Wattles in goats are associated with the FMN1/GREM1 region on chromosome 10

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Summary

The presence of congenital appendages (wattles) on the throat of goats is supposed to be under genetic control with a dominant mode of inheritance. Wattles contain a cartilaginous core covered with normal skin resembling early stages of extremities. To map the dominant caprine wattles (W) locus, we collected samples of 174 goats with wattles and 167 goats without wattles from nine different Swiss goat breeds. The samples were genotyped with the 53k goat SNP chip for a subsequent genome-wide association study. We obtained a single strong association signal on chromosome 10 in a region containing functional candidate genes for limb development and outgrowth. We sequenced the whole genomes of an informative family trio containing an offspring without wattles and its heterozygous parents with wattles. In the associated goat chromosome 10 region, a total of 1055 SNPs and short indels perfectly co-segregate with the W allele. None of the variants were perfectly associated with the phenotype after analyzing the genome sequences of eight additional goats. We speculate that the causative mutation is located in one of the numerous gaps in the current version of the goat reference sequence and/or represents a larger structural variant which influences the expression of the FMN1 and/or GREM1 genes. Also, we cannot rule out possible genetic or allelic heterogeneity. Our genetic findings support earlier assumptions that wattles are rudimentary developed extremities.

Keywords genome sequencing, genome-wide association study, limb development, livestock, skin appendages.
We collected samples of 341 breeding goats from nine different Swiss breeds and scored the presence or absence of wattles (Table S1). Most goats with wattles showed two more or less equally sized wattles on the ventral throat (Fig. 1a). About 7.5% of the collected goats with wattles had only a single wattle on one side (left or right; Fig. 1b). In a single case, we found a goat with two differently sized wattles at an abnormal localization below the ears (Fig. 1d). A histological section of a wattle from a slaughtered goat confirmed the previously described substructure with a cartilaginous core covered with normal skin (Fig. 1e; Imagawa et al. 1994). Therefore, we speculate that caprine wattles, due to their anatomical features, may represent regressed limbs, as was discussed previously (Mouquet 1895). This hypothesis is also supported by our observation that wattles in Swiss goat breeds usually show the same coat color patterning as the limbs in multicolored goat breeds (Fig. S1). The presence of wattles is not correlated with sex or with the presence of horns or beard (data not shown). For some goats, we had the phenotype information for related animals, which confirmed the previously reported monogenic autosomal dominant inheritance (Fig. S2). Taken together, our results are consistent with the limited information about wattles reported in the literature (Mouquet 1895; Siemens 1921; Kronacher & Ogrizek 1924; Lush 1926; Ricordeau 1967; Lauvergne et al. 1987).

A cohort of 174 goats with wattles and 167 goats without wattles was genotyped using Illumina’s goat SNP50 BeadChip containing 53,346 SNP markers (Tosser-Klopp et al. 2014). To map the W locus in Swiss goats, we performed a genome-wide association study (GWAS) for the wattles phenotype and detected a genome-wide significant association on goat chromosome (CHIR) 10 (Fig. 2). The strongest association with a P-value of $8.9 \times 10^{-9}$ was found for SNP 31048-SCAFFOLD 134-1829065 (Table S2). Two SNPs exceeded the Bonferroni significance threshold ($P = 1.02 \times 10^{-6}$). They are located on CHIR 10 at 26,397,973 bp and 26,526,103 bp (goat genome assembly CHIR 1.0; Dong et al. 2013). No other region in the genome showed genome-wide associated SNPs. The most significantly associated SNPs from our GWAS were located in a genomic region with putatively functional candidate genes for the development of extremities (Fig. 2c). The two genes encoding formin 1 (FMN1) and gremlin 1 (GREM1) are known to play a role during limb outgrowth and limb development of mammals and thus represent good functional candidate genes for a developmental phenotype like wattles. The gene annotation of that goat genome region and the order of these genes corresponds well to the syntenic human and mouse chromosome segments. FMN1 is relevant for cell polarization and limb patterning (Mass et al. 1990; Woychik et al. 1990; Evangelista et al. 2003). GREM1, a bone morphogenic protein (BMP) antagonist, controls mammalian limb outgrowth and chondrogenesis (Merino et al. 1999; Zuniga et al. 1999). BMP signaling during limb patterning must be moderated by GREM1 to maintain the signaling loop between the zone of polarizing activity and the apical ectodermal ridge. Mutations in the murine Fnm1 and Grem1 genes were reported in mouse limb deformity phenotypes (Mass et al. 1990; Woychik et al. 1990; Zuniga et al. 2004, 2012; Pavel et al. 2007). Genomic rearrangements of the Grem1–Fnm1 locus were also reported to cause oligosyndactyly in humans (Dimitrov et al. 2010). A 40-kb duplication upstream of GREM1 including the secretogranin V (7B2 protein) gene (SCG5) causes a colorectal polyp syndrome in humans (Jaeger et al. 2012). This mutation is associated with increased allele-specific GREM1 expression. Increased GREM1 expression is predicted to cause reduced BMP pathway activity (Jaeger et al. 2012). Interestingly, the best associated SNP in the GWAS for wattles in the goat was located upstream of GREM1 (Fig. 2c). Therefore, we
speculate that a regulatory mutation influencing the expression of the GREM1–FMN1 locus might be responsible for the development of the polyp-like skin appendages in goats.

