 – Boichard *et al*. [2003][d]
						119±30 – Ashwell *et al*. [2005][j]
	138±8	119±9	131±9			130±9
2			22±11			21±17 – Ashwell *et al*. [2005][n]
	34±15			36±7	32±10	28±20 – Schulman *et al*. [2004]**
			63±11			60±20 – Kuhn *et al.* [2003][f]
						73±27
3	30 – Heyen *et al.* [1999]	29.0±7.8	28.4±4.9	25.3±6.9	25.0± 8.2	35±25
	56.6 ±4.1	56.8±5.2	56.9±4.5	51±6	53.0±4.9	45± – Ashwell *et al*. [2005][j]
			87.5±8.5	72±8		87±26
		104.5±6.8	111.7±6.9		116±15	104±15*
	104.0±8.4					
4	68±9	58±9				71±20*
			104±8			67±15 – Schrooten *et al.* [2004][a]
5		7±7	7±7			7±7
			49.0±8.4			50±9
	69.0±8.4		77±7			101±8
	98.0±5.4	94±10		104±10	98.3±4.5	110±15 – Ashwell *et al.* [2005][j]
6	6±5	7±5	6±5	8±4	9±5	
	28±7	29.5±7.8	30.0±5.0	35 – Freyer *et*	35.0±7.2	50±10*, 55±15
	47.7±3.7	49.0±4.5	47.8±2.8	*al.* 2004	48.4±2.9	52±15 – Schrooten *et al.* [2000][e] –
	62.0±5.6	63.0±4.4	59.6±6.3	50.7±4.2	60.0±5.3	Kuhn *et al*. [2003][g]
	75.7±4.1	80.8±5.1	79.8±3.9	61.6±5.4		85±9
	97.4±5.6	103.1±5.4	92.0 ±5.4	78.0±6.1	101.3±6.4	113±15 – Schnabel *et al.* [2005b][e]
				102±7		

Table 3 continued

BTA	M QTL	P QTL	%P QTL	F QTL	%F QTL	Other QTLs
7	27.0±8.4	24±8	14±8	15±12	19.5±9.2	63±9, 55±15 – Ron *et al.* [2004][f]
						75±10 – Ashwell *et al.* [2004][f]
	80.5±8.8	78.5±8.7	67.5±8.5	72±10		107±12
	117±6	117±8	103.5±7.1			
9	47±7	47±7	48.3±7.7	43±7		45±16 – Boichard *et al.* [2003][b]
						55±15 – Klungland *et al.* [2001]**
	79±6	68±7		66±6		72±15*, 74±15
			84±10	97±8	98±15	98.7±7.5
10			24±7	36±8		7±5*,
						46±20 – Ashwell *et al.* [2005][n]
			63±8			48±10, 75±9
11						24.7±6.6*
	105 – Boichard *et al.* [2003]	99±12	85 – Mosig *et al.* [2003]	88±13		46±8
						93±16
12	35.0±8.5	32.0±8.5	30.5±8.5			
			90±10	86±7		
13	19 – Heyen *et al.* [2005]	19 – Heyen *et al.* 2005	20.0±6.4			
	84±8.5	65.0±6.7	42.0±5.5			
14	5.0±3.2	5±5	5.8±3.0	5±4	4.0±2.9	28±15*, 28±13 –
	27.3±6.8	20±5	31.3±5.5	21±6	21.8±5.6	Schulman *et al.* [2004]**, 34±8
	64±13	65±6	60±7			60±15 – Schnabel *et al.* [2005b][k]
						84±7
		84±10	84±10	86±13		86±15*

Table 3 continued

BTA	M QTL	P QTL	%P QTL	F QTL	%F QTL	Other QTLs
15			35±13		35±14	33±9
17	70±14	92±10		72±8	68±8	69±22 – Ashwell *et al.* [2005][e]
18						54±10 – Ashwell *et al.* [2004][d]
						59±10
	78±15	70±7	80±15	80±7	78±15	78±20 – Kuhn *et al.* [2003][fg]
						82±28 – Kuhn *et al.* 2003][c]
						81±8, 82±11*
19				50±8		51±8, 52±15 – Schrooten *et al.* [2004][m]
					69±6	72±15 – Boichard *et al.* [2003][a]
20	5 – Chamberlain *et al.* [2002]	5±5	5±5	9±4	22±6	29.0±8.4
		22±5				31±12 – Boichard *et al.* [2003][b]
		38±5	36.5±3.8	44±8	41±5	34±9 – Schnabel *et al.* [2005][m]
	22±5					64.0±8.4
	39±5	66 – Olsen *et al.* 2002	61±5		75 – Blott *et al.* [2003]	70±15 – Boichard *et al.* [2003][d]
	54±7					
21	12.5±8.0	15±13	13±8	8±7		25±15*
						32±7
	38.8±5.8	44±8	31±9	55.0±5.4		40±9 – Schnabel *et al.* [2005b][m]
						44±15 – Boichard *et al.* [2003][d]
		72±10	67±9			64±6
22		41±7	76±8			48±10
23	15.0±5.7		9±6			14.5±6.7
						24±16 – Ashwell *et al.* [1997][f],
	33.7±7.5	32.3±7.8	30±5.0	33.3±4.9	36±10	Ashwell *et al.* [2005][j]
						40±12 – Elo *et al.* [1999][a] 45±12**
						45±5
		67±15	66±10		64±15	66.6±7.0

Table 3 continued

BTA	M QTL	P QTL	%P QTL	F QTL	%F QTL	Other QTLs
26	21.7±6.4 50±10	22.3±6.4 50±9	25±6	17±6 43±6	43±6	18±8, 42±15 – Ashwell *et al.* [2005][j] 47±10
27	1 – Rodriguez-Zas *et al.* [2002a] 17±11 64 – Ashwell *et al.* [1997]	0 – Rodriguez-Zas *et al.* [2002a] 17±11 39±8 64 – Ashwell *et al.* [1997]	0 – Mosig *et al.* [2003] 2.5 – Ron *et al.* [2004] 15 – Mosig *et al.* [2003] 64 – Ashwell *et al.* [1997]	5 – Ashwell *et al.* 2004 16±8 36±10 64 – Zhang *et al.* 1998	0 – Mosig *et al.* [2003] 41±10 64 – Ashwell *et al.* [1997]	3 – Kuhn *et al.* [2003], 5 – Ron *et al.* [2004][f] 15±9 21– Ashwell *et al.* [2001][h] 48±13* 62±12 – Ashwell *et al.* [2004][d]
28	22±9					
29	10.7±5.8 37±7	14.8±6.6	1 – Mosig *et al.* 2003	5 – Ashwell *et al.* 2004		9±13 59±10
XY	147 – Harder *et al.* [2006][+]	147 – Harder *et al.* [2006][+]				147 – Harder *et al.* [2006][c,g,q]

Mean and individual QTLs calculated as mean±SD.
M – milk yield, P – protein yield, %P – protein content, F – fat yield, %F – fat content.
Other QTLs: with no mark – somatic cell score QTLs, **mastitis*, **veterinary treatment,
[a]milking speed, [b]udder balance, [c]nonreturn rate on 90d, [d]fertility, [e]calving ease, [f]functional herd life, [g]stillbirth, [h]dairy form, [j]front teat placement, [k]daughter pregnancy rate, [m]fore udder attachment, [n]body depth, [q]dystocia.

question, this example is the simplest event of the inter-trait interference. The most complex events, such as fitness, expressed as health traits or longevity, depended on multiple single traits. The same consideration is not completely suitable for %F QTL (see paragraph Mapping QTLs in cattle). Close study of QTLs for all traits in BTA3 allows to make the following hypothetical assumption of their distribution: 0-10 cM – %P and %F; 20-36 cM – 41-45 cM, 56-66 cM – M, P, F, %P and %F; 70-85 cM – M, %P and F; 100-115 cM – M, P, %P and %F. In the area of 56-66 cM the bifurcation of QTLs can be expected. It is remarkable, that arrangement of QTLs in BTA3 is very similar to that in BTA6. Viitala *et al*. [2003], using their own data gave the position of two %F QTLs at 20 cM and 100 cM. Heyen *et al*. [1999] suggested, that in the region of 30-50 cM three strong QTLs – M, P and F – are located.

