

1    **Bovine gonadotrophs express anti-Müllerian hormone (AMH): Comparison of**  
2    **AMH mRNA and protein expression levels among old Holsteins and young and old**  
3    **Japanese black females**

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14    *Running head: AMH expression in bovine gonadotroph*

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16

17     **Abstract.** Anti-Müllerian hormone (**AMH**) is secreted from ovaries and stimulates  
18     gonadotropin secretion from bovine gonadotroph cells. Other important hormones for  
19     endocrinological gonadotroph regulation (e.g., gonadotropin-releasing hormone, inhibin,  
20     and activin) have paracrine and autocrine roles. Therefore, in this study, AMH expression  
21     in bovine gonadotroph cells and the relationships between AMH expression in the bovine  
22     anterior pituitary (**AP**) and estrous stage, age, and breed were evaluated. *AMH* mRNA  
23     expression was detected in APs of post-pubertal heifers (26 months old) by reverse  
24     transcription-polymerase chain reaction. Based on western blotting using an antibody to  
25     mature C-terminal AMH, the AMH protein was expressed in APs. Immunofluorescence  
26     microscopy utilizing the same antibody indicated that AMH is expressed in gonadotrophs.  
27     The expression of AMH mRNA and protein in APs did not differ among estrous phases  
28     ( $P > 0.1$ ). We compared expression levels among old Holsteins ( $79.2 \pm 10.3$  months old)  
29     and young ( $25.9 \pm 0.6$  months old) and old Japanese black females ( $89.7 \pm 20.3$  months  
30     old). The APs of old Holsteins exhibited lower *AMH* mRNA levels ( $P < 0.05$ ) but higher  
31     AMH protein levels than those of young Japanese black females ( $P < 0.05$ ). In conclusion,  
32     bovine gonadotrophs express AMH, and this AMH expression may be breed-dependent.  
33     **Additional keywords:** Age, Breed, Anterior pituitary, Müllerian-inhibiting substance,  
34     Ruminants, TGF- $\beta$  superfamily

35    **Short summary**

36    Ovaries secrete anti-Müllerian hormone (**AMH**), which stimulates gonadotropin secretion  
37    from gonadotrophs in bovines. This study revealed that gonadotrophs themselves express  
38    AMH. The AMH expression levels in anterior pituitaries (**APs**) were not affected by the  
39    estrous phase. The APs of old Holsteins exhibited lower *AMH* mRNA levels but higher  
40    AMH protein levels than those in young Japanese black APs.

41     **Introduction**

42         Anti-Mullerian hormone (**AMH**) is a glycoprotein belonging to the transforming  
43         growth factor (**TGF**)- $\beta$  superfamily. AMH is secreted by immature granulosa cells in the  
44         ovaries of humans and animals ([Bhide and Homburg 2016](#)). It has important roles in the  
45         ovaries for the regulation of gonadotropin-responsive pre-antral follicle development  
46         ([Hernandez-Medrano \*et al.\* 2012](#)) and the inhibition of follicular atresia ([Seifer \*et al.\*](#)  
47         [2014](#)). Plasma AMH concentrations can predict the number of high-quality embryos  
48         produced by donor goats, ewes, or cows ([Ireland \*et al.\* 2008](#); [Monniaux \*et al.\* 2011](#); [Pinto](#)  
49         [et al. 2018](#)). These data suggest the importance of AMH for proper reproductive function  
50         in animals. In addition to the well-studied roles of AMH in the ovaries of female animals,  
51         recent studies have revealed that secreted AMH affects gonadotrophs in the anterior  
52         pituitary (**AP**). The main AMH receptor, i.e., AMH receptor type 2 (**AMHR2**), is  
53         colocalized with gonadotrophin-releasing hormone (**GnRH**) receptors on the surface of  
54         gonadotrophs ([Kereilwe \*et al.\* 2018](#)). AMH activates the synthesis and secretion of  
55         gonadotropins, e.g., luteinizing hormone (**LH**) and follicle stimulating hormone (**FSH**),  
56         in gonadotrophs of rodents and bovines ([Bédécarrats \*et al.\* 2003](#); [Garrel \*et al.\* 2016](#);  
57         [Kereilwe \*et al.\* 2018](#)). Therefore, AMH has important roles in controlling gonadotropin  
58         secretion.

59        GnRH secreted from the hypothalamus is a well-known endocrine mechanism to  
60        control gonadotropin synthesis and secretion in gonadotrophs. However, GnRH is also  
61        expressed in gonadotrophs themselves, with paracrine or autocrine roles in the control **of**  
62        gonadotropin synthesis and secretion ([Pagesy et al. 1992](#); [Miller et al. 1996](#)). Inhibin and  
63        activin, other family members of the TGF- $\beta$  superfamily, are secreted by the ovaries and  
64        affect gonadotrophs. It is important to note that gonadotrophs synthesize and secrete both  
65        inhibin and activin, with paracrine and autocrine effects on gonadotropin synthesis and  
66        secretion ([Popovics et al. 2011](#)). The coordination of the endocrine, paracrine, and  
67        autocrine control of these hormones is likely important for normal reproductive functions  
68        ([De Kretser et al. 2002](#)).

69        Old age is associated with decreased fertility in beef cows ([Osoro and Wright 1992](#)).  
70        However, little is known about the exact mechanisms underlying this association in  
71        domestic animals. Studies of AMH are promising for understanding these mechanisms.  
72        Blood AMH concentrations are highest in pubertal girls, and decrease gradually from the  
73        age of 25 years until the post-menopausal period ([Dewailly et al. 2014](#)). In contrast, old  
74        Japanese Black cows have higher blood AMH concentrations than those in postpubertal  
75        heifers and young cows ([Koizumi and Kadokawa 2017](#)). These data suggest that age may  
76        be a determinant of the blood AMH concentration.

77 AMH expression in gonadotrophs has not been evaluated in any species. However,  
78 AMH is expressed in the APs of both male and female tilapia ([Poonlaphdecha et al. 2011](#)).  
79 Therefore, we evaluated the hypothesis that AMH is expressed in bovine gonadotrophs  
80 in AP tissues. [Ribeiro et al. \(2014\)](#) reported a difference in blood AMH concentrations  
81 among dairy cow breeds. Infertility in Holsteins is an important issue in dairy industries  
82 worldwide ([Kadokawa and Martin 2006; Adamczyk et al. 2017; Gernand and König  
83 2018](#)). Therefore, we also evaluated the relationship between AMH expression in APs  
84 and various physiological factors, i.e., stage of the estrus cycle, age, and breed.

85

## 86 Materials and Methods

### 87 *AP and ovary sample collection for RT-PCR and western blotting*

88 All experiments were performed according to the Guiding Principles for the Care and  
89 Use of Experimental Animals in the Field of Physiological Sciences (Physiological  
90 Society of Japan) and were approved by the Committee on Animal Experiments of  
91 Yamaguchi University.

92 We obtained AP tissue from post-pubertal (26 months of age) Japanese Black heifers  
93 at a local abattoir, using a previously described method ([Kadokawa et al. 2014](#)) for RNA

94 or protein analyses ( $n = 4$ ) or immunohistochemistry ( $n = 5$ ). The heifers were in the  
95 middle luteal phase, i.e., 8 to 12 days after ovulation, as determined by macroscopic  
96 examination of the ovaries and uterus (Miyamoto *et al.* 2000); the AP show the highest  
97 LH, FSH and GnRHR concentrations in this phase (Nett *et al.* 1987).

98 Granulosa cells in preantral and small antral follicles express AMH (Campbell *et al.*  
99 2012). Therefore, we also collected ovary tissue samples from the same heifers to use as  
100 positive-control of AMH in western blotting ( $n = 4$ ) and immunohistochemistry ( $n = 5$ )  
101 assays.

