A New Linkage Map Of The Rabbit (*Oryctolagus cuniculus*) Chromosome 1 (*OCU1*) And Results Of A QTL Analysis For Carcass Composition and Meat Quality Traits

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Introduction

Genomic resources for the rabbit are still limited compared with other species. Up to now there is not sufficient information available about QTL for carcass composition and meat quality traits in rabbits. In this study, we investigated a F_2 family, which has been produced by crossing *Giant Grey* and *New Zealand White*. The aim of the project is directed towards genome-wide QTL mapping for a multitude of traits including growth, carcass composition and meat quality. Here, we present the results for the rabbit chromosome 1 (*OCU1*).

Material and methods

Animals, phenotypic traits and genotyping. For mapping of QTL, an intercross population was generated from an initial cross between *Giant Grey* (GG) and *New Zealand White* (NZW) rabbits. 279 F_2 animals derived from 25 F_1 does and 5 F_1 bucks were used. The rabbits were fed pellets *ad libitum* and slaughtered at the age of 84 days. More than 40 traits were collected for carcass composition and meat quality (Bieniek, 1997; Sternstein et al. 2009). F_2 animals were genotyped for 173 microsatellite markers (Rico et al. 1994; Surridge et al. 1997; Van Haeringen et al. 1997; Korstanje et al. 2001, 2003; Chantry-Darmon et al. 2005), which are informative in our population. The linkage map of *OCU1* was constructed with 25 markers (Table 1).

Statistical analyses. A family specific linkage map was built using CRI-Map 2.4 software (Green et al. 1990). The first step identified linked markers by two-point analysis. In the second step, the linkage group was examined by multipoint analysis using build and flipsn options. The marker order was accepted if LOD score > 3. For QTL mapping, data were analysed with least squares regression interval mapping using family and season as fixed effects (Grid-QTL, Seaton et al. 2006). The sex was included as fixed effect in the model for meat colour and head weight. Litter size was included as fixed effect for the analyses of birth weight and weight after five weeks. Significance thresholds of the F-statistics for single QTL with additive and dominance effects were determined by 1000 permutations for each trait.

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Results and discussion

The distribution of alleles in the resource population is presented in Table 1. In the F_1 generation, the number of alleles per locus ranged from two to four, with heterozygosities between 0.31 and 1.00. The polymorphism information content varied from 0.20 to 0.64. The number of informative meioses ranged between 177 and 560 (Table 1).

Table 1: Information and properties of microsatellite markers used for linkage analyses on *OCU1*

Microsatellite	Acc. number	Location	GG	NZW	h[1]	IM[2]	PIC[3]
D1UTR2	AF389367	1[4]	1,2,3	2,3	0.67	330	0.38
D1L1B10	AF398352	nd[4,7]	1,2,3	1	0.52	392	0.41
Sol51	X94685	nd[7]	1,2,3	1,3	0.66	467	0.45
D1L2B4	AF389358	nd[4,7]	1,2,3	1	0.54	241	0.28
D1UTR7	AF389355	1[4]	1,2,3	2,4	0.81	513	0.64
INRACCDDV0269	AJ874595	1p21.3-21.1[5]	1,2	1	0.31	177	0.20
INRACCDDV0236	AJ874569	1p21.3-21.1[5]	1,2	1	0.31	178	0.20
Sat13	X99892	1[4]	2	1,2	0.50	308	0.31
INRACCDDV0345	AJ874661	1p12[5]	1,2,3	2,3	0.62	343	0.39
INRACCDDV0299	AJ874621	nd[4,7]	1,2	2	0.72	464	0.37
INRACCDDV0240	AJ874573	1p11dist[5]	1,2	1	0.48	245	0.26
D1UTR3	AF389359	1[4]	1	2	1.00	560	0.38
D1L7C11	AF389369	nd[4,7]	1,2	2	0.86	512	0.37
INRACCDDV0271	AJ874597	1q14[5]	1,2	2	0.48	259	0.25
INRACCDDV0252	AJ874583	1q14[5]	1,2,3,4	4	0.55	264	0.28
INRACCDDV0320	AJ874640	1q14[5]	1,3	1,2,3	0.66	519	0.54
D1L8C9	AF389374	nd[4,7]	2	1,2	0.66	426	0.36
OCPRG5	-	nd[6,7]	2,3	1,3	0.66	366	0.44
INRACCDDV0136	AJ874476	nd[4,7]	1,2	1	0.55	429	0.35
D1UTR4	AF389353	1[4]	1	1,2	0.44	379	0.34
INRACCDDV0302	AJ874624	nd[4,7]	1,3	1,2,3	0.71	487	0.50
INRACCDDV0169	AJ874508	1q21.5[5]	1,2,3	1	0.90	523	0.44
D1UTR5	AF389357	1[4]	1	1,2	0.41	366	0.33
D1UTR6	AF389354	1[4]	1,2	1	0.83	488	0.37
INRACCDDV0298	AJ874620	1q27dist[5]	1	1,2	0.97	551	0.37