For F-QTL 25.3+/-6.9 (Table III) annexin 9 protein gene (*ANXA9*) and fatty acid transporter protein type 3 gene (*SLC27A3*) have been offered as candidate genes on BTA3 [Calva *et al*., 2006].

BTA 5. The *OLR1* gene encoding the oxidised low-density lipoprotein receptor has been proposed as a candidate marker [Khatib *et. al*. 2006]. The location of the gene was estimated to be in the interval of 106-108 cM of BTA5, where M, P, F and %F QTLs were mapped (Tab. 1 and 3). In the 3'-untranslated region (UTR) the quantitative trait-associated nucleotide (QTAN) the substitution A/C was found, which had an effect on milk yield and fat content [Khatib *et. al*. 2006]. But the authors could not completely exclude the possibility that the observed effects were caused by linkage disequilibrium (LD) with another functional SNP in control regions of OLR1 or by LD with other nearby genes.

BTA 6. In the pericentromeric region of BTA6 firstly the M, P and F QTL was reported. Moreover, in relation to the trait M it is in repulsion with the M QTL near the BM143 marker [Ron *et al.* 1998]. A complete BTA6 scan for QTLs of the American Holstein population has revealed the M, P, F, %P and %F QTLs in this region as well [Schnabel *et al*. 2005a]. A preliminary position of these QTLs was given of 6±5 cM (Tab. 3). A second milk production QTL-cluster (M, P, F, %P, %F) is supposed to be within the region 28-35 cM (Fig. 1). From the covariance analysis it appears that these QTLs may coincide as a pleiotropic %P and %F MQR (multiple trait quantitative trait region) – Schrooten *et al.* [2004]. The central region of BTA6 is very complex for interpretation. In this region the interference might exist between different QTLs, in some cases resulting from pleiotropy. Freyer *at al*. [2003] was able to detect two M QTLs, one of a strong magnitude (F=12.1) at 40 cM and another of a weaker magnitude (F=4.19) at 59 cM. Moreover, these data coincide with those presented by Ron *et al.* [2001] and Velmala *et al*. [1999], who also point out the M QTL at about 40 cM. Olsen *et al*. [2004] draw attention to a very weak M QTL located at 64 cM. Near the BM143 marker there is a strong magnitude M QTL reported by many laboratories and authors, and also the %P QTL. Thus, apparently there is an evidence for three M QTLs in the central region of BTA6 (Fig. 1).

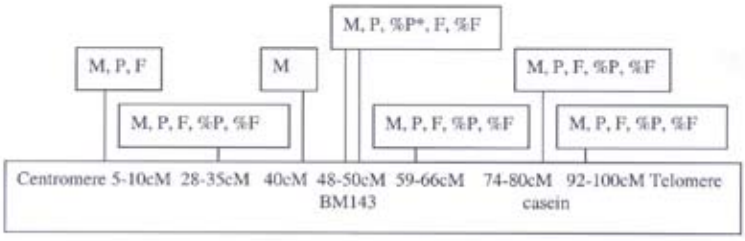

Fig. 1. Presumable QTL map of BTA6. *Region of a hypothetical bifurcation.

The character of distribution of these M QTLs does not allow dissecting the M QTL at 40 cM, but this should be possible for the M QTL at 58-64 cM (Tab. 1). The mean calculated is 47.7±3.7 cM and appears very similar to that got for the P QTL, *i.e.* 49.0 ± 4.5 cM (Tab. 3).

The exact position of the %P QTLs in the middle of BTA6 might been the effect of interference between as much as three M QTLs and two P QTLs (Fig. 1). There are three precisely localized positions for %P QTLs in the vicinity of BM143: one by Ron *et al.* [1998] at 50±4 cM, second by Olsen *et al.* [2004] at 46±4 cM, and third by Schnabel *et al*. [2005a] at 48±4 cM. We computed the mean position for this %P QTL to reach 47.8±2.8 cM (Tab. 3). This is a very remarkable result, mostly because the mean position of the QTL from twelve independent investigations coincides with three individual reports. Moreover, the results testify the normal distribution of these QTLs (Tab.1). Apparently, in the 40-53 cM region (Tab. 1) there are no other strong-magnitude QTLs that could affect distribution of %P QTLs, or they may be located nearby and thus could not be resolved.

How many QTLs of %P in the central 48-65 cM region of BTA6 exist? There is one triple QTL of relatively weak-magnitude (M, P and %P) at 58-64 cM. The strong-magnitude QTL located near the BM143 marker has five alleles: (+M, -%P), (+M, --%P), (weak M, --%P), (+M, -P, -%P), and (-M, -P, +%P), where + or - means increase or decrease in a given trait, respectively [Georges *et al*. 1995, Spelman *et al*. 1996, Zhang *et al*. 1998, Kuhn *et al*. 1999, Velmala *et al*. 1999, Wiener *et al*. 2000, Ron *et al*. 2001, Olsen *et al*. 2002, Schnabel *et al*. 2005a]. Out of the five alleles mentioned there are apparently two or three which display a different phenotype in relation to genetic background and accuracy of phenotype calculation[1]. Therefore, the question arises, whether these five alleles belong to one QTL? The possibility exists that the region around BM143 is apt to bifurcation (Fig. 1). In support to this hypothesis are facts given below: (i) another candidate genes have recently been found, which are

[1]Empirically (from different papers) there are 5 alleles, but because of different genetic background and accuracy of phenotype calculation we may suppose that in fact there are only 2-3 alleles.

located proximally to BM143, namely osteopontin *(OPN)* – Schnabel *et al*. [2005a], polycystin 2 *(PKD2)* – Olsen *et al*. [2005], and *ABCG2* – Cohen-Zinder *et al.* [2005]; (ii) one of the most probable causative genes for region 46-48 cM is *ABCG2* and (iii) the *OPN* gene is expressed in mammary gland, and area *OPN-PKD2-ABCG2* exhibits a very strong linkage disequilibrium. So, in different populations of cattle some of the these genes may serve as causative for %P QTL, and epistatic interaction can not be excluded between genes of that region. Cohen-Zinder *et al*. [2005] consider another QTL proximate to centromere from the HERC6 marker that is responsible for milk, fat, and protein production, but QTL which located distally to LAP3 mainly affects milk, fat yield and protein concentration.

The following question remains unanswered: are the QTLs of F at position 50.7±4.2 cM and of %F at 48.4±2.9 cM the same as of %P at 47.8±2.8 cM? In other words, is it a pleiotropic QTL? Formally, three of five alleles mentioned above also included the F and/or %F phenotype and the presence of pleiotropic QTL coincides with the data of Ron *et al*. [2001] and Cohen-Zinder *et al.* [2005]. Distally to the BM143, peroxysome proliferator-activated receptor-gamma coactivator-1 alpha *(PPARGC1A*) at 51 cM have been offered as causative gene for F QTL [Weikard *et al*. 2005]. The quantitative trait-associated nucleotide (QTAN) of PPARGC1A gene lays in intron 9, so it might be questioned if it really is a QTN (quantitative trait nucleotide – *i.e*. the one that gives a mutation). In cattle, the mean LD (linkage disequilibrium) reaches the value of 30 cM [Farnir *et al*. 2000], what may be the consequence of haplotypes long up to several megabases, as compared to human LD that is only 1-2 cM, with its maximum haplotype length of 0.8Mb [Wall and Pritchard 2003]. If it is true the QTL linked with QTAN of *PPARGC1A* may belong to F QTL 50.7±4.2 cM or to F QTL 61.6±5.4 cM (Tab.3). Ongoing research will further elucidate this supposition.

Apparently, there are M, P, F, %P and %F QTLs at 59-64 cM in BTA6 (Tab. 3). In favour of that hypothesis is the evidence of pleiotropy of P and F QTLs at 58 cM [Freyer *et. al*. 2003] and data presented by Szyda *et al.* [2005] and Schnabel *et al.* [2005a] reporting QTLs of M, P, F, %P and %F in the same region.