102 The AP and ovary samples for RNA or protein extraction were immediately frozen  
103 in liquid nitrogen and stored at  $-80^{\circ}\text{C}$ . The AP and ovary samples for  
104 immunohistochemistry were fixed with 4% paraformaldehyde at  $4^{\circ}\text{C}$  for 16 h.  
105

106 *RT-PCR, sequencing of amplified products, and homology search in gene databases*  
107 Total RNA was extracted from the AP samples ( $n = 4$ ) using RNAzol RT Reagent  
108 (Molecular Research Center Inc., Cincinnati, OH, US) according to the manufacturer's  
109 protocol. The extracted RNA samples were treated with ribonuclease-free  
110 deoxyribonuclease (Thermo Fisher Scientific, Waltham, MA, US) to eliminate possible  
111 genomic DNA contamination. Using a NanoDrop ND-1000 spectrophotometer

112 (NanoDrop Technologies Inc., Wilmington, DE, USA), the concentration and purity of  
113 each RNA sample were evaluated to ensure the A<sub>260</sub>/A<sub>280</sub> nm ratio was in the acceptable  
114 range of 1.8–2.1. The mRNA quality of all samples was verified by electrophoresis of  
115 total RNA followed by staining with ethidium bromide, and the 28S:18S ratios were 2:1.  
116 The cDNA was synthesized from 1 µg of the total RNA per AP using SuperScript IV  
117 Vilo Master Mix (Thermo Fisher Scientific) according to the manufacturer's protocol.

118 In order to determine the expression of AMH mRNA in the AP, PCR was conducted  
119 using a primer pair designed by Primer3 based on reference sequence of bovine AMH  
120 [National Center for Biotechnology Information ([NCBI](#)) reference sequence of bovine  
121 AMH is NM\_173890]. The expected PCR-product size of AMH using the primer pair is  
122 328 bp (nucleotides 1486-1813; forward primer: 5'-GCTCATCCCCGAGACATACC- 3';  
123 reverse primer: 5'-TTCCCGTGTAAATGGGGCA-3'). Using a Veriti 96-Well Thermal  
124 Cycler (Thermo Fisher Scientific), PCR was performed using 20 ng of cDNA and  
125 polymerase (Tks Gflex DNA Polymerase, [Takara Bio Inc.](#), Shiga, Japan) under the  
126 following thermocycles: 94 °C for 1 min for pre-denaturing followed by 35 cycles of  
127 94°C for 60 s, 60°C for 15 s, and 68°C for 30 s. PCR products were separated on 1.5%  
128 agarose gel by electrophoresis with a molecular marker [Gene Ladder 100 (0.1-2kbp),  
129 [Nippon Gene](#), Tokyo, Japan], stained with fluorescent stain (Gelstar, Lonza, Allendale,

130 NJ), and observed using a charge-coupled device ([CCD](#)) imaging system (GelDoc; [Bio-](#)  
131 [Rad](#), Hercules, CA, US). The PCR products were purified with the NucleoSpin Extract II  
132 kit (Takara Bio Inc.) and then sequenced with a sequencer (ABI3130, Thermo Fisher  
133 Scientific) using one of the PCR primers and the Dye Terminator v3.1 Cycle Sequencing  
134 Kit (Thermo Fisher Scientific). The sequences obtained were used as query terms with  
135 which to search the homology sequence in the DNA Data Bank of  
136 Japan/GenBank/European Bioinformatics Institute Data Bank using the basic nucleotide  
137 local alignment search tool ([BLAST](#)) optimized for highly similar sequences (available  
138 on the NCBI website).

139

140 *Antibodies used in this study*

141 Human AMH is secreted as a homodimeric precursor consisting of two identical  
142 monomers (560 amino acids; NCBI accession number AAA98805.1) ([Mamsen et al.](#)  
143 [2015](#)). Each monomer consists of two domains, (i) a mature C-terminal region, which  
144 becomes bioactive after proteolytic cleavage and binds to AMHR2, and (ii) a pro-region,  
145 which is important for AMH synthesis and extracellular transport. The human AMH  
146 precursor is cleaved at amino acid 451 (arginine) between the two domains. The pro-  
147 region has another cleavage site at amino acid 229 (arginine), giving rise to three potential

148 cleavage products: pro-mid-mature, mid-mature, and mature ([Mamsen et al. 2015](#)). The  
149 bovine AMH precursor monomer (575 amino acids; NCBI accession number  
150 NP\_776315.1) has 91% sequence similarity to the human protein [evaluated using  
151 Genetyx ver. 11 (Genetyx, Tokyo, Japan)]. The bovine AMH precursor contains an  
152 arginine cleavage site between the two domains at amino acid 466. However, the bovine  
153 AMH precursor does not contain arginine at the residue corresponding to amino acid 229  
154 of the human pro-region of AMH. A rabbit polyclonal anti-AMH antibody  
155 ([ARP54312\\_P050; Aviva Systems Biology, CA, USA](#)) that recognizes the mature C-  
156 terminal form of human AMH (corresponding to amino acids 468–517;  
157 SVDLRAERSVLIPETYQANNCQGVCGWPQS DRNPRYGNHV VLLKMQARG)  
158 was used. This sequence had 98% homology to amino acids 483–532 of the mature C-  
159 terminal form of bovine AMH but no homology to other bovine proteins, as determined  
160 using protein BLAST.

161 We used also a specific guinea pig polyclonal anti-bovine GnRHR ([Kadokawa et al. 2014](#)),  
162 a specific mouse monoclonal anti-LH  $\beta$  ([LH \$\beta\$](#) ) subunit antibody (clone 518-B7;  
163 [Matteri et al. 1987; Iqbal et al. 2009](#)), and a specific mouse monoclonal anti-FSH  $\beta$   
164 ([FSH \$\beta\$](#) ) subunit antibody (clone A3C12; [Borromeo et al. 2004](#)) for immunohistochemical  
165 analysis of AP tissue. These antibodies are utilized for immunohistochemical analysis of

166 AP tissue in our previous papers ([Kadokawa et al. 2014](#); [Pandey et al. 2017a, 2017b;](#)  
167 [Kereilwe et al. 2018](#))

168

169 *Western Blotting for AMH detection*

170 Proteins were extracted from the AP (n = 4) or ovary samples (n = 4, used as positive  
171 controls) and western blotting was performed as previously described ([Kereilwe et al.](#)  
172 [2018](#)). The extracted protein sample (33.4 $\mu$ g of total protein in 37.5 $\mu$ l) was mixed in  
173 12.5 $\mu$ l of 4x Laemmli sample buffer (Bio-rad) containing 10% (v/v)  $\beta$ -mercaptoethanol,  
174 then boiled for 3 min at 100 °C. The boiled protein samples were quickly cooled down in  
175 ice, then the protein samples (2, 4, 8, or 16  $\mu$ g of total protein) were loaded onto a  
176 polyacrylamide gel along with a molecular weight marker (Precision Plus Protein All  
177 Blue Standards; Bio-Rad), and resolved by electrophoresis on sodium dodecyl sulfate  
178 polyacrylamide gels at 100 V for 90 min. Proteins were then transferred to polyvinylidene  
179 fluoride ([PVDF](#)) membranes. Blocking was done with 0.1% Tween 20 and 5% non-fat  
180 dry milk for 1h at 25 °C then immunoblotting was performed with the anti-AMH rabbit  
181 antibody (1:25,000 dilution) overnight at 4 °C. After washing membrane with 10 mM  
182 Tris-HCl (pH 7.6) containing 150 mM NaCl and 0.1% Tween 20, the PVDF membrane  
183 was incubated with horseradish peroxidase ([HRP](#))-conjugated anti- rabbit IgG goat

184 antibody ([Bethyl laboratories, Inc.](#), Montgomery, TX, USA; 1:50,000 dilution) at 25 °C  
185 for 1 h. Protein bands were visualized using an ECL-Prime chemiluminescence kit ([GE](#)  
186 [Healthcare](#), Amersham, UK) and CCD imaging system ([Fujifilm](#), Tokyo, Japan). [Mamsen](#)  
187 *et al.* (2015) utilized western blotting to detect AMH in the human testis or immature  
188 granulosa cells and identified 2 to 5 bands. In this previous study, the pro-mature form  
189 was detected as 3 or 4 bands (12.5, 16, 35, or 55 kDa) and the precursor was 98 kDa. We  
190 defined bovine AMH bands based on mobility as the AMH precursor or the pro-mature  
191 form (4 sizes) according to these previous studies ([Pierre et al. 2016](#); [Mamsen et al. 2015](#);  
192 [Di Clemente et al. 2010](#)). Antibodies were removed from the PVDF membrane with  
193 stripping solution ([Nacalai Tesque Inc.](#), Kyoto, Japan), then, the membrane was used for  
194 immunoblotting with the anti- $\beta$ -actin mouse monoclonal antibody (A2228, 1:50,000  
195 dilution; [Sigma-Aldrich](#), St. Louis, MO, USA).

