Exploring the genetic basis of cattle grazing behaviour for the sustainable use of the Swiss Alps

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Abstract

Sustainable use of pastures requires suitable grazing livestock. Novel research has revealed the glutamate metabotropic receptor 5 gene (*GRM5*) to be associated with the movement of Hereford cows grazing steep and rugged grasslands in New Zealand. The study also reported a predominance of variants *C* and *B*, and much lower frequency of *A* in this population. In the current exploratory study, we asked if similar *GRM5* variant frequencies and behavioural relationships are observed in different cattle breeds elsewhere. Grazing behaviours were derived from GPS-tracked mature cows (*n*=17; 12 Highland and 5 Original Brown) when grazing in the Swiss Alps. Gene variation was determined using PCR-single-strand conformation polymorphism analysis. The Swiss cattle had only three of a potential six *GRM5* genotypes: *AC*, *BC* and *CC* (3:3:11). Variant *C* was the most common (frequency 82%) and present in all the cows, while the *A* and *B* variants were equally represented (9%). The results suggest differences in grazing behaviour among *GRM5* genotypes in Swiss cattle, although such differences did not reflect those observed in the New Zealand cattle. The unbalanced frequency of *GRM5* genotypes found in the Swiss cattle herds may bring opportunity for genetic selection to adapt their grazing behaviour to alpine landscapes. A larger sampling is needed to establish the effects of *GRM5* variation on grazing behaviours.

Keywords: genetic associations, grazing personalities, home range, GPS-tracking collars

Introduction

Differences in space use and movement between and within cattle breeds suggest a genetic basis for grazing behaviour (Bailey *et al*., 2004; Pauler *et al*., 2020). Recent research has revealed that variation in the glutamate metabotropic receptor 5 gene (*GRM5*) is associated with the behaviour of Hereford cows grazing in steep and rugged grasslands in New Zealand (Moreno Garcia *et al*., 2022): Cows' home range, movement tortuosity, elevation range and travelled distance were related to *GRM5* genotypes. The study also reported a predominance of *GRM5* variants *B* and *C*, and a much lower frequency of *A*. A subsampling analysis on the New Zealand data revealed linkages between cattle *GRM5* variation and fifteen key grazing behaviours, and highlighed the consequences on rangelands functioning (Moreno Garcia *et al*., 2024). We therefore investigated if *GRM5* variant frequencies and relationships with grazing behaviours are similar in cattle farmed elsewhere.

Materials and methods

The Swiss GPS data originated from two grazing experiments on subalpine pastureland in Switzerland. In the first experiment, Pauler *et al*. (2020) compared the grazing behaviour of cattle breeds in a latin-square design in independent repetitions of relatively small grazing areas (0.3–1.2 ha). In the second experiment, Svensk *et al*. (2021) investigated the grazing behaviour of Highland cattle in shrub-encroached pastures. These paddocks were larger (approx. 5 ha) and included patches of dense shrub as well as open grassland. Nine cows (four Highland and five Original Brown) from Pauler's study and eight cows (Highland) from Svensk's study were still available for blood sampling (*n*=17), and grazing behaviours were calculated by combining 5-min GPS data and digital elevation models as described in Moreno Garcia *et al*. (2022).

Blood samples were collected from the tail vein of the cows (animal testing authorization GR/16/2021). These samples were air dried onto FTA papers for subsequent genotyping of *GRM5* exon 5 using PCR-single-strand conformation polymorphism analysis (Moreno Garcia *et al*., 2022). After genotyping, linear mixed models were fitted to four grazing behaviours that had been previously associated (home range and movement tortuosity) or trended towards association (horizontal distance travelled and elevation range) with variation in the gene. The models were initially constructed with the New Zealand data of Moreno Garcia *et al*. (2022) and *GRM5* genotype and cow age class were fitted as explanatory variables (fixed factors) when significant. The random structure was nested by cow identity (15-day repeated measurements) and adjusted by herd. Models with lowest Akaike information criterion were then fitted to the Swiss data. The models' predicted mean grazing behaviour for the New Zealand and Swiss cattle were determined for subsequent comparisons.