In linkage maps the casein genes were mapped to BTA6 83±5 cM (Prinzenberg *et al.* 2003). It is therefore highly probable that casein genes are candidates for P QTLs at 80.8±5.1 cM and %P QTLs at 79.8±3.9 cM. In the same region located is the F QTL at 78.0±6.1 cM (Tab. 3). Apparently, F QTL is a pleiotropic one as in this region, at 81.5-83.0 cM, another QTL was found affecting the fat thickness on the back [Li *et al.* 2004]. Regarding the 94-100 cM region, it is still not clear how many QTLs it contains (Fig. 1). Schrooten *et al*. [2004] have found there two MQR (%F and %P – 12 cM, and P and %P – 121 cM). Thus, in our opinion in BTA6 there are minimum six regions where QTLs for milk production traits are concentrated: 5-10 cM, 15-35 cM, 47-50 cM, 59-66 cM, 74-80 cM, and 92-103 cM. In each region there may be one or two pleiotropic QTLs (Fig. 1).

The positions we found there for QTLs partly coincide with the data based on meta-analysis [Kathar *et al*. 2004] – M QTL 49.5±5.0 cM, 86.7±7.9 cM; P QTL 51.6±7.2 cM; %P QTL 49.4±1.8 cM, 91.1±7.6 cM; F QTL 50.8±6.0 cM, and %F QTL 48.1±2.8 cM, 113±15 cM except the pericentromeric region 7-30 cM (Tab. 3), for which no data are available from the cited paper of Kathar *et al*. [2004].

BTA7 and BTA 9. Despite the fact that BTA7 is longer than BTA6, its QTLs are distributed sparcely. Only in the 15-30 cM, 60-80 cM, and 115-125 cM regions the QTLs are concentrated (Tab. 1 and 3). In BTA9 (110 cM) there is a gap in QTLs close to the middle of the chromosome (Tab. 1), the phenomenon that represents a non-uniform distribution of the QTLs in bovine chromosomes. The BTA6, being saturated with the milk production trait QTLs as compared to other chromosomes, is an exception in this respect.

BTA 14. The gene *DGAT1* was the first candidate gene discovered in dairy cattle [Grisart *et al*. 2002, 2004]. It seemed that the diallelic state of *DGAT1* was in accordance with the animal's phenotype. Later on, supplementary alleles with VNTR repeats were discovered in the promoter region of *DGAT1* [Kuhn *et al*. 2004]. There is a discussion ongoing whether the existence of additional alleles in the promoter region of *DGAT1* (forming intragenic haplotypes with the diallelic polymorphism of *DGATI* coding region) or another F, P, %P or %F QTL occurring near the gene [Bennewitz *et al.* 2004b, Furbass *et al*. 2006] best explain the total phenotypic variation. From our analysis it appears that there are M, P, F, %P and %F QTLs in the region of 20-30 cM (Tab. 3).

The nature cares for a reliable lipid metabolism. There is a family of several DGAT genes, active in different parts of the body [Cases *et al*. 2001]. No relationship has been found between DGAT1 and fat thickness on the back in cattle Moore *et al.* [2003]. The same authors suppose the presence of another QTL in the region of 5-15 cM, responsible for the back fat trait. This shall be clarified in nearest future. A DNA segment spanning 576 kb, including DGAT1 gene [Winter *et al*. 2004], was isolated and cloned. Attention should be drawn to the fact, that in the region of 7-13 cM there is a MQR between M, P, %P, F, %F and the udder conformation [Schrooten *et al*. 2004] as also pregnancy rate QTLs found [Ashwell *et al.* 2004]. It is questionable, whether all these traits are determined (or at least significantly affected) by *DGAT1*. In this study a QTL, which was not mapped exactly, has roughly been located in the 0.1 cM region, and was not considered in calculations (Tab. 1). In the 60-70 cM region of BTA14 a pleiotropic M, P and %P QTL (or few QTLs) is located (Tab. 3). On the contrary, in the 80-90 cM region located are the P, %P and F QTLs (Tab.3).

BTA 19. The growth hormone gene (*GH*) is located at 66 cM in BTA19. Our statistical analysis shows that only the reported %F QTL at 69±6 cM may have some relation to the GH gene. Therefore, as a %F QTL candidate gene, the one coding for fatty acid synthase (FASN) has been proposed [Roy *et al*. 2005], located nearby the SCS QTL at 51±8 cM and fore udder attachment QTL at 52±15 cM (Tab. 3). The expectation of geneticists that genes coding for hormones could be candidates for moderate or major QTLs of milk production traits has not been confirmed. The

unsolved problem is which genes determining significant variation in milk traits (milk variation-keeping genes) allow a population of dairy cattle to response accordingly to the pressure of selection. Are these transcription factors, genes encoding hormones and other regulatory genes, or they belong to genes of metabolic pathways. There are not enough causative genes discovered until now to answer this question.

BTA 20. In the central region of the BTA20, at 40 cM, the growth hormone receptor (GHR) gene (*GHR*) has been mapped, probably responsible for effects on traits M, %P and %F. Blott *et al*. [2003] demonstrated that the F279Y substitution in the transmembrane domain of *GHR* contributes to the phenotype variation – M (0.7-2.9%), %P (5.3-9.4%) and %F (2.3-5.5%) – in Holstein-Friesian cattle. Statistical analysis of the distribution of QTLs led to determination an outlier M QTL at 54 cM ($P<0.05$) (Tab. 1). We calculated a mean value for the M QTL position at 39±5 cM. Altogether, in BTA20 there are four M QTLs (22±5 cM, 39±5 cM, 54±7 cM) – Cohen *et al*. [2002], four P QTLs (5±5 cM, 22±5 cM, 38±5, 66 cM) – Olsen *et al.* [2002], and three %P QTLs (5±5 cM, 36.5±3.8 cM, 61±5 cM) – Table 3). There is a possible bifurcation of %P QTL at 36.5 ± 3.8 cM on two other QTLs – 31 cM and at 40 cM (Tab.1). As far as M, P and %P traits are concerned, BTA20 could be referred to as an autosome saturated with QTLs. Liu *et al*. [2004] claim that QTLs M and P at 20 cM are probably pleiotropic. Blott *et al*. [2003] reported a %P and %F QTLs at 75 cM. Most likely on BTA20 there are following regions where QTL concentrate: 0-10 cM – M, P, F and %P; 20- 25 cM – M and P; 39-41 cM – M, P, %P, F and %F; 55-75 cM – M, P, %P and %F. There are also data available from a meta-analysis of BTA20 showing M QTL at 37.7±8.2 cM and %P QTL at 38.5±1.9 cM and 49.6±5.0 cM) – Kathar *et al.* [2004]. Blott *et al.* [2003] have not found a relationship between haplotypes under investigation and the trait F, nevertheless they noted a weak magnitude F QTL at 42 cM. Earlier Arranz *et al.* [1998] found a weak magnitude of F QTL at 53 cM ($P<0.07$) while Ashwell *et al.* [2005] pointed out on strong magnitude of QTLs affecting thurl width, body depth, and strength in region where gene *GHR* occurs.

BTA 23. This autosome is remarkable as it harbours the complex major histocompatibility *locus* (*BoLA*) at 35 cM and the gene coding for prolactin (*PRL)* at 43 cM. No somatic cell score (SCS) QTLs were located near BoLA *locus* (Tab. 3). This is the evidence that SCS QTLs are not of immunological nature. In the region 15-25 cM, where only one SCS QTL has been identified, QTLs for structural parametres of the udder are concentrated. Referring to gene *PRL,* there is some hope in considering it as a candidate gene for F QTL at 41-42 cM (Tab. 1). It should be taken into account that these QTLs segregate only in American and Canadian populations of dairy cattle. It is interesting to note that also QTL of thickness of back fat in cattle (45.1-50.9 cM) – Li *et al*. [2004] – may be related to *PRL*. From Table 1 the following arrangement of QTLs in BTA23 can be assumed: 10-20 cM for M and %P; 30-35 cM for M, P, %P, F and %F and 64-67 cM for P, %P and %F.