196

197 *Fluorescent immunohistochemistry and confocal microscopy*

198 We collected tissue blocks of AP (n=5) in 4% paraformaldehyde PBS. The tissue  
199 blocks were stored at 4°C for 16 h, after which they were placed in 30% sucrose PBS  
200 until the blocks were infiltrated with sucrose. For the immunofluorescence analysis of AP  
201 tissues, previously described methods were used ([Kadokawa et al. 2014](#)). Briefly, 15- $\mu$ m

202 sagittal sections were prepared and mounted on slides. The sections were treated with  
203 0.3 % Triton X-100-PBS for 15 min, then, blocking done by incubating with 0.5 mL of  
204 PBS containing 10% normal goat serum ([Wako Pure Chemicals](#), Osaka, Japan) for 1 h at  
205 room temperature. The slides were incubated with a cocktail of primary antibodies (anti-  
206 GnRHR guinea pig antibody, anti-AMH rabbit antibody, and either anti-LH $\beta$  or anti-  
207 FSH $\beta$  mouse antibody [all diluted as 1:1,000]) for 12 h at 4°C, then followed by  
208 incubation with a cocktail of fluorochrome-conjugated secondary antibodies (Alexa Fluor  
209 Alexa Fluor 488 goat anti-rabbit IgG, Alexa Fluor 546 goat anti-mouse IgG, and Alexa  
210 Fluor 647 goat anti-guinea pig IgG [all from Thermo Fisher Scientific and diluted as 1  
211  $\mu$ g/mL]) and 1  $\mu$ g/mL of 4', 6'-diamino-2-phenylindole ([DAPI](#); [Wako Pure Chemicals](#))  
212 for 2 h at room temperature.

213 The stained sections on slides were observed by confocal microscopy (LSM710; [Carl](#)  
214 [Zeiss](#), Göttingen, Germany) equipped with a diode lasers (405nm, argon laser 488nm,  
215 HeNe laser 533nm, and HeNe laser 633nm). Images obtained by fluorescence microscopy  
216 were scanned with a 40 $\times$  or 63 $\times$  oil-immersion objective and recorded by a CCD camera  
217 system controlled by ZEN2012 black edition software (Carl Zeiss). GnRHR, AMH and  
218 LH $\beta$  or FSH $\beta$  localization were examined in confocal images of triple-immunolabeled  
219 specimens. In the confocal images obtained after immunohistochemistry analysis, the

220 GnRHR is shown in light blue, AMH is shown in red, and LH $\beta$  or FSH $\beta$  is shown in green.  
221 To verify the specificity of the signals, we included several negative controls in which the  
222 primary antiserum had been omitted or pre-absorbed with 5 nM of the same antigen  
223 peptide, or in which normal rabbit IgG (Wako Pure Chemicals) was used instead of the  
224 primary antibody. Percentage of single- and double-labeled AMH- and GnRHR-positive  
225 cells were determined from 12 representative confocal images per pituitary gland.

226

227 *AP sample collection for comparisons among estrus stages*

228 AP tissues were collected from the heads of adult (26-month-old) non-pregnant  
229 healthy Japanese Black heifers in the pre-ovulation [day 19 to 21 (day 0 = day of estrus);  
230 n = 5], early luteal (day 2 to 5; n = 5), mid-luteal (day 8 to 12; n = 5), or late luteal (day  
231 15 to 17; n = 5) phase, as determined by the macroscopic examination of the ovaries and  
232 uterus ([Miyamoto et al. 2000](#)). Samples were obtained at a local abattoir as previously  
233 described ([Rudolf and Kadokawa 2014](#)) and immediately frozen in liquid nitrogen and  
234 stored at -80°C until RNA or protein extraction.

235

236 *AP sample collection for comparisons among ages or breeds*

237 AP tissues were obtained during the luteal phase from healthy post-pubertal Japanese  
238 Black heifers ( $25.9 \pm 0.6$  months of age; n = 5; [young JB group](#)), old Japanese Black cows  
239 ( $89.7 \pm 20.3$  months of age;  $5.2 \pm 0.5$  parity; n = 5; [old JB group](#)), and old Holstein cows  
240 ( $79.2 \pm 10.3$  months of age;  $6.6 \pm 0.9$  parity; n = 5; [old Hol group](#)) from the local abattoir.  
241 It was not possible to obtain AP samples from post-pubertal Holstein heifers because they  
242 are kept in dairy farms for milking purposes. All of the heifers and cows in the three  
243 groups were non-lactating and non-pregnant and they had no follicular cysts, luteal cysts,  
244 and other ovarian disorders based on macroscopic examinations of the ovaries ([Kamomae](#)  
245 [2012](#)). All cows in the old Hol group had endometritis as determined by the macroscopic  
246 examination of the uterus with mucopurulent vaginal discharge ([Kamomae 2012](#)). All of  
247 their endometritis clinical scores ([Sheldon and Dobson 2004](#)) were 1, since the mucus  
248 character was clear or translucent with flecks of white pus, and the mucus odor was not  
249 unpleasant. The old Holstein cows were slaughtered owing to infertility, diagnosed after  
250 at least 5 artificial insemination attempts. The old Japanese Black cows were slaughtered  
251 after completing parturition a sufficient number of times, as planned by farmers to obtain  
252 beef.

253

254 *Real-time PCR to evaluate the factors affecting AMH expression*

255 Real-time PCR was performed to compare *AMH* expression among estrous phases or  
256 among the young JB, old JB, and old Hol groups. The preparation of high-quality total  
257 RNA and cDNA synthesis were performed as described above.

258 [Table 1](#) shows the primers designed for real-time PCR using Primer Express  
259 Software V3.0 (Thermo Fisher Scientific) based on the reference sequences. The amount  
260 of gene expression was measured in duplicate by real-time PCR analyses with 20 ng  
261 cDNA, using CFX96 Real Time PCR System ([Bio-Rad](#), Hercules, CA, USA) and Power  
262 SYBR Green PCR Master Mix (Thermo Fisher Scientific), together with a 6-point  
263 relative standard curve, non-template control, and no reverse-transcription control.  
264 Standard 10-fold dilutions of purified and amplified DNA fragments were prepared.  
265 Temperature conditions for all genes were as follows: 95°C for 10 min for pre-  
266 denaturation; five cycles each of 95°C for 15s and 66°C for 30s; and 40 cycles each of  
267 95°C for 15s and 60°C for 60s. Melting curve analyses were performed at 95°C for each  
268 amplicon and each annealing temperature to ensure the absence of smaller non-specific  
269 products such as dimers. To optimize the real-time PCR assay, serial dilutions of a cDNA  
270 template were used to generate a standard curve by plotting the log of the starting quantity  
271 of the dilution factor against the C<sub>q</sub> value obtained during amplification of each dilution.  
272 Reactions with a coefficient of determination (R<sup>2</sup>) >0.98 and efficiency between 95 and

273 105% were considered optimized. The concentration of PCR products was calculated by  
274 comparing C<sub>q</sub> values of unknown samples with the standard curve using appropriate  
275 software (CFXmanagerV3.1, Bio-Rad). The gene expression levels for *AMH* genes were  
276 normalized to the geometric mean of the expression levels of two house-keeping genes,  
277 *GAPDH* and *RANBP10*. We selected these two housekeeping genes from among 20 that  
278 have been previously described (Rekawiecki et al. 2012; Walker et al. 2009) because they  
279 had the smallest inter-heifer coefficients of variation of reads per kilobase of transcript  
280 per million mapped reads value upon deep sequencing of the transcriptome (Pandey et al.  
281 2017c).