GG - *Giant Grey*, NZW - *New Zealand White*, numbers are identifiers of different alleles, [1]observed heterozygosity in the F_1, [2]number of informative meioses, [3]polymorphism information content (F_2), [4]Korstanje et al. (2001), [5]Chantry-Darmon et al. (2005, 2006), [6]Van Hearingen et al. (1997), [7]not determined

We were able to assign nine previously unmapped markers to chromosome 1. By two-point analyses, the marker *D1L1B10* mapped 20cM from *D1UTR7* (LOD 14.29), Sol51 14cM from *D1UTR7* (LOD 35.60), *D1L2B4* 8cM from *D1UTR7* (LOD 17.37), *D1L7C11* 0cM from *INRACCDDV0252* (LOD 38.38), *INRACCDDV0299* 2cM from *D1UTR3* (LOD 81.35), *INRACCDDV0136* 2cM from *D1UTR4* (LOD 51.01), *INRACCDDV0302* 13cM from *D1UTR4* (LOD 31.19), *D1L8C92* 2cM from *INRACCDDV0320* (LOD 64.19) and *OCPRG5* 3cM from *INRACCDDV0320* (LOD 51.22). The constructed map of this chromosome spans 146.2 cM with an average marker distance of 5.8 cM (Figure 1). The maternally derived map

is 1.2 times longer than the paternal map. The order of the marker loci is in agreement with the previously published maps (Korstanje et al. 2001; Chantry-Darmon et al. 2005, 2006), but the distances between the comparable loci are different in our population.

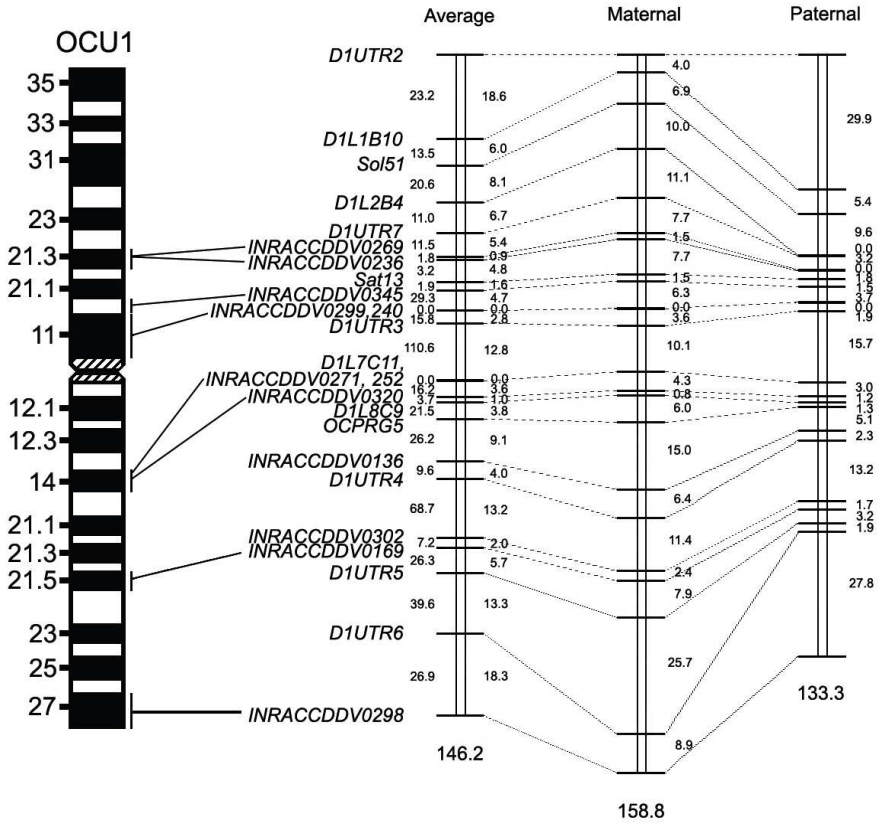

Figure 1: Cytogenetic associated linkage maps of rabbit chromosome 1 (*OCU1*)
The cytogenetic map (left) followed by the sex average map, the maternal map and the paternal map (right). The numbers on the right hand side of the linkage maps show the estimated distances between loci in cM (Kosambi). The statistical supports for the pair wise order of markers are given on the left hand side of the sex averaged map. The total lengths of the maps are shown at the bottom of each bar.

