1 TITLE

2	Specific locations and amounts of denatured collagen and collagen-specific
3	chaperone HSP47 in the oviducts and uteri of old cows as compared to those of
4	heifers
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15	Running head: Denatured collagen in bovine oviducts and uteri

17 Abstract

Collagen, the most abundant extra-cellular matrix in oviducts and uteri, performs critical 18 19 roles in pregnancies. We hypothesised that the locations and amounts of both denatured collagen and the collagen-specific molecular chaperone, 47-kDa heat shock protein 2021(HSP47), in the oviducts and uteri of old cows are different compared to those of young heifers because of repeated pregnancies. Since detecting damaged collagen in tissues is 2223challenging, in the first part of this study, we developed a new method that uses a denatured collagen detection reagent. Then, we compared damaged collagen in the 24oviducts and uteri between post-pubertal growing nulliparous heifers $(22.1 \pm 1.0 \text{ months})$ 2526old) and old multiparous cows (143.1 \pm 15.6 months old). Further, we evaluated the 27relationship between denatured collagen and HSP47 by combining this method with fluorescence immunohistochemistry. Picro-sirius red staining showed collagen in almost 28all parts of the oviducts and uteri. Expectedly, damaged collagen was increased in the 29oviducts and uteri of old cows. However, damaged collagen and HSP47 were not located 30 in the same area in old cows. The number of fibroblasts increased, suggesting the presence 31of fibrosis in the oviducts and uteri of old cows. These organs of old cows showed higher 3233 HSP47 protein amounts than those of heifers. However, the uteri, but not oviducts, of old cows showed lower HSP47 mRNA amounts than those of heifers. These findings revealed 34 the specific location and amounts of denatured collagen and HSP47 in the oviducts and 35uteri of old cows compared to those of heifers. 36

Additional keywords: aging, fibroblast, fibrosis, infertility, ruminants, serpin family H
 member 1.

39 Introduction

Infertility increases after aging in various animals, including cows (Osoro and Wright 40411992). However, little is known about the exact pathophysiological mechanisms in oviducts and uteri. Collagen, one of the most abundant extra-cellular matrix (ECM) 42proteins, exerts a critical role in successful pregnancies, and abnormal collagen 43expression is associated with recurring miscarriages in women (Li et al. 2019, Shi et al. 44 2020). The bovine endometrium, similar to that of other mammalians, changes 45morphologically throughout the oestrous cycle (Arai et al. 2013). Furthermore, 46dysregulation of ECM remodelling in bovine endometrium may impair fertility (Scolari 4748 et al. 2016).

49Denaturation of collagen is increased due to various diseases, including cancer, osteoporosis, and arthritis (Fields 2013, Ito and Nagata 2019). Denatured collagen was 50studied by electron microscopy for corneal immune injury (Mohos and Wagner 1969). It 51was technically challenging to detect damaged collagen in tissues until the recent 52development of a collagen hybridising peptide (Zitnay et al. 2017) and a denatured 53collagen detection reagent (Takita et al. 2019). The latter is a biotin-labelled collagen-54mimetic peptide that hybridises with the denatured portion of collagen. It enables the 55detection of denatured collagen via western blotting as well as through visualisation of 56heat damaged collagen fibrils in mouse fibroblasts (Takita et al. 2019). 57

58 Forty-seven kilodalton heat shock protein, HSP47, encoded by *SERPINH1*, is a sole 59 procollagen-specific molecular chaperone that is essential for correct folding of the 60 unique, triple-helical structure of collagen (Ito and Nagata 2019). HSP47 also plays 61 important roles in the synthesis of collagen as well as in the prevention of procollagen 62 aggregation (Duarte and Bonatto 2018). Therefore, HSP47 is central in detecting the 63 location of active collagen synthesis in the oviducts and uteri.

In this study, we hypothesised that the locations and amounts of both denatured 64 collagen and HSP47 in the oviducts and uteri of old cows are different compared to those 65 of young heifers. In the first part of this study, we developed a new method using the 66 denatured collagen detection reagent to compare young and old oviducts and uteri. Then, 67 we evaluated the relationship between denatured collagen and HSP47 in heifers and old 68 cows utilising this method followed by fluorescence immunohistochemistry. Further, we 69 compared the amounts of the mRNA and protein of HSP47 in oviducts and uteri between 70the old cows and heifers. 71

72

73 Materials and Methods

74 Sample collection

All experiments were performed according to the Guiding Principles for the Care and Use of Experimental Animals in the Field of Physiological Sciences (Physiological Society of Japan) and approved by the Committee on Animal Experiments of Yamaguchi University (approval no. 301).