282

283 *Western blotting to evaluate the factors affecting AMH expression*  
284 Western blotting was performed to compare AMH protein levels in APs among  
285 different estrous phases or among the young JB, old JB, and old Hol groups. Sample  
286 collection and western blotting were performed as described above. Briefly, 15 µL (8 µg  
287 of total protein) of boiled sample was loaded on a polyacrylamide gel along with the  
288 molecular weight marker and four standard samples (2, 4, 8, and 16 µg total protein for  
289 each of five randomly selected AP samples diluted with protein extraction reagent).  
290 MultiGauge v.3.0 software (Fujifilm) was used to quantify the signal intensity of the

291 protein bands. The intensities of band of AMH (as mature C-terminal form) for 16-, 8-,  
292 4-, and 2- $\mu$ g AP protein samples were set as 100%, 50%, 25%, and 12.5%, respectively,  
293 and the intensity of other samples was calculated as a percentage of these standards using  
294 MultiGauge software. After antibodies were removed from the PVDF membrane with  
295 stripping solution, the membrane was used for immunoblotting with the anti- $\beta$ -actin  
296 mouse monoclonal antibody. The intensities of the  $\beta$ -actin band for 16-, 8-, 4-, and 2- $\mu$ g  
297 AP protein samples were set as 100%, 50%, 25%, and 12.5%, respectively, and the  
298 intensity of other samples was calculated as a percentage of these standards using  
299 MultiGauge software. AMH expression level was normalized to that of  $\beta$ -actin in each  
300 sample.

301

302 *Analysis of the AMH gene 5'-flanking region*

303 The 5000-nucleotide sequence of the 5'-flanking region of the *AMH* gene  
304 (chromosome 7: 22691978-22696977) was obtained using the online Ensembl  
305 ([www.ensembl.org](http://www.ensembl.org)) and BLAT Search Genome program (<http://genome.ucsc.edu>) (Cow  
306 Jun. 2014, *Bos\_taurus\_UMD\_3.1.1/bosTau8*). The sequence was analyzed using Genetyx  
307 software ver. 13 (Genetyx, Tokyo, Japan) for the presence of consensus response element  
308 (RE) sequences for estrogen—i.e., ERE (5'-GGTCANNNTGACC-3') ([Gruber et al.](#)

309     2004), and half ERE (GGTCA, TGACC, or TGACT) (Liu et al. 1995), as well as for

310     progesterone—i.e., PRE (5'-G/A G G/T AC A/G TGGTGTTCT-3') (Geserick *et al.* 2005).

311

312     *Statistical analysis*

313     The statistical analysis was done by one-factor ANOVA followed by *post-hoc*

314     comparisons using Fisher's protected least significant difference (**PLSD**) test using

315     StatView version 5.0 for Windows (**SAS Institute**, Inc., Cary, NC, USA). The level of

316     significance was set at  $P < 0.05$ . Data are expressed as mean  $\pm$  standard error of the mean

317     (**SEM**).

318

319     **Results**

320     *Expression of AMH mRNA in APs of post-pubertal heifers*

321     PCR products of the expected size (328 bp), indicating AMH, were obtained by

322     agarose gel electrophoresis (Fig. 1). Homology searching in the gene databases for the

323     obtained sequence of amplified products revealed that the best match alignment was

324     bovine AMH (NM\_173890.1), which had a query coverage of 100%, an e-value of 0.0, and

325     a maximum alignment identity of 99%. There was no other bovine gene found to have a

326     homology for the obtained sequences of amplified products, which lead to the conclusion

327 that the sequences of the amplified products were identical with the sequence of bovine  
328 AMH.

329

330 *AMH protein expression in APs*

331 Western blotting confirmed the presence of AMH in both the AP and ovary samples,  
332 with differences in intensity between sample type ([Fig. 2A](#)). Weaker bands for the AMH  
333 precursor (70 kDa) were detected in the AP samples than in the ovary samples. Stronger  
334 bands for the mature C-terminal form were observed for the AP samples than the ovary  
335 samples, and there was a difference in molecular weights between AP (20 kDa) and ovary  
336 (25 kDa) samples. [Figure 2B](#) shows representative β-actin bands for both tissue types.

337

338 *Immunofluorescence analysis of AMH expression in bovine small follicles and AP tissues*  
339 [Figure 3](#) shows immunofluorescence signals in the granulosa cells of small follicles  
340 in the ovary tissues of post-pubertal heifers.

341 Also the expression of GnRHR, AMH, LH $\beta$ , and FSH $\beta$  in bovine AP tissues was  
342 investigated by immunohistochemistry. AMH was localized in the majority of LH $\beta$ -  
343 positive ([Fig. 4a](#)) and FSH $\beta$ -positive ([Fig. 4b](#)) cells. In AP samples, there were  $53.2 \pm 2.1$   
344 GnRHR-positive cells,  $43.2 \pm 2.5$  AMH-positive cells, and  $30.2 \pm 1.6$  double-positive

345    cells; 57.0%  $\pm$  3.4% of GnRHR-positive cells were AMH-positive, whereas 82.0%  $\pm$   
346    5.5% of AMH-positive cells were GnRHR-positive.

347

348    *Relationship between AMH in APs and the estrous phase*

349    We used real-time PCR and western blotting to evaluate the relationship between the  
350    estrous phase and AMH expression at the mRNA and protein levels in APs. There were  
351    no differences among phases of the estrous cycle in AMH expression at the mRNA ( $P >$   
352    0.05; [Fig. 5](#)) or protein levels ( $P > 0.05$ ; [Fig. 6](#)).

353

354    *AMH expression in APs of Holstein cows, Japanese black heifers, and Japanese black*  
355    *cows*

356    Real-time PCR and western blotting were used to analyze AMH expression at the  
357    mRNA and protein levels in the AP. The levels of *AMH* mRNA were lower in the old Hol  
358    group than in young JB group ( $P < 0.05$ ; [Fig. 7](#)). The old JB group had tendency to express  
359    lower levels *AMH* mRNA than those in the young JB group ( $P = 0.10$ ). AMH protein  
360    levels were greater in the old Hol group than in the old JB and young JB groups ( $P < 0.05$ ;  
361    [Fig. 8](#)). There was no difference in AMH levels between the young JB and old JB groups  
362    ( $P > 0.10$ ).

363

364     *ERE, and PRE in the 5'-flanking region of bovine AMH gene*

365         The 5'-flanking region of the bovine *AMH* gene was analyzed for EREs, PREs, and

366         similar sequences. There were no ERE, no half ERE, nor PRE sequences.

367

## 368     **Discussion**

369         The APs of tilapia express AMH but the specific cells expressing AMH are unclear

370         ([Poonlaphdecha et al. 2011](#)). This study is the first to evaluate gonadotrophs expressing

371         AMH. AMH activates the synthesis and secretion of gonadotropins from the

372         gonadotrophs of rodents and bovines ([Bédécarrats et al. 2003](#); [Garrel et al. 2016](#);

373         [Kereilwe et al, 2018](#)). Therefore, the coordination of the endocrine, paracrine, and

374         autocrine control of AMH may be important for normal reproductive functions, similar to

375         GnRH, inhibin, and activin ([Pagesy et al. 1992](#); [Miller et al. 1996](#); [Popovics et al. 2011](#)).

376         Immunohistochemistry using an anti-AMH antibody has shown a strong signal in the

377         granulosa cells of small antral follicles, which express *AMH* mRNA ([Campbell et al.](#)

378         [2012](#)), consistent with AMH expression in granulosa cells of ruminants ([Rocha et al.](#)

379         [2016](#)). Additionally, the band patterns observed by western blotting were similar to those

380         of a previous study of AMH ([Mamsen et al. 2015](#)). Therefore, the anti-AMH antibody

381         can be used for immunohistochemical analyses of bovine samples. Gonadotrophs are a

382 heterogeneous cell population including LH and FSH monohormonal and bihormonal  
383 subsets in rats, equines, and bovines ([Townsend et al. 2004](#); [Pals et al. 2008](#); [Kadokawa](#)  
384 *et al. 2014*). Our results showed that both LH $\beta$ -positive cells and FSH $\beta$ -positive cells  
385 express AMH, suggesting that AMH secreted from the three types of gonadotrophs have  
386 paracrine or autocrine roles.