BTA 26. In BTA26 several M, P, F and %P QTLs were identified (Tab.1). The QTLs in this chromosome might be used for MAS (marker-assisted selection). For

the F QTL (43±6 cM, Tab. 3) two candidate genes have been proposed: mitochondrial glycerol-3-phospate acyltransferase (*GPAM*) – Roy *et al*. [2005] – or insulin 1 precursor *(INS1)* – Gautier *et al*. [2005]. For F QTL (17±6 cM) the candidate is the gastric lipase (LIPF) gene [Gautier *et al*. 2005]. Related study shows the linkage between QTAN – a C/T substitution in the bovine *TCF7L2* gene (40cM) in BTA26 and M, P, F, %P QTL [Jiang *et al*. 2005]. It means that in the 35-50 cM region one F QTL and one pleiotropic M, P, F, %P QTL are located (Tab. 3). The presence of %P trait in the pleiotropic QTL reported by Jiang *et al*. [2005] and absence of the %P QTL from Table I results from different methods used for identification of these QTLs. It is to be noted, that at nearly the same position (47±10 cM) QTL of SCS and udder type are located (Tab. 3).

BTA 27. It was shown that in chromosome BTA27 a strong-magnitude QTL of dairy conformation (DF) is located, next to the BMS689 marker at 34 cM [van Tassel *et al*. 2004]. Selection for improved DF may lead to selecting cows that are more prone to reproductive and metabolic diseases [Van Tassel *et al*. 2004]. In the same region the F and %F QTLs are located (Tab. 3). So, identification of genes that determine DF QTL would help to elucidate the genetic and physiological mechanisms of fat metabolism in dairy cattle. On the other hand, however, the DF QTL may be useful in selecting animals which are more resistant to metabolic disorders without forfeiting substantial genetic improvement in production traits [van Tassel *et al*. 2004]. According to Table 1 and 3 there are three regions in BTA27 where milk production traits QTLs are concentrated: (i) in pericentromeric region at 0-17 cM – M, P, F, %P and %F QTLs, (ii) in central region at 34-40 cM – P and F QTLs, and (iii) next to telomere – at 64 cM – M, P, F, %P and %F QTLs. It should be noted that at 45 cM the M and P QTLs (Tab. 1) are located even more "telomerical" than at 64 cM because only two markers have been used for its mapping [Viitala *et al*. 2003]. Van Tassel *et al*. [2004] have mentioned BTA27 as a promising object for MAS, especially for F QTLs at 36 cM, %F QTLs at 41 cM and DF QTL at 34 cM (Tab. 3).

X-chromosome. It seems strange, that there are very few investigations on QTLs in relation to the X-chromosome. This is apparently due to technical difficulties in simultaneous mapping QTLs in autosomes and X-chromosome using daughter and granddaughter designs. Two QTLs for lactation persistency and QTLs for dystocia, stillbirths and non-return rate were found on BTAX/Y [Kuhn *et al.* 2003, Harder *et al.* 2006]. The haplotype analysis revealed that the lactation persistency QTLs and QTLs for the three fertility traits were segregating together in one family. This indicates that both traits may be affected by a single *locus* in the pseudoautosomal region of BTAX/Y, and suggests that X-chromosome is a very interesting object for searching QTLs for all milk production traits.

Arrangement of QTLs in cattle autosomes

Modern dairy cattle breeds have been obtained as a result of domestication and selection for dairy traits. Selection was carried out using natural alleles of

genes responsible for milk production traits. Studying phenotype contribution and arrangement of QTLs it is possible to define which QTLs are fixed in a given population. If some candidate genes of these QTLs belong to one metabolic pathway, the cluster arrangement of QTLs on chromosome(s) is possible. To check this assumption with the help of a *chi*-square and Kolmogorow-Smirnov criterions the distribution of QTLs in chromosomes has been estimated. H_0 hypothesis assumes the uniform (normal?) distribution of QTLs in bovine chromosomes. On the basis of the results obtained the following basic conclusions can be made:

(1) In most cases M, P, F, %P, %F QTLs settle down in clusters that testify the display of one or two pleiotropic QTLs. This feature of QTLs of milk production traits in cattle may be used for reduction the standard error (SE). For example, the %P QTL at 47.8±2.8 cM located next to BM143 in the BTA6 (Tab. 3) has the SE of 2.8 cM, but hypothetically pleiotropic M, P, F, %P and %F QTL 48.7±1.6 cM localized in the same position has SE 1.8 cM. That results in SE nearly two times less than well-defined SE for %P QTL, which has been identified with LA/LD mapping [Olsen *et al*. 2005].

(2) For each separate trait the cluster arrangement of QTLs has not been revealed. As it follows from Table 3, the resolving power of applicable statistic analysis used could dissect two QTLs on distance not less than 12 cM. It means that each QTL from Table 3 may be potentially complex. In other words it might consist of several QTLs. But in cattle no QTLs have been found so far at the distance less than 12 cM.

***Mastitis* (MST)**

Mastitis, and also subclinical *mastitis*, causes tremendous economical losses (in USA two billion dollars each year – van Tassel *et al*. [2004]) due to direct treatment costs, culling of cows, or indirect losses in milk production as well as changes in milk quality. SCS (somatic cell score) is a suitable parameter for evaluation of udder health. Its correlation with *mastitis* is 0.7±0.1 [Shook *et al*. 2006]. Moreover, a positive relationship exists between *mastitis* incidence and high milk yield of cows. That fact may point out on combined selection for MST QTLs and QTLs of milk production traits. Consequently for MAS, the positions of MST-QTLs need to be taken into account. Using the data from Table 3 it is possible to reveal favourable and(or) unfavourable positions of MST QTLs. For example, in the central region of BTA6 there is the MST QTL at 50±10 cM, while the SCS QTL occurs at 85±9 cM (Tab. 3). Moreover, in Table 3 QTLs for veterinary treatment, fertility, calving ease *etc*. are shown. Taken into account the imprecise location of QTLs at 10-20 cM, their positions must be considered as preliminary. But in some cases undesirable QTLs located close to each other can lead to consequences unfavourable for selection. Nevertheless, some facts are obvious: for BTAs 3, 6, 8, 9, 14, 18, 21 and 27 the SCS QTLs and MST QTLs occupy the same region (Tab. 4). In BTA 14, the candidate gene for SCS QTL at 34±8 cM (Tab. 3) might be the DNA-dependent protein kinase gene *(PRKDC)* – Schwerin

et al. [2003]. The nearest future should clarify what candidate genes determine SCS/ MST QTLs. Table 4 summarizes the co-location regions between MST-QTLs and QTLs for milk production traits.

Table 4. Locations of *mastitis* and other milk production traits QTLs (cM) on selected *Bos taurus* autosomes (BTA)

BTA	MST QTL	M QTL	P QTL	%P QTL	F QTL	%F QTL	SCS QTL
3	104±15	84-125	84-120	84-116	-	-	83-120
4	71±20	44-96	-	50-100	54-100	46-98	-
6	50±10	37-57	40-61	39-59	39-63	39-61	43-63
8	31±15	-	-	17-53	-	-	17-59
9	72±15	58-92	58-92				68-100
10	7±5	0-22	-	-	-	-	-
14	28±15	7-47	3-43	8-42	9-41	8-40	13-47
	86±15	52-86	51-86	62-86	-	-	65-86
18	82±11	54-82	63-82	63-82	64-82	64-82	64-82
21	25±15	1-37	0-40	0-40	0-40	-	11-47
27	48±13	35-67	35-67	49-71	30-62	34-66	25-65

Mean MST QTLs – mean±SD.
Regions within each cell are shown of co-location of a given QTL ($P<0.05$).
MST – *mastitis*, M – milk yield, P – protein yield, %P – protein content, F – fat yield, %F – fat content, SCS somatic cell score.

According to calculations by Pong-Wong *et al.* [2002] the MAS may effectively spread up to 10 cM with decreasing significancy, depending on a trait. So, if two QTLs are located at a distance of up to 10 cM, then they shall be subjected to effective co-selection. Thus, MAS programmes need to draw attention to unfavourable QTLs within ±10 cM from a marker selected.

Results and discussion

It follows from the analysis presented here that QTLs are still localized imprecisely and it would be difficult to search for, or to define candidate genes in these regions. The only solution to this situation is to map the QTLs precisely. Microsatellite markers reach limitations for that purpose. Presently, other type of genetic markers – SNPs (single nucleotide polymorphisms) – gain increasing popularity in gene mapping studies, due to their high accuracy and reproducibility. Moreover, they are indispensable for identification of positional candidate genes [Vignal *et al*. 2002]. First results of such approach are now available. For example Blott *et al*. [2003],

Olsen *et al.* [2004], Schnabel *et al*. [2005a] and Cohen-Zinder *et al*. [2005] used SNP for mapping candidate genes.