We obtained oviductal and uterine samples from cattle managed by contract farmers in western Japan. All cattle born in Japan since 2003 are registered at birth with an individual identification number in a database of National Livestock Breeding Center of Japan. We utilised both individual identification numbers to search the database and information given by the contract farmers for the cattle in this study.

84	We used a previously reported method (Ferdousy et al. 2020) to obtain the ampulla,
85	isthmus, caruncular (CAR), and intercaruncular (ICAR) areas as well as the uterine
86	myometrium from healthy postpubertal, growing, young nulliparous heifers (22.1 \pm 1.0
87	months old; Young group), and old multiparous Japanese Black beef cows (143.1 ± 15.6
88	months old; 9 ± 1 parities; sacrificed at least 3 months after the last parturition; Old group)
89	at a local abattoir. The heifers and cows were at days 2 to 3, 8 to 12, 15 to 17, or 19 to 21
90	of the oestrous cycle (day $0 =$ day of oestrus), as determined via macroscopic examination
91	of the ovaries and uterus (Miyamoto et al. 2000). The samples collected were from the
92	side ipsilateral to ovulation from days 2 to 3, 8 to 12, or 15 to 17 but were from the side
93	ipsilateral to the dominant follicle from days 19 to 21. We collected at least five samples
94	per group per day. Half of the samples (whole tissue fragment; about 1 cm length of
95	ampulla and isthmus; about 5 mm in width, 5 mm in length, and 2 mm in thickness of
96	CAR, ICAR, and myometrium) were frozen in liquid nitrogen and preserved at -80°C
97	until RNA or protein extraction was performed. The remaining half was embedded in a
98	cryo-mould containing an optimum cutting temperature compound (Sakura Fintechnical
99	Co. Ltd., Tokyo, Japan), and then the cryo-mould was wrapped with an aluminium foil.
100	The cryo-moulds were then frozen in liquid nitrogen and preserved at -80°C until in situ
101	detection of denatured collagen and immunohistochemistry studies were conducted.

Additionally, we measured the total collagen in tissue using picro-sirius red staining. For this purpose, we obtained the ampulla, isthmus, CAR, and ICAR from four different young nulliparous heifers (21.5 ± 0.6 months old), and four old multiparous Japanese Black beef cows (148.8 ± 12.0 months old; 9 ± 1 parities; sacrificed at least 3 months after the last parturition) at the local abattoir. The samples were stored in 4% paraformaldehyde (PFA) at 4°C for 16 h.

108

109 Development of the method for in situ detection of denatured collagen

We developed a new method for *in situ* detection of denatured collagen. As describedbelow, this method can be combined with fluorescent immunohistochemistry.

112 Unfixed tissue blocks were sectioned into 15-µm-thick sections using a cryostat (CM1950, Leica Microsystems, Wetzlar, Germany) and mounted on slides (MAS coat 113Superfrost, Matsunami-Glass, Osaka, Japan). Next, the tissue was fixed with 4% PFA in 114 PBS for 15 min. Some sample sections from the young group were placed on slides 115treated with 100 °C PBS for 2 min (pre-heated slides) or with 25 °C accutase cell 116 117detachment solution (Nacalai Tesque, Kyoto, Japan) for 30 min (digested slides) to 118 denature collagen, whereas others were treated with ice-cold PBS (non-treated slides). 119 We used accutase because it is a proteolytic and collagenolytic enzyme, and it is not 120inhibited by the possible presence of calcium and magnesium in the tissues. We tried to 121use also collagenase, but the structures of the tissues were broken after staining, while 122accutase did not significantly damage the structure. Blocking was performed by 123incubating the tissue sections in PBS (0.5 mL) containing 10% normal goat serum (Wako 124Pure Chemicals, Osaka, Japan) for 1 h at room temperature. Tissues were then treated with an avidin/biotin blocking kit (Vector Laboratories, Burlingame, CA, USA) following 125

the manufacturer's protocol. After washing twice with PBS, the slide was loaded with 5 126 127µg/mL of denatured collagen detection reagent (Funakoshi, Tokyo, Japan) and incubated 128for 60 min at room temperature in a humid box. After washing twice with PBS, the tissues 129were incubated with streptavidin, Alexa Fluor 546 conjugate (diluted to 1 µg/mL in PBS, Thermo Fisher Scientific, Waltham, MA, USA), and 1 µg/mL of 4, 6-diamino-2-130 phenylindole (DAPI; Wako Pure Chemicals) for 60 min at room temperature. After 131132washing thrice, cover glasses were mounted using Vectashield HardSet Mounting Medium (Vector Laboratories). 133