387 Western blotting showed differences in band strength or size between APs and  
388 ovaries. The APs exhibited weaker bands for the AMH precursor (70 kDa) than those for  
389 ovary samples, suggesting that APs store less AMH precursor than ovaries. The band size  
390 for the mature C-terminal form was smaller for APs (20 kDa) than for ovaries (25 kDa).  
391 We did not observe a 25-kDa band in the AP lane or a 20-kDa band in the ovary lane,  
392 even after longer exposure periods (data not shown). A potential explanation for the band  
393 size difference for the mature C-terminal form may be a difference in O-glycosylation  
394 among organs ([Medzihardszky et al. 2015](#); [Skaar et al. 2011](#)).

395 AMH expressed by gonadotroph has not been evaluated previously in any species;  
396 accordingly, it was impossible to compare our data with the results of previous studies.  
397 Our results that AMH expression at the mRNA and protein levels in APs differ between  
398 the young JB and old Hol groups. Jerseys have higher blood AMH concentrations than  
399 those of Holsteins ([Ribeiro et al. 2014](#)). Therefore, the difference in AMH expression in

400 APs may be explained by a difference among breeds or any factor related to breed. The  
401 APs of the old Hol group expressed lower levels of *AMH* mRNA than those of the young  
402 JB group. In contrast, the APs of the old Hol group exhibited higher AMH protein levels  
403 than those of the young and old JB groups. However, the results for the effects of breed  
404 and age on AMH expression in APs should be interpreted with caution because we could  
405 not obtain APs from young Holsteins. Further studies are required to clarify whether  
406 AMH secretion from APs is decreased in old Hol and results in higher AMH protein levels  
407 within APs.

408 We previously reported that old Japanese Black cows have significantly higher  
409 blood AMH concentrations (100 pg/mL) than those of young Japanese Black cows (1–10  
410 pg/mL) throughout the postpartum period (Koizumi and Kadokawa 2017). However, we  
411 observed a small difference in AMH expression at the mRNA and protein levels in APs  
412 between the young and old JB groups in this study. Therefore, AMH secreted by the ovary,  
413 rather than AMH secreted by the AP, may explain the difference in blood AMH  
414 concentrations between young and old cows.

415 Previous studies have not detected significant changes in the blood AMH  
416 concentration during the estrous cycle in ruminants (Pfeiffer *et al.* 2014; Koizumi and  
417 Kadokawa 2017; El-Sheikh Ali *et al.* 2013). Our data also showed no significant changes

418 in AMH at the mRNA and protein levels in APs during the estrous cycle. The 5'-flanking  
419 region of the bovine *AMH* gene does not contain ERE, half ERE, or PRE sequences.  
420 Therefore, AMH expression in APs, similar to the blood AMH concentration, is unlikely  
421 to change during the estrous cycle. In conclusion, bovine gonadotrophs express AMH,  
422 and the AMH expression may be breed-dependent. Further studies are needed to  
423 determine the precise effects of age and breed on AMH expression.

424

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431

#### 432 **Conflicts of Interest**

433 The authors declare no conflicts of interest.

434

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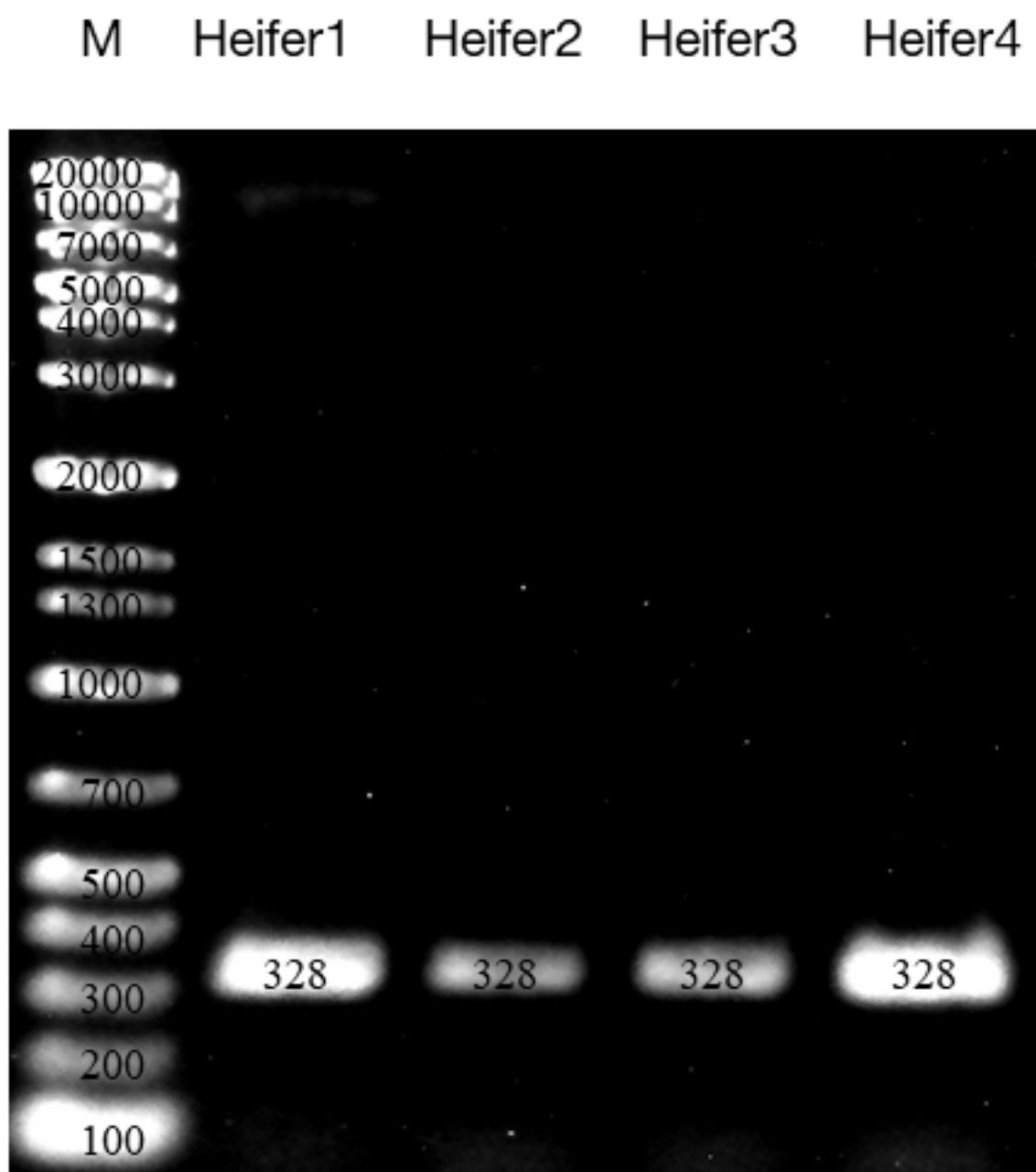
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610