In light of this, identification of candidate genes in moderate and major QTL regions will involve the following steps: (i) rough mapping by segregation analysis of QTLs; (ii) more precisely mapping using combined LA/LD analysis; (iii) fine mapping at 1-100 kb using SNP (method of overlapping haplotypes). Such approach promoted creation of a more dense microsatellite map [Ihara *et al*. 2004], SNP maps [Werner *et al*. 2004], BAC-maps [Schibler *et al.* 2004], EST maps [Everts-Van der Wind *et al*. 2004], and finally the sequence of whole cattle genome [Andersson *et al*. 2004].

There is an intensive search going on for candidate genes in target regions, combining comparative mapping across human and laboratory animal maps, cattle maps and whole genome sequencing projects. Projects like HapMap on human genome (http://www. hapmap.org), which now might be applied also for cattle, will speed up ongoing research. First results can be expected in near future.

REFERENCES

1. ANDERSSON L., GEORGES M., 2004 – Domestic animal genomics: deciphering the genetics of complex traits. ***Nature*** 5, 202-212.
2. ARRANZ J.J., COPPIETERS W., BERZI P., CAMBISANO N., GRISART B., KARIM L., MARCQ F., MOREAU L., MEZER C., RIQUET J., SIMON P., VANMANSHOVEN P., WAGENAAR D., GEORGES M., 1998 – A QTL affecting milk yield and composition maps to bovine chromosome 20: a confirmation. ***Animal Genetics*** 29, 107-115.
3. ASHWELL M.S., REXROAD C.E.J.R., MILLER R.H., Van RADEN P.M., DA Y., 1997 – Detection of loci affecting milk production and health traits in an elite US Holstein population using microsatellite markers. ***Animal Genetics*** 28, 216-222.
4. ASHWELL M.S., Van TASSELL C.P., SOENSTEGAARD T.S., 2001 – A genome scan to identify QTL affecting economically important traits in a US Holstein population. ***Journal of Dairy Science*** 84, 2535-2542.
5. ASHWELL M.S., HEYEN D.W., SOENSTEGAARD T.S., Van TASSELL C.P., DA Y., Van RADEN P.M., RON M., WELLER J.I., LEWIN H.A., 2004 – Detection of QTL affecting milk production, health, and reproductive traits in Holstein cattle. ***Journal of Dairy Science*** 87, 468-475.
6. ASHWELL M.S., HEYEN D.W., WELLER J.I., RON M., SOENSTEGAARD T.S., Van TASSELL C.P., LEWIN H.A., 2005 – Detection of quatitative trait loci influencing conformation traits and calving ease in Holstein-Friesian cattle. ***Journal of Dairy Science*** 88, 4111-4119.
7. BENNEWITZ J., REINSCH N., GROHS C., LEVEZIEL H., MALAFOSSE A., THOMSEN H., XU N., LOOFT C., KUHN C., BROCKMANN G.A., SCHWERIN M., WEIMANN C., HIENDLEDER S., ERHARDT G., MEDJUGORAC I., RUSS I., FORSTER M., BRENIG B., REINHARDT F., REENTS R., AVERDUNK G., BLUMEL J., BOICHARD D., KALM E., 2003 – Combined analysis of data from two granddaughter designs: A simple strategy for QTL confirmation and increasing experimental power in dairy cattle. ***Genetics, Selection, Evolution*** 35, 319-338.
8. BENNEWITZ J., REINSCH N., GUIARD V., FRITZ S., THOMSEN H., LOOFT C., KUHN C., SCHWERIN M., WEIMANN C., ERHARDT G., REINHARDT F., REENTS R., BOICHARD D., KALM E., 2004a – Multiple QTL mapping with cofactors and application of alternative variants of the false discovery rate in an enlarged granddaughter design. ***Genetics*** 168, 1019-1027.

9. BENNEWITZ J., REINSCH N., PAUL S., LOOFT C., KAUPE B., WEIMANN C., ERHARDT G., THALLER G., KUHN C., SCHWERIN M., THOMSEN H., HEINHARDT F., REENTS R., KALM E., 2004b – The DGAT1 K232A mutation is not solely responsible for the milk production QTL on the bovine chromosome 14. ***Journal of Dairy Science*** 87, 431-442.
10. BLOTT S., KIM J.J., MOISIO S., SCHMIDT-KUNTZEL A., CORNET A., BERZI P., CAMBISANO N., FORD C., GRISART B., JOHNSON D., KARIM L., SIMON P., SNELL R., SPELMAN R.,WONG J., VILKKI J., GEORGES M., FARNIR F., COPPIETERS W., 2003 – Molecular dissection of a QTL: A phenylalanine-to-tyrosine substitution in the transmembrane domain of the bovine growth hormone receptor is associated with a major effect on milk yield and composition. ***Genetics*** 163, 253-266.
11. BOICHARD D., BISHOP M.B., 1997 – Detetion of QTLs influencing milk production and mastitis resistance with a granddaughter design in Holstein cattle. Proceedings of the 48th Annual Meeting of the EAAP, Vienna, Austria.
12. BOICHARD D., GROHS C., BOURGEOIS F., CERQUEIRA F., FAUGERAS R., NEAU A., RUPP R., AMIGUES Y., BOSCHER M.Y., LEVEZIEL H., 2003 – Detection of genes influencing economic traits in three French dairy cattle breeds. ***Genetics, Selection, Evolution*** 35, 77-101.
13. BOVENHUIS H., SCHROOTEN C., 2002 – QTL for milk production traits in dairy cattle. Proceedings of the 7th World Congress on Genetics Applied to Livestock Production, 19-23 August, Montpellier, France. Paper 09-07.
14. CALVA J.H., MARTINEZ-ROYO A., SILVERI L., FLORIOT S., EGGEN A., MARCOS-CARCAVILLA A., SERRANO M., 2006 - Isolation, mapping and identification of SNPfor four genes (ACP6, CGN, ANXA9, SLC27A3) from a Bovine QTL region on BTA3. ***Cytogenetics and Genome Research*** 114, 32-43.
15. CARLBORG O., HALEY C.S., 2004 – Epistasis: too often neglected in complex trait studies? ***Nature*** 5, 618-625.
16. CASES S., STONE S.J., ZHOU P., YEN E., TOW B., LARDIZABAL K.D., VOELKER T., FARESE JR. R.V., 2001 – Cloning of DGAT2, a second mammalian diacylglycerol acyltransferase, and related family members. ***Journal of Biological Chemistry*** 276, 38870-38876.
17. CHAMBERLAIN A., MCPARLAN H., BALASINGHAM T., CARRICK M., BOWMAN P., ROBINSON N., GODDARD M., 2002 – Mapping QTL affecting milk composition traits in dairy cattle using a complex pedigree. Proceedings of the 7th World Congress on Genetics Applied to Livestock Production, 19-23 August, Montpellier, France. Paper 09-08.
18. COHEN M., SERROUSI E., RON M., REICHENSTEIN M., PLIS-FINAROV A., SHANI M.,WELLER J.I., 2002 – Population-wide linkage disequilibrium between a SNP and a QTL affecting milk protein production on BTA6 in dairy cattle. Proceedings of the 7th World Congress on Genetics Applied to Livestock Production, 19-23 August, Montpellier, France. Paper 09-12.
19. COHEN-ZINDER M., SEROUSSI E., LARKIN D.M., LOOR J.J., EVERTS vAN DER WIND A., LEE J.H., DRACKLEY J.K., BAND M.R., HERNANDEZ A.G., SHANI M., LEWIN H.A., WELLER J.I., RON M., 2005 – Identification of a missense mutation in the bovine ABCG2 gene with a major effect on the QTL on chromosome 6 affecting milk yield and composition in Holstein cattle. ***Genome Research*** 15 (7), 936-944.
20. COPPIETERS W., RIQUET J., ARRANZ J.J., BERZI P., CAMBISANO N., GRISART B., KARIM L., MARCQ F., MOREAU L., NEZER C., SIMON P., VANMANSHOVEN P., WAGENAAR D., GEORGES M., 1998 – A QTL with major effect on milk yield and composition maps to bovine chromosome 14. ***Mammalian Genome*** 9, 540-544.
21. ELO K.T., VILKKI J., De KONING D.J., VELMALA R.J., MAKI-TANILA A.V., 1999 – A QTL for live weight maps to bovine chromosome 23. ***Mammalian Genome*** 10, 831-835.

