

## Single nucleotide polymorphisms in the growth hormone and insulin-like growth factor 1 genes are associated with production and fertility traits in dairy cows

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**Introduction** The *somatotropic axis* has been shown to be a key regulator of growth and development in animals and affects performance traits including milk production, growth rate, body composition and fertility. The action of growth hormone (GH) is mediated through controlling expression of many genes among which is the insulin-like growth factor-1 (*IGF-1*). A positive association between systemic concentrations of IGF-1 in the early postpartum period and subsequent cow fertility has been reported (Patton *et al.*, 2007). Additionally, we have also found associations between single nucleotide polymorphisms (SNPs) in *IGF-1* and *GH* and production traits in cattle (Mullen *et al.*, 2010). The objective of this study was to determine if an association exists between these SNPs and fertility and milk production traits in lactating dairy cows.

**Material and methods** DNA was extracted and subsequently genotyped for 10 SNPs in the *IGF-1* gene and 7 SNPs in the *GH* gene on 610 Holstein-Friesian dairy cows from 10 herds (6 commercial and 4 research herds) calving between 1997 to 2007. Pregnancy rate, assessed by ultrasound scanning initially 30 to 50 days and subsequently at 100 days post-insemination, and calving to 1st service interval (CFS) was available on 362 cows for the year 2006; 241 of these cows also had records of body condition score (BCS) at calving. Information was obtained from the Irish Cattle Breeding Federation on calving interval from 369, 242 and 148, first, second and third parity cows, respectively and on milk production for first, second and third lactation from 392, 237 and 152 cows, respectively. Experimental treatments within the four research herds were treated as separate herds and contemporary group was subsequently defined as herd-year-month of calving. The association between each of the SNPs and performance was determined using mixed animal linear models in ASREML (Gilmour *et al.*, 2009) accounting for the additive genetic relationship among animals. Analyses were undertaken within parity for milk production and calving interval. Fixed effects included in the model were Holstein breed fraction and contemporary group. Only one record on calving to first service interval, pregnancy rate to first service, and pregnancy rate overall was available for all animals and therefore the association between each SNP and these fertility traits was undertaken across all parities with parity, as well as contemporary group and Holstein breeding fraction, included in the model as a fixed effect.

**Results** No SNP was associated with calving to first service interval. The G allele of *IGF1i3* was associated with increased milk yield in lactation 1 (b=398 kg; SE=173.0 kg) and 2 (b=751.3 kg; SE=262.0), increased fat yield in lactation 1 (18.8 kg; SE=6.8 kg) and 2 (21.3 kg; SE=10.2 kg) and increased protein yield in lactation 2 (16.5 kg; SE=8.0). Both *IGF1i1* and *IGF1i2* were associated with BCS at calving (Table 1). None of the other seven *IGF-1* SNPs were associated with any of the performance traits evaluated. *GHi33* was the only *GH* SNP associated with milk production with the T allele associated with an increased in milk protein yield in lactation 2 of 9.8 kg (SE=5.0 kg). However, several of the *GH* SNPs were associated with fertility, as measured by calving interval, pregnancy rate to first service and pregnancy rate overall (Table 1).

**Table 1** Associations (standard errors in parenthesis) between SNPs in the *GH* and *IGF-1* genes and calving interval (days), body condition score ([Scale 1 to 5\*10]), pregnancy rate to first service (PRFS; %\*100) and pregnancy rate overall (Overall; %\*100)

SNP <sup>a</sup>	Allele substitution	Calving interval			BCS	PRFS	Overall
		Parity 1	Parity 2	Parity 3			
<i>IGF1i1</i>	A → T	-4.6 (6.2)	4.9 (7.9)	-9.6 (11.7)	-1.34 (0.52)*	1.75 (3.8)	-1.56 (2.22)
<i>IGF1i2</i>	C → T	-2.6 (6.8)	1.3 (8.8)	12.2 (12.2)	1.92 (0.57)***	0.17 (4.14)	1.07 (2.44)
<i>IGF1i3</i>	G → A	4.5 (13.1)	0.3 (16.5)	-3 (22.6)	0.29 (1.12)	1.71 (8.07)	3.73 (4.71)
<i>GHi32</i>	T → C	4.0 (6.6)	5.3 (8)	22.5 (11.4)*	0.08 (0.59)	10.03 (4.20)*	5.34 (2.48)*
<i>GHi33</i>	T → A	-4.4 (10.2)	-11.2 (14.2)	-15.4 (19.3)	0.66 (1.13)	5.5 (7.20)	1.49 (4.23)
<i>GHi35</i>	T → C	3.4 (6.2)	3.5 (7.7)	13 (10.5)	0.08 (0.59)	10.12 (4.14)*	5.01 (2.42)*
<i>GHi38</i>	T → C	4/0 (6.6)	5.3 (8)	22.4 (11.3)*	0.45 (0.59)	9.84 (4.22)*	5.29 (2.48)*

\* = P<0.05; \*\*\* = P<0.001 significance from zero. <sup>a</sup>: i = Intronic SNP

**Conclusions** SNPs in *IGF-1* were associated with milk production traits and BCS; however there was no evidence of an association with any fertility traits measured. SNPs in *GH* were associated with calving interval, pregnancy rate and milk protein yield. The associations found in this study warrant further investigation including additional sequencing to understand the causative mechanisms involved.

### References

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