611 Table 1. Name, accession number, and details of the primers used for real-time PCRs

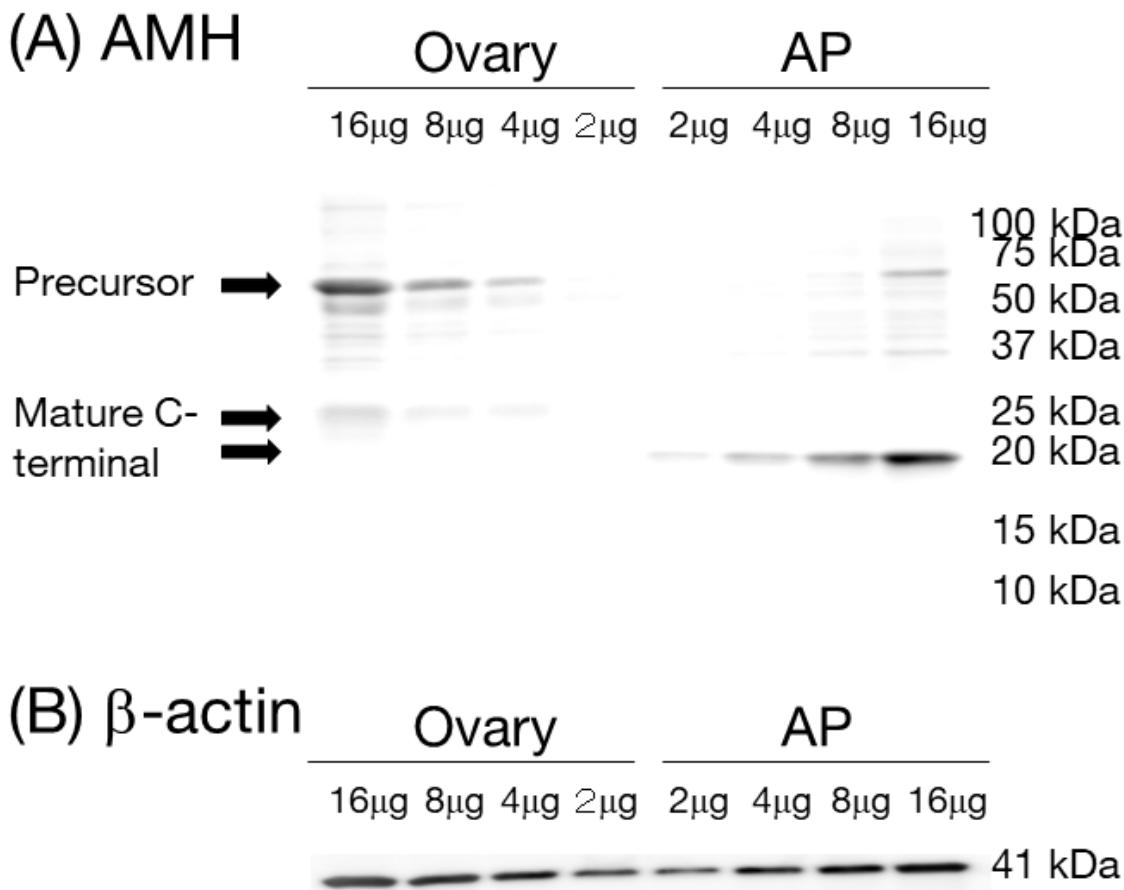
Gene name	Accession number	Primer	Sequence 5'-3'	Size (bp)
<i>GAPDH</i>	NM_001034034	Forward	TGGTGAAGGTCGGAGTGAAC	91
		Reverse	ATGGCGACGATGTCCACTTT	
<i>RANBP10</i>	NM_001098125	Forward	CCCAGTCCTACCAGCCTACT	133
		Reverse	CCCCCAGAGTTGAATGACCC	
<i>AMH</i>	NM_173890	Forward	GGGTTAGCCCTTACCCCTGC	121
		Exon 3 4	Reverse	GTAACAGGGCTGGGGTCTT

612



613 **Fig. 1.** Expression of anti-Müllerian hormone (*AMH*) mRNA, as detected by RT-PCR.  
614  
615 Electrophoresis of PCR-amplified DNA products using the primer pair for bovine *AMH*  
616 and cDNA derived from the anterior pituitary (*AP*) of post-pubertal heifers. The lanes  
617 labeled Heifers 1 to 4 demonstrate that the DNA products were of the expected size, i.e.,  
618 328 bp. Lane M showed the band sizes of the DNA marker.

619



620

621 **Fig. 2.** Western blotting results using extracts (2, 4, 8, or 16  $\mu$ g of total protein) from the  
622 APs or ovaries of post-pubertal heifers and an anti-AMH rabbit antibody (A) or anti-  
623  $\beta$ -actin mouse antibody (B).

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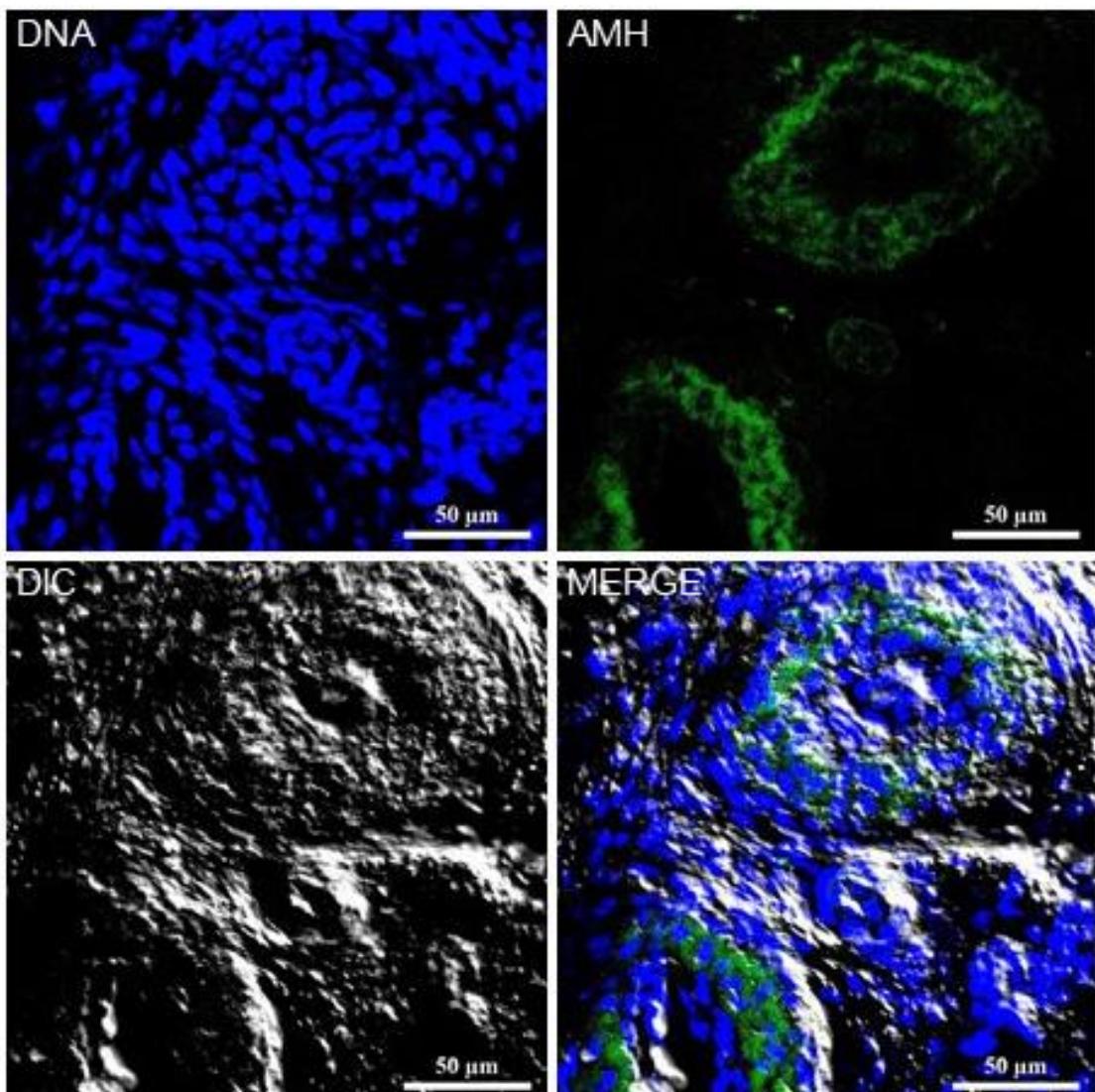
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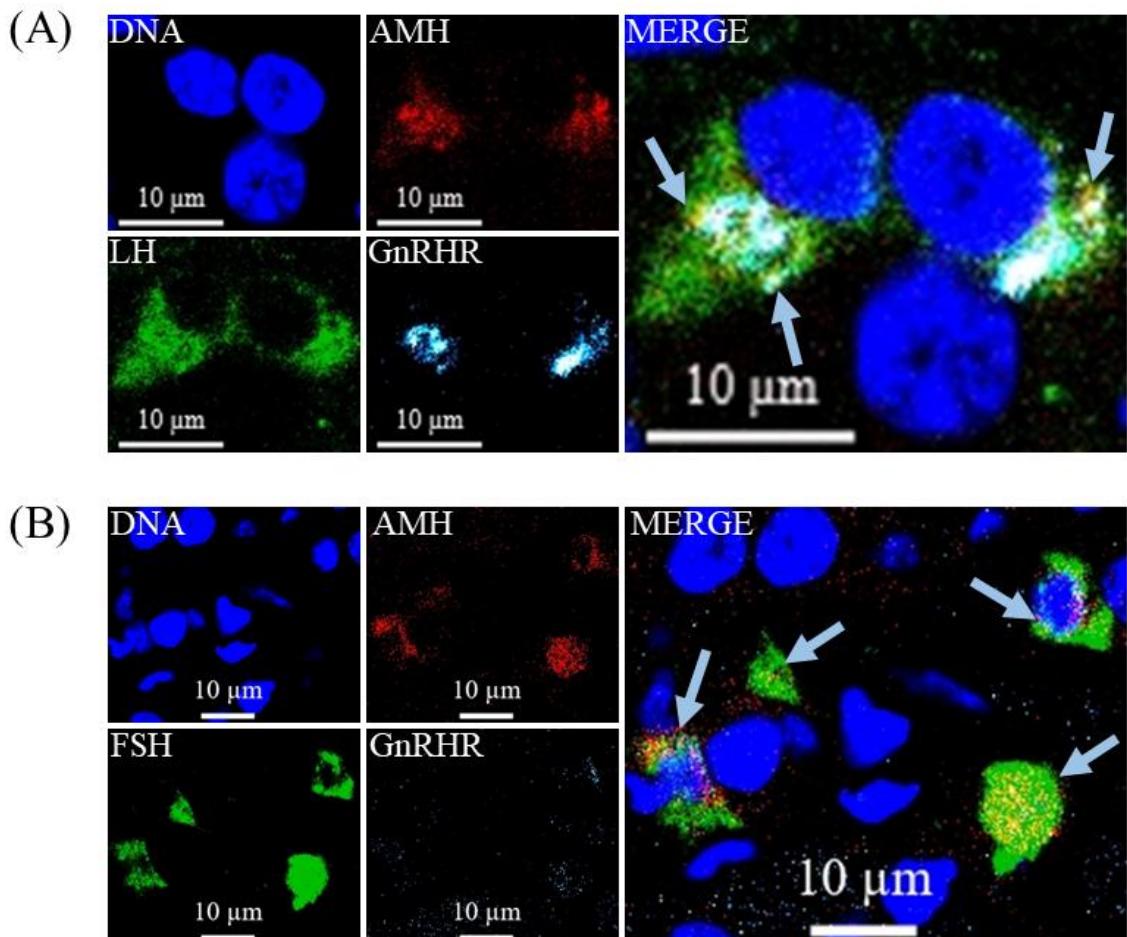