22. EVERTS-Van der WIND A., KATA S.R., BAND M.R., REBEIZ M., LARKIN D.M., EVERTS R.E., GREEN C.A., LIU L., NATARAJAN S., GOLDAMMER T., LEE J.H., MCKAY S., WOMACK J.E., LEWIN H.A., 2004 – A 1463 gene cattle-human comparative map with anchor points defined by human genome sequence coordinates. ***Genome Research*** 14, 1424-1437.
23. FARNIR F., COPPIETERS W., ARRANZ J-J., BERZI P., CAMBISANO N., GRISART B., KARIM L., MARCQ F., MOREAU L., MNI M., NEZER C., SIMON P., VANMANSHOVEN P., WAGENAAR D., GEORGES M., 2000 – Extensive genome-wide linkage disequilibrium in cattle**.** ***Genome Research*** 10, 220-227.
24. FARNIR F., GRISART B., COPPIETERS W., RIQUET J., BERZI P., CAMBISANO N., KARIM L., MNI M., MOISIO S., SIMON P.,WAGENAAR D., VILKKI J., GEORGES M., 2002 – Simultaneous mining of linkage and linkage disequilibrium to fine map QTL in outbred half-sib pedigrees. Revisiting the location of a QTL with major effect on milk production on bovine chromosome 14. ***Genetics*** 161, 275-287.
25. FISHER P.J., SPELLMAN R.J., 2004 - Verification of selective DNA pooling methodology through identification and estimation of the DGAT1 effect. ***Animal Genetics*** 35, 201-205.
26. FREYER G., KUHN C., WEIKARD R., ZHANG Q., MAYER M., HOESCHELE I., 2002 - Multiple QTL on chromosome six in dairy cattle affecting yield and content traits. ***Journal of Animal Breeding and Genetics*** 119, 69–82.
27. FREYER G., SOERENSEN P., KUHN C., WEIKARD R., HOESCHELE I., 2003 – Search for pleiotropic QTL on chromosome BTA6 affecting yield traits of milk production. ***Journal of Dairy Science*** 86, 999-1008.
28. 27 FREYER G., SOERENSEN P., KUHN C., WEIKARD R., 2004 - Investigation in the character of QTL affecting negatively correlated milk traits. ***Journal of Animal Breeding and Genetics*** 121, 40-51.
29. FURBASS R., WINTER A., FRIES R., KUHN C., 2006 – Alleles of the bovine DGAT1 variable number of tandem repeat associated with a milk fat QTL at chromosome 14 can stimulate gene expression. ***Physiological Genomics*** 25, 116-120.
30. GAUTIER M., BARCELONA R.R., FRITZ S., GROHS C., DRUET T., BOICHARD D., EGGEN A., MEUWISSEN T.H.E., 2005 – Fine mapping and physical characterization of two linked QTLs affecting milk fat. ***Genetics*** 172, 425-436.
31. GEORGES M., NIELSEN D., MACKINNON M., MISHRA A., OKIMOTO R., PASQUINO A.T., SARGEANT L.S., SOERENSEN A., STEELE M.R., ZHAO X., WOMACK J.E., HOESCHELE I., 1995 – Mapping QTL controlling milk production in dairy cattle by exploiting progeny testing. ***Genetics*** 139, 907-920.
32. GRISART B., COPPIETERS W., FARNIR F., KARIM L., FORD C., CAMBISANO N., MNI M., REID S., SIMON P., SPELMAN R., GEORGES M., SNELL R., 2002 – Positional candidate cloning of a QTL in dairy cattle: Identification of a missense mutation in the bovine DGAT1 gene with major effect on milk yield and composition. ***Genome Research*** 12, 222–231.
33. GRISART B., FARNIR F., KARIM L., CAMBISANO N., KIM J.J., KVASZ A., MNI M., SIMON P., FRERE J.M., COPPIETERS W., GEORGES M., 2004 – Genetic and functional confirmation of the causality of the DGAT1 K232A quantitative trait nucleotide in affecting milk yield and composition. ***Proceedings of the National Academy of Sciences of the USA*** 101, 2398-2403.
34. HARDER B., BENNEWITZ J., REINSCH N., THALLER G., THOMSEN H., KUHN C., SCHWERIN M., ERHARDT G., FORSTER M., REINHARDT F., KALM E., 2006 – Mapping of quantitative trait loci for lactation persistency traits in German Holstein dairy cattle. ***Journal of Animal Breeding and Genetics*** 123, 89-96.
35. HAYES B., GODDARD M.E., 2001 – The distribution of the effects of genes affecting QTL in livestock. ***Genetics, Selection, Evolution*** 33, 209-229.

36. HEYEN D.W., WELLER J.I., RON M., BAND M., BEEVER J.E., FELDMESSER E., DA Y., WIGGANS G.R., Van RADEN P.M., LEWIN H.A., 1999 – A genome scan for QTL influencing milk production and health traits in dairy cattle. ***Physiological Genomics*** 1, 165-175.
37. HEYEN D.W., WELLER J.I., RON M., BAND M., BEEVER J.E., FELDMESSER E., DA Y., WIGGANS G.R., Van RADEN P.M., LEWIN H.A., 2005 – A genome scan for QTL influencing milk production and health traits in dairy cattle, http://cagst.animal.uiuc.edu [consulted: March 2005]
38. HOLMBERG M., ANDERSSON-EKLUND L., 2004 – Quantitative trait loci affecting health traits in Swedish dairy cattle. ***Journal of Dairy Science*** 87, 2653-2659.
39. HURST L.D., PAL C., LERCHER M.J., 2004 – The evolutionary dynamics of eukaryotic gene order. ***Nature Review Genetics*** 5, 299-310.
40. IHARA N., TAKASUGA A., MIZOSHITA K., TAKEDA H., SUGIMOTO M., MIZOGUCHI Y., HIRANO T., ITOH T., WATANABE T., REED K.M., SNELLING W.M., KAPPES S.M., BEATTIE C.W., BENNETT G.L., SUGIMOTO Y., 2004 – A comprehensive genetic map of the cattle genome based on 3802 microsatellites. ***Genome Research*** 14, 1987-1998.
41. JIANG Z., DE S., GARCIA M.D., GRIFFIN K.B., WU X.L., XIAO O., MICHAL J.J., SHARMA B.S., JANSEN G.B., 2005 – An independent confirmation of a quantitative trait locus for milk yield and composition traits on bovine chromosome 26**.** ***Journal of Animal Breeding and Genetics*** 122, 281-284.
42. KATHAR M.S., THOMSEN P.C., TAMMEN I., RAADSMA H.W., 2004 – QTL mapping in dairy cattle: review and meta-analysis. ***Genetics, Selection, Evolution*** 36, 163-190.
43. KHATIB H., LEONARD S.D., SCHUTZKUS V., LUO W., CHANG Y.M., 2006 – Association of the OLR1 gene with milk composition in Holstein dairy cattle. ***Journal of Dairy Science*** *89*, 1753-1760.
44. KIM J.J., FARNIR F., COPPIETERS W., JOHNSON D., GEORGES M., 2002 – Evaluation of a new QTL fine-mapping method exploiting linkage disequilibrium on BTA14 and BTA20 in a dairy cattle. Proceedings of the 7th World Congress on Genetics Applied to Livestock Production, 19-23 August, Montpellier, France. Paper 21-23.
45. KLUNGLAND H., SABRY A., HERINGSTAD B., OLSEN H.G., GOMEZ-RAYA L., VAGE D.I., OLSAKER I., ODEGARD J., KLEMETSDAL G., SCHULMAN N., VILKKI J., RUANE J., AASLAND M., ROENNINGEN K., LIEN S., 2001 – QTL affecting clinical mastitis and somatic cell count in dairy cattle. ***Mammalian Genome*** 12, 837-842.
46. De KONING D.J., SCHULMAN N.F., ELO K., MOISIO S., KINOS R., VILKKI J., MAKI-TANILA A., 2001 – Mapping of multiple QTL by simple regression in half-sib designs. ***Journal of Animal Science*** 79, 616-622.
47. KUHN C., FREYER G., WEIKARD R., GOLDAMMER T., SCHWERIN M., 1999 – Detection of QTL for milk production traits in cattle by application of a specifically developed marker map of BTA6. ***Animal Genetics*** 30, 333-340.
48. KUHN C., BENNEWITZ J., REINSCH N., XU N., THOMSEN H., LOOFT C., BROCKMANN G.A., SCHWERIN M., WEIMANN C., HIENDLEDER S., ERHARDT G., MEDJUGORAC I., FORSTER M., BRENIG B., REINHARDT F., REENTS R., RUSS I., AVERDUNK G., BLUMEL J., KALM E., 2003 – QTL mapping of functional traits in the German Holstein cattle population. ***Journal of Dairy Science*** 86, 360-368.
49. KUHN C., THALLER G., WINTER A., BININDA-EMONDS O.R.P., KAUPE B., ERHARDT G., BENNEWITZ J., SCHWERIN M., FRIES R., 2004 – Evidence for multiple alleles at the DGAT1 locus better explains a quantitative trait locus with major effect on milk fat content in cattle. ***Genetics*** 167, 1873-1881.