Results and discussion

The *GRM5* genotypes found in the Swiss cattle were *AC*, *BC* and *CC* in the proportions of 2:3:4 in Pauler's experiment (Pauler *et al*., 2020) and 1:0:7 in Svensk's study (Svensk *et al*., 2021). The overall frequency of variant *C* was 82% and a 9% frequency was revealed for both variants *A* and *B*. Although the *CC* genotype was the most common (65% of tested individuals), cows in the Pauler's study had three genotypes with two to four individuals in contrast with the two genotypes found in the Svensk's herd being seven *CC* cows and one *AC* cow. A possible explanation might be that in the Svensk's herd, all the cows belonged to one farmer, while Pauler's herd was put together with animals from different farmers who may have used diverse selection criteria. The lack of *AB* and *BB* genotypes in the Swiss cattle tested might be attributable to the small sample size, the breeding decisions made by the farmers, or because these genotypes are generally uncommon: within the 306 New Zealand cows all six possible genotypes were present; however, the *AA* genotype was found in only three cows, and *AB* and *BB* (not found in the Swiss cattle) represented only 6% and 12% of the New Zealand herd, respectively (Moreno Garcia *et al*., 2022). In contrast to the Swiss cattle, the New Zealand cattle seem to be more commonly *BC* or *CC*, with 35% and 36% of individuals respectively, and 10% of cows had the *AC* genotype. These frequencies are similar to the composition found in Pauler's herd with lower proportion of *AC* and higher proportion of *CC*. Despite the geographic distance between the Swiss and New Zealand cattle populations, and the differences in the breeds and livestock systems, we still found an unbalanced frequency of *GRM5* genotypes in favour of variant *C* and, a much lower presence of *A*.

The *GRM5* genotypes in the Swiss cattle seemed to have behavioural relationships that were different to the associations observed in the New Zealand study, where *BC* cows travelled longer distances (significantly different; Figure 1A) but had smaller elevation ranges (Figure 1B), than was displayed by the *AC* and *CC* cows. The three genotypes had similar searching patterns with no differences observed (Figure 1C). The *CC* genotype tended to have a larger home range than the *AC* or *BC* cows (Figure 1D). In contrast, with the New Zealand cattle, Moreno Garcia *et al*. (2022) reported larger home ranges for *AC* (7.82 ha day^{-1}) than *CC* cattle (7.29 ha day^{-1}) or the *BC* cattle (7.25 ha day^{-1}), while the opposite was observed with the Swiss cattle. The *AC* New Zealand cows displayed smaller searching patterns than *BC* and *CC* genotypes, whereas no differences were observed for the Swiss cows.

Conclusion

This preliminary study exploring relationships between *GRM5* genotypes and grazing behaviours in Swiss cattle found different results to those found with a previous study from New Zealand (Moreno Garcia *et al*., 2022). It also investigated *GRM5* variant frequencies and revealed the *GRM5* variant *C* to be common, suggesting a potential opportunity for genetic selection to adapt grazing behaviours of cattle to the heterogeneity of the Swiss Alps.
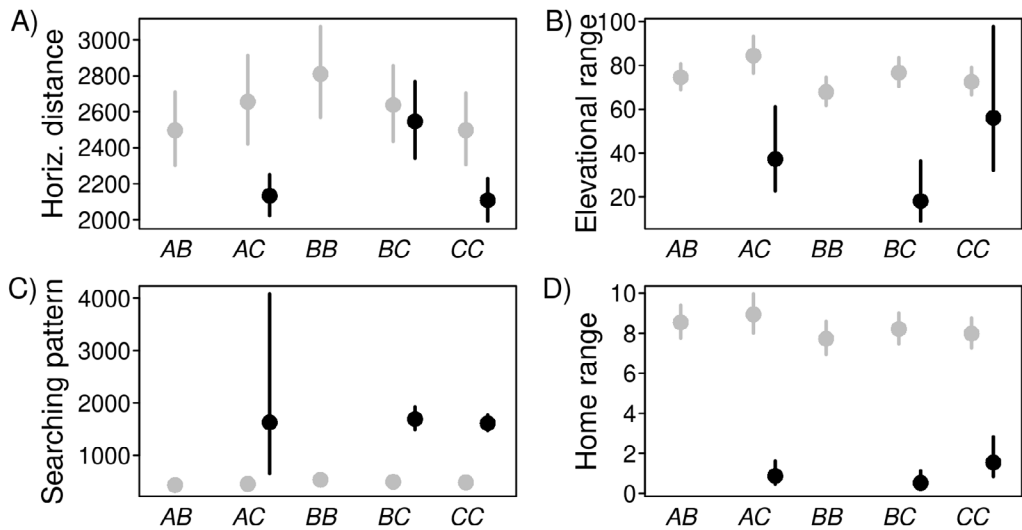
Figure 1. Daily grazing behaviours for Swiss (black) and New Zealand (grey) cows. Dots indicate the marginal means predicted by the linear mixed models for five *GRM5* genotypes. The bars indicate the back-transformed standard errors.

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