Sections were observed with a confocal microscope (LSM710; Carl Zeiss, Göttingen, 134135Germany) equipped with a 405 nm diode laser, 488 nm argon laser, 533 nm HeNe laser, and 633 nm HeNe laser. Images obtained by fluorescence microscopy were scanned with 136a 20× or 40× oil-immersion objective and recorded with a CCD camera system controlled 137by ZEN2012 black edition software (Carl Zeiss). The exact same microscope settings 138139were used throughout immunofluorescence imaging of the ampulla, isthmus, CAR, ICAR, or myometrium to compare between young and old cows. We distinguished between the 140 layers or parts of oviducts and uteri according to Banu et al. (2005), Hayashi et al. (2017), 141 142and Godoy-Guzman et al. (2018).

143

144 Picro-sirius red staining for total collagen

The fixed tissues were dehydrated and embedded in paraffin using the Handed autokinette (model 1400P, Shiraimatsu Corp. Ltd., Osaka, Japan). Thin sections (10 μm thick) were cut with a sliding microtome (Yamato Kohki, Saitama, Japan) attached onto

148	a slide glass. The paraffin-embedded sections were de-parafinised thrice in xylene, for 5
149	min each, followed by de-alcohol in 100%, 100%, 90%, and 70% ethanol and ultrapure
150	water for 5 min each. The slides were then covered in pico-sirius red staining solution
151	(Picro-Sirius Red Stain Kit, ScyTek laboratories Inc., Logan, UT, USA) for 1 h. Following
152	staining, the slides were washed twice with 0.5% acetic acid solution. The sections were
153	dehydrated through three changes of 100% ethanol and cleared in three changes of xylene.
154	After attaching the cover slip with Entellan new mounting medium (Sigma-Aldrich, St.
155	Lous, MO, USA), the stained sections were observed under a light microscope fitted with
156	a digital camera (Eclipse Ci, Nikon, Tokyo, Japan). The staining and light microscopy
157	results showed collagen in red, muscle fibres and cytoplasm in yellow, and complex in
158	orange.

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RT-PCR, sequencing of amplified products, and homology search in gene databases 160

161 Total RNA (at least four per tissue) was extracted using the RNAzol RT isolation reagent (Molecular Research Centre Inc., Cincinnati, OH, USA) and treated with 162163deoxyribonuclease. The concentration and purity of each RNA sample were evaluated by 164spectrophotometry (acceptable 260/280 nm ratio of absorbance, 1.8-2.1) and electrophoresis (28S:18S ratios were 2:1). Complementary DNA was synthesised using 165the Verso cDNA Synthesis Kit (Thermo Fisher Scientific). No reverse transcription 166

167 controls (NRCs) were prepared for RT-PCR; they were generated by treating the
168 extracted RNA with the same deoxyribonuclease but not with cDNA synthetase.

169	To determine the amount of HSP47 mRNA, a primer pair was designed by Primer
170	Express v3.0 (Thermo Fisher Scientific) based on the reference sequence of bovine
171	HSP47 [National Center for Biotechnology Information (NCBI) reference sequence of
172	bovine HSP47 is NM_001046063]. Table 1 details the primers. PCR was performed using
173	20 ng of cDNA, 20 ng RNA as the NRC or water as the no template control (NTC), and
174	polymerase (Tks Gflex DNA Polymerase, Takara Bio Inc., Shiga, Japan) under the
175	following thermocycle conditions: 94 °C for 1 min for pre-denaturation followed by 35
176	cycles of 98°C for 10 s, 60°C for 15 s, and 68°C for 30 s. PCR products were separated
177	on 1.5% agarose gel by electrophoresis with a molecular marker (Nippon Gene, Tokyo,
178	Japan), stained with Gelstar (Lonza, Allendale, NJ, USA), and observed using a charge-
179	coupled device (CCD) imaging system (GelDoc; Bio-Rad, Hercules, CA, US). The PCR
180	products were purified with the NucleoSpin Extract II kit (Takara Bio Inc.) and then
181	sequenced using one of the PCR primers and the Dye Terminator v3.1 Cycle Sequencing
182	Kit (Thermo Fisher Scientific). The sequences obtained were used as query terms with
183	which to search the homology sequence using the basic nucleotide local alignment search
184	tool (BLAST) (available on the NCBI website).