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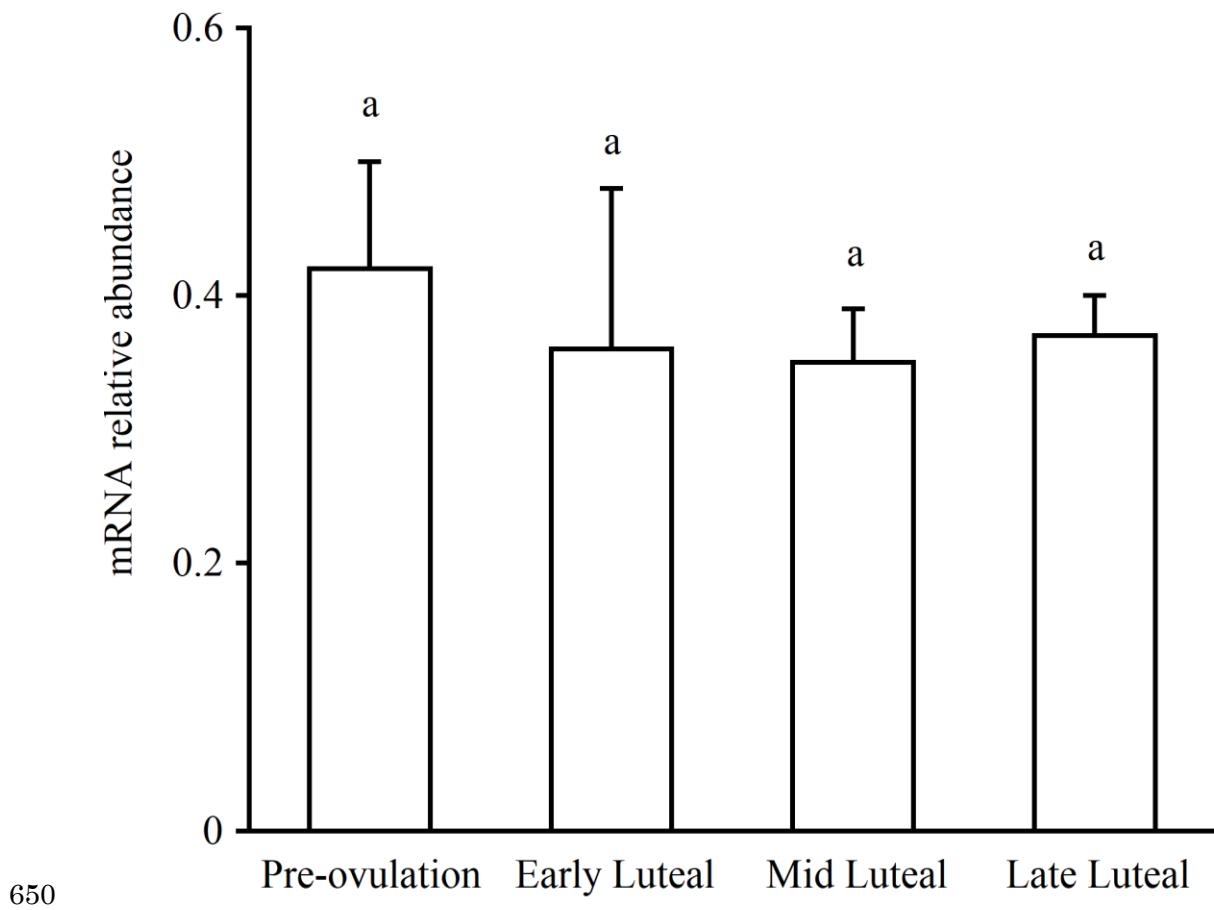
636 **Fig. 3.** Fluorescence immunohistochemical analysis of AMH on small antral follicles in  
637 ovaries of post-pubertal heifers. Images were captured by laser confocal microscopy for  
638 AMHR2 (green) with counter-staining by DAPI (dark blue, indicating DNA) and  
639 differential interference contrast (DIC). Scale bars represent 50  $\mu$ m.