Two distinct QTL were identified on OCU1 for fat weight loin and the pH value 24h *p.m.* of *M. biceps femoris* ($pH_{24}BF$, chromosome-wide significance level $p<0.05$, Table 2, Figure 2). The observed QTL explained 4.67 and 5.29% of the phenotypic variance, respectively.

Table 2: QTL effects for carcass composition and meat quality traits on *OCU1*

Trait	*F* ratio	Position (cM)	CI	a± SE	d± SE	VF_2 (%)
Fat weight loin (g)	5.71*	143.0	21.0-146.0	1.99±0.87	3.36±1.34	4.67
$pH_{24}BF$[1]	6.87*	119.0	4.0-136.0	-0.00±0.02	-0.09±0.02	5.29

[1]pH-value 24 hours *p.m.* of *M. biceps femoris*, * significant at $p< 0.05$ chromosome wide threshold, a-additive effect, d-dominance effect, CI-confidence interval, VF_2 (%)-percentage of F_2 phenotypic variance explained by the QTL.

The peak positions of the QTL were at 143 and 119 cM for fat weight loin and the $pH_{24}BF$, respectively.

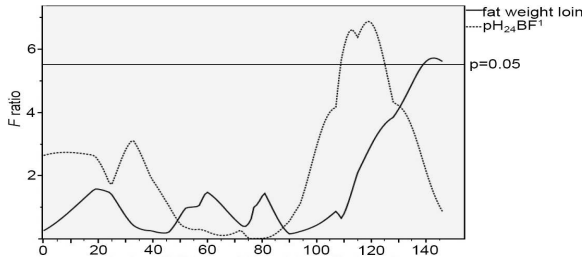

Figure 2: *F* ratio curves for fat weight loin and pH value 24 h *p.m.* of *M. biceps femoris*[1] on *OCU1*, p = 0.05 indicates the chromosome-wide threshold.

Conclusion

Novel QTL for carcass composition and meat quality traits were detected on rabbit chromosome 1 in our F_2 cross bred population. Additional animals will be genotyped in another family to confirm the QTL positions and effects and to identify additional QTL on other chromosomes.

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References

Bieniek, J. (1997). *Zeszyty Naukowe A.R. w Krakowie*. Rozprawy 233.

Chantry-Darmon C., Rogel-Gaillard C., Bertaud M. *et al.* (2003). *Cyt. Gen. Res.*, 103:192–201.

Chantry-Darmon, C., Urien, C., Hayes, H. *et al.* (2005). *Mam. Genome*, 16:442-459.

Chantry-Darmon, C., Urien, C., Rochambeau, H. *et al.* (2006). *Anim. Genet.*, 37:335-341.

Green, P., Falls, K., Crooks, S. (1990). *Washington University School of Medicine*.

Korstanje, R., Gillissen, G.F., Versteeg, S.A. *et al.* (2001). *Anim. Genet.*, 32:308-312.

Korstanje, R., Gillissen, G.F., Versteeg, S.A. *et al.* (2003). *J. Hered.*, 94(2):161-169.

Rico, C., I. Rico, I., Webb, N. (1994). *Anim. Genet.*, 25:367.

Seaton, G., Hernandez, J., Crunchec, J.A. *et al.* (2006). *In Proc 8th WCGALP*.

Sternstein, I., Brockmann, G.A., Maj, D. *et al.* (2009). *In Proc 16th Int. Symp. on Housing and Diseases of Rabbits*, 13.-14.05.2009 in Celle, pages 170-182.

Surridge, A.K., Bell, J., Rico, C. *et al.* (1997). *Anim. Genet.*, 28:302-305.

Van Haeringen, W.A., Den Biemann, M., Van Zutphen, L.F.M. *et al.* (1997). *J. Exp. Anim. Sci.*, 38:49-57.