50. LEONARD S., KHATIB H., SCHUTZKUS V., CHANG Y.M., MALTECCA C., 2005 – Effects of the osteopontin gene variants on milk production traits in dairy cattle. ***Journal of Dairy Science*** 88, 4083-4086.
51. LI C., BASARAB J., SNELLING W.M., BENKEL B., KNEELAND J., MURDOCH B., HANSEN C., MOORE S.S., 2004 – Identification and fine mapping of quantitative trait loci for backfat on bovine chromosomes 2, 5, 6, 19, 21, and 23 in a commercial line of Bos taurus**.** ***Journal of Animal Science*** 82, 967-72.
52. LINDERSSON M., ANDERSSON-EKLUND L., De KONING D.J., LUNDEN A., MAKI-TANILA A., ANDERSSON L., 1998 – Mapping of serum amylase-1 and QTL for milk production traits to cattle chromosome 4. ***Journal of Dairy Science*** 81, 1454-1461.
53. LIU Y., JANSEN G.B., LIN C.Y., 2004 – QTL mapping for dairy cattle production traits using a maximum likelihood method. ***Journal of Dairy Science*** 87, 491-500.
54. MAKI-TANILA A., De KONING D.J., ELO K.T., MOISIO S., VELMALA R., VILKKI H.J., 1998 – Mapping multiple QTL by regression in half sib designs. Proceedings of the 6th World Congress on Genetics Applied to Livestock Production, Armidale. Published by the Armidale.University of New England, Armidale, 26, 269–272.
55. MOORE S.S., LI C., BASARAB J., SNELLING W.M., KNEELAND J., MURDOCH B., HANSEN C., BENKEL B., 2003 – Fine mapping of QTL and assessment of positional candidate genes for backfat on bovine chromosome 14 in a commercial line of Bos taurus. ***Journal of Animal Science*** 81, 1919-1925.
56. MOSIG M.O., LIPKIN E., KHUTORESKAYA G., TCHOURZYNA E., SOLLER M., FRIEDMANN A., 2003 – A whole genome scan for QTL affecting milk protein percentage in Israeli-Holstein cattle by means of selective milk DNA pooling in a daughter design, using an adjusted false discovery rate criterion*.* ***Genetics*** 157, 1683-1698.
57. NADESALINGAM J., PLANTE Y., GIBSON J.P., 2001 – Detection of QTL for milk production on chromosomes 1 and 6 of Holstein cattle. ***Mammalian Genome*** 12, 27-31.
58. OLSEN H.G., GOMEZ-RAYA L., VAGE D.I., OLSAKER I., KLUNGLAND ., SVENDSEN M., AADNOEY T., SABRY A., KLEMETSDA G., SCHULMAN N., KRAMER W., THALLER G., ROENNINGEN K., LIEN S., 2002 – A genome scan for QTL affecting milk production in Norwegian dairy cattle. ***Journal of Dairy Science*** 85, 3124-3130.
59. OLSEN H.G., LIEN S., SVENDSEN M., NILSEN H., ROSETH A., AASIAND OPSAI M., MEUWISSEN T.H.E., 2004 – Fine mapping of milk production QTL on BTA6 by combined linkage and linkage disequilibrium analysis. ***Journal of Dairy Science*** 87, 690-698.
60. OLSEN H.G., LIEN S., GAUTIER M., NILSEN H., ROSETH A., BERG P.R., SUNDSAASEN K.K., SVENDSEN M., MEUWISSEN T.H., 2005 – Mapping of a milk production QTL to a 420 kb region on bovine chromosome 6. ***Genetics*** 169, 275-283.
61. ORR H.A., 1998 – The population genetics of adaptation: The distribution of factors fixed during adaptive evolution. ***Evolution*** 52, 935-949.
62. PLANTE Y., GIBSON J.P., NADESALINGAM J., MEHRABANI-YEGANEH H., LEFEBVRE S., VANDERVOORT G., JANSEN G.B., 2001 – Detection of QTL affecting milk production traits on 10 chromosomes in Holstein cattle. ***Journal of Dairy Science*** 84, 1516-1524.
63. PONG-WONG R., HALEY C.S., WOOLLIAMS J.A, 1999 – Behaviour of the additive finite locus model. ***Genetics, Selection, Evolution*** 31, 193-211.
64. PONG-WONG R., VILLANUEVA B., WOOLLIAMS J.A., 2002 – Comparision of direct and marker-assisted selection with optimised contributions. Proceedings of the 7th World Congress on Genetics Applied to Livestock Production, Montpellier, France. August 19-23, Paper 22-17.

65. PRINZENBERG E.M., WEIMANN C., BRANDT H., BENNEWITZ J., KALM E., SCHWERIN M., ERHARDT G., 2003 – Polymorphism of the bovine CSN1S1 promoter: Linkage mapping, intragenic haplotypes, and effects on milk production traits. ***Journal of Dairy Science*** 86, 2696-2705.
66. REINSCH N., THOMSEN H., LOOFT C., KALM E., GRUPE S., KUHN C., SCHWERIN M., LEYHE-HORN B., HIENDLEDER S., ERHARDT G., MEDJUGORAC I., RUSS I., FORSTER M., BRENIG B., REENTS R., AVERDUNK G., 1998 – First results on somatic cell count loci from the ADR bovine mapping project. Proceedings of the 6th World Congress on Genetics Applied to Livestock Production, Armidale. Published by the University of New-England, Armidale, 26, 426–428.
67. RODRIGUEZ-ZAS S.L., SOUTHEY B.R., HEYEN D.W., LEWIN H.A., 2002a – Interval and composite interval mapping of somatic cell score, yield, and components of milk in dairy cattle. ***Journal of Dairy Science*** 85, 3081-3091.
68. RODRIGUEZ-ZAS S.L., SOUTHEY B.R., HEYEN D.W., LEWIN H.A., 2002b – Detection of QTL influencing dairy traits using a model for longitudinal data. ***Journal of Dairy Science*** 85, 2681-2691.
69. RON M., HEYEN D.W., WELLER J.I., BAND M., FELDMESSER E., PASTERNAK H., DA Y., WIGGANS G.R., VAN RADEN P.M., EZRA E., LEWIN H.A., 1998 – Detection and analysis of a locus affecting milk concentration in the US and Israeli dairy cattle populations. Proceedings of the 6th World Congress on Genetics Applied to Livestock Production, Armidale. Published by the University of New England, Armidale, 26, 422–425.
70. RON M., KLIGER D., FELDMESSER E., SEROUSSI E., EZRA E., WELLER J.I., 2001 – Multiple QTL locus analysis of bovine chromosome 6 in the Israeli Holstein population by a daughter design. ***Genetics*** 159, 727-735.
71. RON M., FEIDMESSER E., GOLIK M., TAGER-COHEN I., KLIGER D., REISS V., DOMOCHOVSKY R., ALUS O., SEROUSSI E., EZRA E., WELLER J.I., 2004 – A complete genome scan of the Israeli Holstein population for QTL by a daughter design. ***Journal of Dairy Science*** 87, 476-490.
72. ROY R., GAUTIER M., ZARAGOZA P., EGGEN A., RODELLAR C., 2005 – Radiation hybrid and genetic linkage mapping of two genes related to fat metabolism in cattle: Fatty Acid Synthase (FASN) and Glycerol-3-phosphate acyltransferase mitochondrial (GPAM). ***Animal Biotechnology*** 16(1), 1-9.
73. SCHIBLER L., ROIG A., MAHE M.F., SAVE J-C., GAUTIER M., TAOURIT S., BOICHARD D., EGGEN A., CRIBIU E.P., 2004 – A first generation bovine BAC-based physical map. ***Genetics, Selection, Evolution*** 36, 105-122.
74. SCHNABEL R.D., KIM J.J., ASHWELL M.S., SOENSTEGAARD T.S., VAN TASSELL C.P., CONNOR E.E., TAYLOR J.F., 2005a – Fine-mapping milk production quantitative trait loci on BTA6: Analysis of the bovine osteopontin gene. ***Proceedings of the National Academy of Science of the USA*** 102, 6896-6901.
75. SCHNABEL R.D., SOENSTEGAARD T.S., TAYLOR J.F., ASHWELL M.S., 2005b – Whole-genome scan to detect QTL for milk production, conformation, fertility and functional traits in two US Holstein families. ***Animal Genetics*** 36, 408-416.
76. SCHROOTEN C., BOVENHUIS H., COPPIETERS W., VAN ARENDONK J.A.M., 2000 – Whole genome scan to detect QTL for conformation and functional traits in dairy cattle. ***Journal of Dairy Science*** 83, 795-806.
77. SCHROOTEN C., BINK M.C.A.M., BOVENHUIS H., 2004 – Whole genome scan to detect chromosomal regions affecting multiple traits in dairy cattle. ***Journal of Dairy Science*** 87, 3550-3560.