640

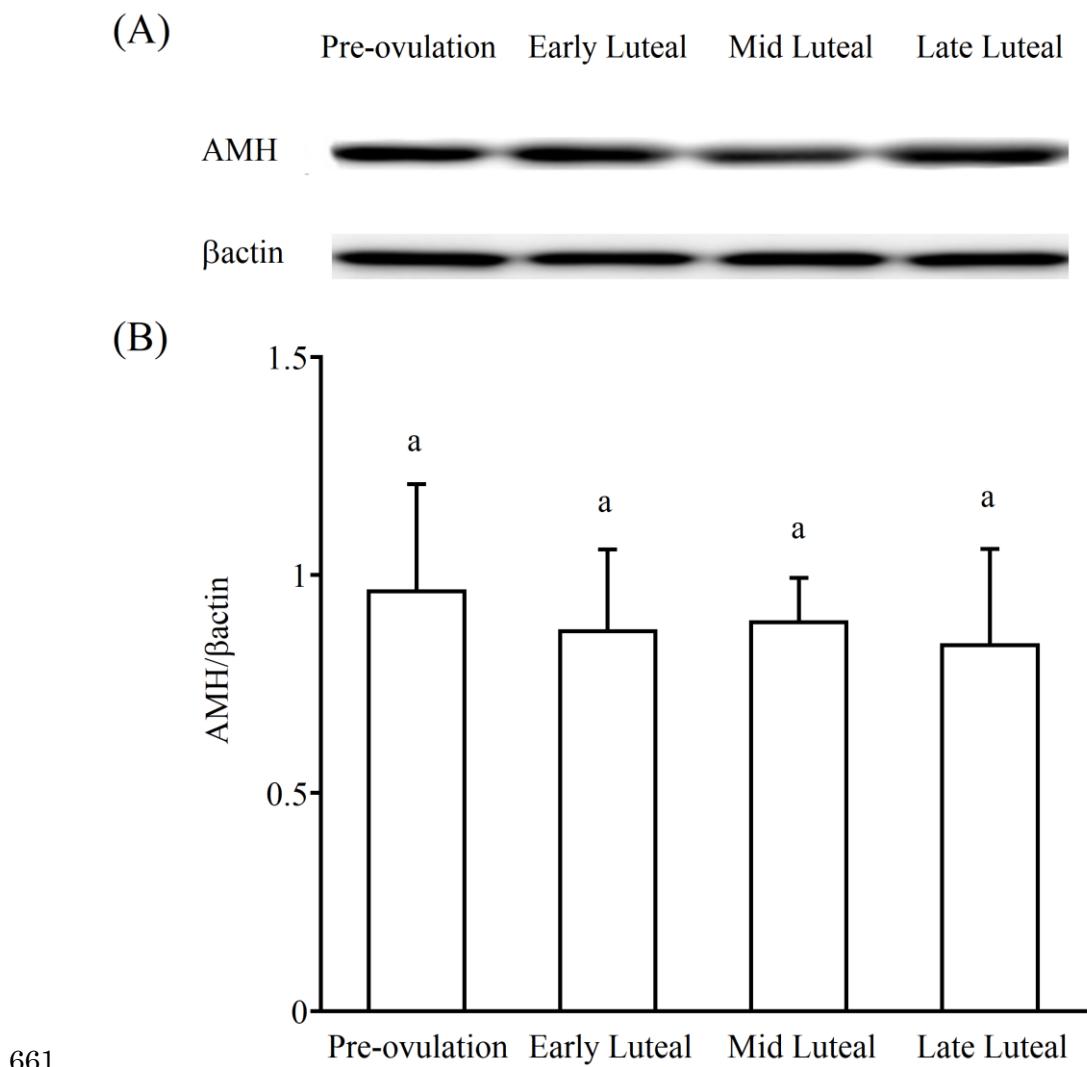


643 **Fig. 4.** Triple-fluorescence immunohistochemistry of AP tissues in post-pubertal heifers  
644 for the detection of gonadotropin-releasing hormone receptor (GnRHR), AMH, and LH  
645 (A) or FSH (B). Images were captured by laser confocal microscopy for GnRHR (cyan),  
646 AMH (red), and LH or FSH (green) with counter-staining by DAPI for DNA (dark blue).  
647 Yellow indicates the colocalization of AMH and LH/FSH, indicated by blue arrows. Scale  
648 bars represent 10  $\mu$ m.

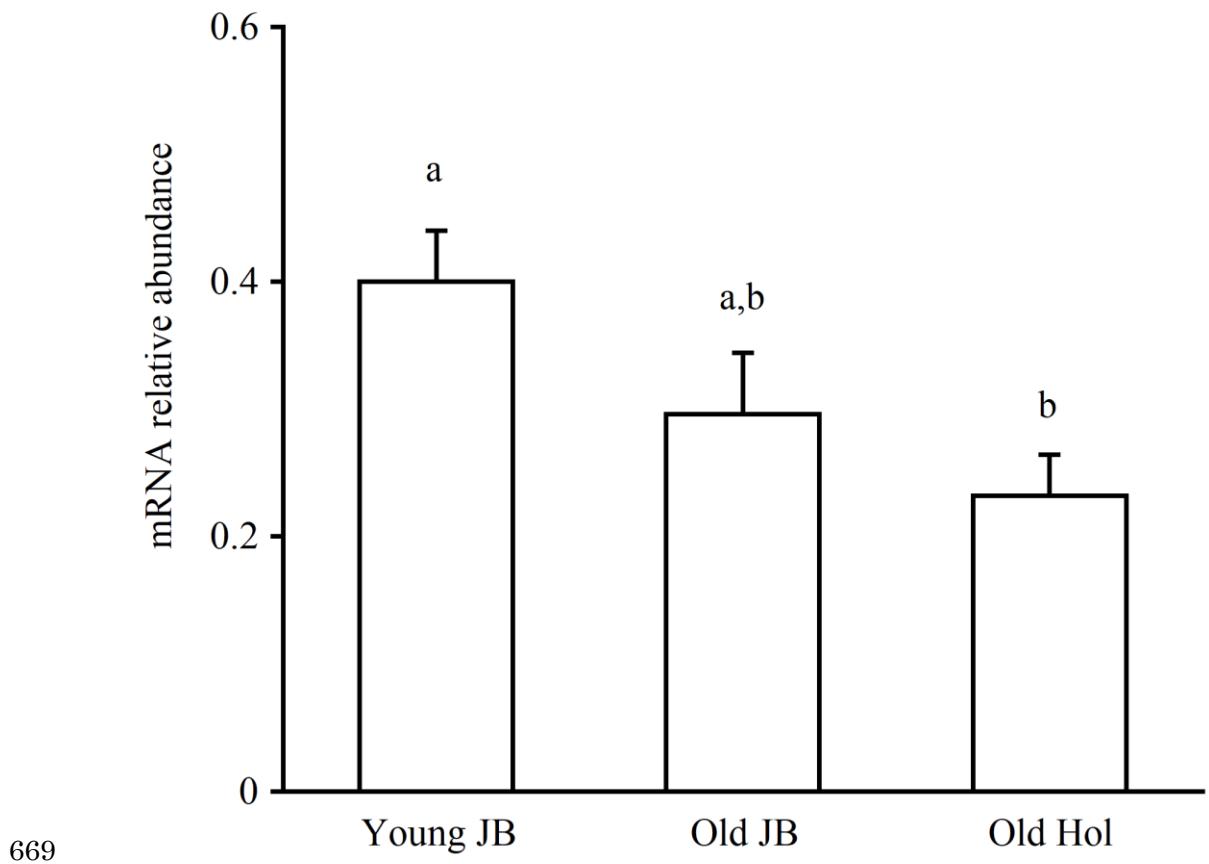
649



652 **Fig. 5.** Relative *AMH* mRNA levels (mean  $\pm$  SEM) in bovine APs during pre-ovulation  
 653 [day 19 to 21 (day 0 = day of estrus)], early luteal (day 2 to 5), mid-luteal (day 8 to 12),  
 654 or late luteal (day 15 to 17) phases, as determined by real-time PCR. Data were  
 655 normalized to the geometric means of *GAPDH* and RAN-binding protein (*RANBP10*)  
 656 levels. The same letters indicate no significant differences ( $P>0.05$ ) across phases.  
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661      Fig. 6. (A) Representative AMH (as mature C-terminal form) and  $\beta$ -actin protein  
662      expression in bovine AP tissues obtained during the pre-ovulation, early luteal, mid luteal,  
663      or late luteal phases of estrous, as detected by western blotting. (B) AMH protein  
664      expression level of AMH normalized to that of  $\beta$ -actin in healthy post-pubertal heifer AP  
665      tissues obtained during pre-ovulation ( $n = 5$ ), early luteal ( $n = 5$ ), mid-luteal ( $n = 6$ ), and  
666      late luteal ( $n = 5$ ) phases. The same letters indicate no significant differences ( $P > 0.05$ )  
667      across phases.



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673 **Fig. 7.** Relative *AMH* mRNA levels (mean  $\pm$  SEM) in bovine AP tissues obtained from

674 healthy young Japanese heifers (young JB), old Japanese black cows (old JB), and old

675 Holsteins cows (old Hol), as determined by real-time PCR. Data were normalized to the

676 geometric means of *GAPDH* and *RANBP10* levels. Letters (a vs. b) indicate significant

677 differences ( $P < 0.05$ ) among groups.

678