186 Western blotting for HSP47 detection

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187	G*Power 3 for windows (Faul et al. 2007) was used to estimate the required
188	number of samples with an alpha-error probability of 0.05 and a statistical power of 0.95.
189	Five samples per day in each tissue of each group (total of 20 samples in each tissue of
190	each group) were assessed and analysed statistically. The samples were ground in liquid
191	nitrogen and homogenised using tissue protein extraction reagent (T-PER; Thermo Fisher
192	Scientific) containing Halt protease inhibitor cocktail (Thermo Scientific). The total
193	protein content of each tissue homogenate was estimated using a bicinchoninic acid kit
194	(Thermo Fisher Scientific). The extracted protein sample was boiled with Sample Buffer
195	Solution with Reducing Reagent (6x) for SDS-PAGE (09499-14; Nacalai Tesque) for 3
196	min at 100 °C. The protein samples (8,000 ng of total protein) were loaded onto a
197	polyacrylamide gel (Any KD Criterion TGX gel, Bio-Rad) along with a molecular weight
198	marker (Precision Plus Protein All Blue Standards; Bio-Rad). Then, the proteins were
199	resolved using sodium dodecyl sulphate-polyacrylamide gel electrophoresis at 100 V for
200	90 min. The proteins were transferred onto polyvinylidene fluoride (PVDF) membranes
201	(Trans-blot turbo PVDF, Bio-Rad) with electroblotting at 2.5 A and 25 V for 7 min using
202	a Trans-blot Turbo system (Bio-Rad).

We used a Can Get Signal Immunoreaction Enhancer kit (Toyobo Co. Ltd, Osaka,

204	Japan) for membrane blocking (1 h at 25 °C), primary antibody reaction (1 h at 25 °C)
205	with an anti-HSP47 rabbit polyclonal antibody (1:400,000 dilution with immunoreaction
206	enhancer solution; AP7366B; Abcepta Inc., San Diego, CA, USA), and secondary
207	antibody reaction (1 h at 25 °C) with goat anti-rabbit IgG horseradish peroxidase-
208	conjugated antibody (Bethyl Laboratories Inc., Montgomery, TX, USA; 1:400,000
209	dilution with immunoreaction enhancer solution). The anti-human HSP47 rabbit antibody
210	recognizes the mature C-terminal form of human HSP47 (corresponding to amino acids
211	390 to 418; FLVRDTQSGSLLFIGRLVRPKGDKMRDEL). This sequence had 100%
212	homology to amino acids 390 to 418 of the mature C-terminal form of bovine HSP47 but
213	no homology to other bovine proteins, as determined using protein BLAST (NCBI
214	reference sequences of human and bovine HSP47 are NP_001193943.1 and
215	NP_001039528.1, respectively).

The protein bands were visualised using an ECL-Prime chemiluminescence kit (GE Healthcare, Amersham, UK) and a CCD imaging system (LAS-3000 Mini; Fujifilm, Tokyo, Japan). The images were exported using the Multigauge (version 3.0; Fujifilm) software. To verify the specificity of the signals, we included several negative controls in which the primary antibodies had been omitted or normal rabbit IgG (Wako Pure Chemicals) antibodies were used instead of the primary antibodies. Signal specificity was

222	also confirmed using negative controls in which the primary antibodies were pre-
223	absorbed with 5 nM antigen peptide (Scrum Inc., Tokyo, Japan).
224	The antibodies were removed from the PVDF membrane with a stripping solution
225	(Nacalai Tesque) prior to the blocking and subsequent immunoblotting with an anti- β -
226	actin mouse monoclonal antibody (1:400,000 dilution; Sigma-Aldrich).
227	All relevant bands were cropped from the exported file using Adobe Photoshop
228	element ver. 2020 (Adobe, San Jose, CA, USA) and pasted onto a graph created using
229	DeltaGraph ver. 7.5.2J (Red rock software, Salt Lake, UT, USA). ImageQuant TL
230	(version 8.2; Cytiva, Marlborough, MA, USA) software was used to measure the band
231	sizes and volumes (calculated using rolling ball background subtraction). The expression
232	protein amount of HSP47 was normalised against β -actin.
233	
234	RT-qPCR analysis of HSP47

After preparation of high-quality total RNA and cDNA synthesis using the previously described protocol, *HSP47* mRNA amount was compared among the young and old groups via the relative standard curve method of RT-qPCR and data analyses, as described previously (Nahar and Kadokawa 2017, Ferdousy *et al.* 2020). G*Power 3 for windows (Faul *et al.* 2007) was used to estimate the required number of samples with an alpha-error probability of 0.05 and a statistical power of 0.95. Five cDNA samples per day in each tissue of each group (total of 20 cDNA samples in each tissue of each group)
were assessed and analysed statistically.