For mutation analysis, we selected an informative trio of Saanen goats for whole genome sequencing (WGS). Under the assumption of a monogenic dominant inheritance, the parents are obligate heterozygotes carrying a single copy of the \( W \) allele and the daughter is homozygous for the alternative \( w \) allele (Fig. S2b). We identified sequence variants (SNPs and short indels) from the WGS data in a 947-kb segment containing the GREM1–FMN1 locus (Fig. 2c). Besides the coding regions, we included the up- and downstream regions of both candidate genes, which are supposed to contain regulatory important sequence elements. This region also contained the SCG5 gene and an uncharacterized locus (LOC102168731). In this 947-kb interval, we detected a total of 1267 variants, of which 1055 perfectly co-segregated with the alleles at the \( W \) locus, meaning that the offspring was homozygous and both parents were heterozygous (Table S3). As we were not aware of the exact wattles phenotype of the Chinese goat, which was sequenced for the establishment of the reference genome, we included all variants at which the offspring was homozygous for either the reference or the alternative allele. Initially, we focussed on coding variants in the annotated genes of the associated region, but genotyping data of a variable number of animals with and without wattles belonging to different goat breeds revealed that none of the three detected exonic variants of FMN1 were perfectly associated with the wattles phenotype (Table S4). In addition, we have genotyped the single missense mutation in all available relatives to evaluate whether this variant might be a candidate causal mutation in the selected goat family used for whole genome sequencing. This showed that the inheritance of the alleles at this SNP located in exon 3 of FMN1 is not perfectly linked with the assumed segregation of the \( W \) mutation (Fig. S2b) and can be ruled out as being causative. Finally, the variant lists of whole genome sequencing data from five goats without wattles and three goats with wattles of various breeds produced in our laboratory in the course of other ongoing studies allowed us to exclude all other detected intronic and intergenic variants as being causative for wattles (Table S3). In addition, we performed visual inspection of the mapped sequence data but did not find evidence of structural variants such as larger sized indels or segmental duplications. The sensitivity of our variant detection might have been compromised by the limited sequence coverage in combination with the presence of many gaps in the reference sequence of the critical interval and the employed short-read sequencing technology.
In conclusion, nearly 90 years after the first breeding experiments revealed that wattles follow a Mendelian inheritance, we have mapped the responsible mutation on goat chromosome 10. This study provides one of the first examples of successful application of the recently developed SNP chip for goats (Kijas et al. 2014; Tosser-Klopp et al. 2014). As caprine wattles resemble early stages of developing limbs, the obtained association to the FMN1 and GREM1 genes, which are known to play an important role during mammalian limb patterning, supports earlier speculations on the anatomical origin of wattles. By sequencing the whole genomes of several goats, we unsuccessfully tried to identify the causative W mutation. We speculate that this is probably due to the draft status of the goat reference genome and the employed sequencing method, which impairs the ability to detect all kinds of variants but in particular large structural variants. In addition, we cannot exclude that genetic and/or allelic heterogeneity may influence the phenotype.

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References


Supporting information

Additional supporting information may be found in the online version of this article.

Figure S1. Identical coat color patterning of the wattles and limbs in different goat breeds.

Figure S2. Pedigree of two goat families showing the autosomal dominant inheritance of the wattles (W).

Table S1. Number of animals from nine Swiss goat breeds with and without wattles used in this study.

Table S2. Two best associated SNPs of the genome-wide association study (GWAS).

Table S3. Sequence variants of 11 sequenced animals in the critical region on goat chromosome 10.

Table S4. Coding FMN1 variants in the associated CHIR 10 region.

Appendix S1 Supplementary methods.