78. SCHULMAN N.F., VIITALA S.M., De KONING D.J., VIRTA J., MAKI-TANILA A., VILKKI J.H., 2004 – QTL for health in Finnish Ayrshire cattle. ***Journal of Dairy Science*** 87, 443-449.
79. SCHWERIN M., CZERNEK-SCHAFER D., GOLDAMMER T., KATA S.R., WOMACK J.E., PAREEK R., PAREEK C., WALAWSKI K., BRUNNER R.M., 2003 – Application of disease genes – Mining for functional candidate genes for mastitis resistance in cattle. ***Genetics, Selection, Evolution*** 35 (supplement), S19-S34.
80. SHOOK G.E., 2006 – Major advances in determining appropriate selection goals. ***Journal of Dairy Science*** 89, 1349-1361.
81. SPELMAN R.J., COPPIETERS W., KARIM L., VAN ARENDONK J.A.M., BOVENHUIS H., 1996 – QTL analysis for five milk production traits on chromosome six in the Dutch Holstein-Friesian population. ***Genetics*** 144, 1799-1808.
82. SZYDA J., LIU Z., REINHARDT F., REENTS R., 2005 – Estimation of QTL parameters for milk production traits in German Holstein dairy cattle population. ***Journal of Dairy Science*** 88, 356-367.
83. Van TASSELL C.P., SOENSTEGAARD T.S., ASHWELL M.S., 2004 – Mapping QTL affecting dairy conformation to chromosome 27 in two Holstein grandsire families. ***Journal of Dairy Science*** 87, 450-457.
84. THOMSEN H., REINSCH N., XU C., LOOFT C., GRUPE S., KUHN C., BROCKMANN G.A., SCWERIN M., LEYHEHORN B., HIENDLEDER S., ERHARD G., MEDJUGORAC I., FORSTER I.R.M., BRENIG B., REINHARDT F., REENTS R., BLUMEL J., AVERDUNK G., KALM E., 2001 – Comparison of estimated breeding values, daughter yield deviations and deregressed proofs within a whole genome scan for QTL. ***Journal of Animal Breeding and Genetics*** 118, 357-370.
85. VELMALA R.J., VILKKI H.J., ELO K.T., De KONING D.J., MAKI-TANILA A.V., 1999 – A search for QTL for milk production traits on chromosome 6 in Finnish Ayrshire cattle. ***Animal Genetics*** 30, 136-143.
86. VIGNAL A., MILAN D., SAN CRISTOBAL M., EGGEN A., 2002 – A review on SNP and other types of molecular markers and their use in animal genetics. ***Genetics, Selection, Evolution*** 34, 275-305.
87. VIITALA S.M., SCHULMAN N.F., De KONING D.J., ELO K., KINOS R., VIRTA A., VIRTA J., MAKI-TANILA A., VILKKI J.H., 2003 – QTL affecting milk production traits in Finnish Ayrshire dairy cattle. ***Journal of Dairy Science*** 86, 1828-1836.
88. VILKKI H.J., De KONING D.J., ELO K.T., VELMALA R., MAKI-TANILA A., 1997 – Multiple marker mapping of QTL of Finnish dairy cattle by regression. ***Journal of Dairy Science*** 80, 198–204.
89. WALL J.D., PRITCHARD J.K., 2003 – Haplotype blocks and linkage disequilibrium in the human genome**.** ***Nature Reviews Genetics*** 4, 587-597.
90. WEIKARD R., KUHN C., GOLDAMMER T., FREYER G., SCHWERIN M., 2005 – The bovine PPARGC1A gene: molecular characterization and association of an SNP with variation of milk fat synthesis. ***Physiological Genomics*** 21, 1-13**.**
91. WELLER J.I., GOLIK M., SEROUSSL E., EZRA E., RON M., 2003 – Population- wide analysis of a QTL affecting milk-fat production in Israeli Holstein population. ***Journal of Dairy Science*** 86, 2219-2227.
92. WELLER J.I., SHLEZINGER M., RON M., 2005 – Correcting for bias in estimation of quantitative trait loci effects. ***Genetics, Selection, Evolution*** 37, 501-522.

93. WERNER F.A.O., DURSTEWITZ G., HABERMANN F.A., THALLER G., KRAMER W., KOLLERS S., BUITKAMP J., GEORGES M., BREM G., MOSNER J., FRIES R., 2004 – Detection and characterization of SNPs useful for identity control and parentage testing in major European dairy breeds. ***Animal Genetics*** 35, 44-49.
94. WIENER P., MACLEAN I., WILLIAMS J.L., WOOLLIAMS J.A., 2000 – Testing for the presence of previously identified QTL for milk production traits in new populations. ***Animal Genetics*** 31, 385-395.
95. WINTER A., ALZINGER A., FRICT R., 2004 – Assessment of the gene content of the chromosomal regions flanking bovine DGAT1. ***Genomics*** 83, 172-180.
96. ZHANG Q., BOICHARD D., HOESCHELE I., ERNST C., EGGEN A., MURKVE B., PFISTER-GENSKOW M., WITTE L.A., GRIGNOLA F.E., UIMARI P., THALLER G., BISHOP M.D., 1998 – Mapping QTL for milk production and health of dairy cattle in a large outbred pedigree. ***Genetics*** 149, 1959-1973.

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Mapowanie QTLs u bydła – aspekt teoretyczny i praktyczny

S t r e s z c z e n i e

Opierając się na piśmiennictwie zebranym do kwietnia 2006 roku przedstawiono położenie QTLs cech produkcji mleka dla gatunku *Bos taurus* ze szczególnym uwzględnieniem *loci* warunkujących *mastitis*, płodność i inne cechy ważne w selekcji wspomaganej markerami (MAS). Przeanalizowano rozkład QTLs w autosomach, jak również wskazano najbardziej prawdopodobne ich położenie. Szczególną uwagę poświęcono autosomom 1, 2, 3, 5, 6, 7, 9, 14, 19, 20, 23, 26 i 27 oraz chromosomowi X. Przedstawiono dowody istnienia plejotropii QTLs jako zjawiska powszechnie występującego u bydła.