To prepare external standards for amplified fragments of cDNA products containing target sequences for RT-qPCR of *HSP47*(800 bp) and two housekeeping genes, *C2orf29* (562 bp) and *SUZ12* (1169 bp), PCRs were conducted as described previously (Nahar and Kadokawa 2017). The primers were designed by Primer Express Software v3.0 (Table 1). The PCR-amplified products were purified to prepare the standards, as well as to verify the DNA sequence. Then, we prepared a 6-point relative standard by 10fold diluting the PCR products for the relative standard method.

HSP47 mRNA levels were normalised to the geometric mean of the levels of two
house-keeping genes, *C2orf29* and *SUZ12*, selected using Normfinder program
(Vandesompele *et al.* 2002) and amplified using previously reported primers (Rekawiecki *et al.* 2012; Nahar and Kadokawa 2017), since they are among the most stable and reliable
housekeeping genes in the bovine oviducts and uterus (Walker *et al.* 2009; Nahar and
Kadokawa 2017).

256The mRNA level was measured in duplicate by RT-qPCR analyses with 20 ng 257cDNA, using CFX96 Real Time PCR System (Bio-Rad) and Power SYBR Green PCR Master Mix (Thermo Fisher Scientific), together with the 6-point relative standards, NTC, 258and NRC to generate the standard curve by plotting the log of the starting quantity of the 259260dilution factor against the C_q value using appropriate software (CFXmanagerV3.1, Bio-261Rad). Temperature conditions for all genes were as follows: 95°C for 10 min for pre-262denaturation; five cycles each of 95°C for 15s and 66°C for 30s; and 40 cycles each of 26395°C for 15s and 60°C for 60 s. Melting curve analyses were performed at 95°C for each amplicon and each annealing temperature to ensure the absence of smaller non-specific 264

products, such as dimers. All the C_q values of the unknown samples (22.85 \pm 0.15) were 265266between the highest (8.00) and lowest (30.33) standards for HSP47 in RT-qPCR. Further, 267all the C_q values of the unknown samples were between the highest and lowest standards 268for C2orf29 or SUZ12 in RT-qPCR. Reactions with a coefficient of determination (\mathbb{R}^2) > 2690.98 and efficiency between 95 and 105% were considered optimised. The coefficients of variation of RT-qPCRs were less than 6%. The concentration of PCR products was 270calculated by comparing C_q values of unknown samples with the standard curve using 271272CFXmanagerV3.1. Then, the HSP47 amount was divided by the geometric mean of 273C2orf29 and SUZ12 in each sample.

274

275 Immunofluorescence staining and confocal microscopy

For immunofluorescence staining, we randomly selected at least five tissue samples 276 per day in each tissue of each group. To evaluate the association between HSP47-rich 277areas and denatured collage-rich areas, the tissues on slides were washed once after 278279incubation with streptavidin, Alexa Fluor 546 conjugate, and DAPI. Then, the sections 280were treated with 0.3% Triton X-100 for 15 min, blocked with 10% normal goat serum 281in PBS for 1 h at room temperature, and subjected to a primary antibody reaction with the 282anti-HSP47 antibody (1:1,000 dilution for overnight at 4°C). Subsequently, the samples 283were subjected to a secondary antibody reaction with Alexa Fluor 647 goat anti-rabbit 284IgG (diluted to 1 µg/mL, Thermo Fisher Scientific) and 1 µg/mL DAPI for 2 h at room temperature. After washing the sections four times, the slides were mounted in 285286preparation for confocal microscopy. To verify the specificity of signals, we included 287several negative controls in which the primary antiserum had been omitted or preabsorbed with 5 nM antigen peptide, or in which normal rabbit IgG was used instead of 288

the primary antibody. We also included negative controls in which the secondary antibodies had been omitted or normal goat IgG (Wako Pure Chemicals) antibodies were used instead of the secondary antibodies. Signal specificity was also confirmed using negative controls in which the secondary antibodies were pre-absorbed with 5 nM normal rabbit IgG.

Additionally, we performed immunohistochemistry to identify whether cytokeratin-rich areas or vimentin-rich areas express HSP47. For this purpose, we included anti-bovine pancytokeratin mouse monoclonal antibody or anti-bovine vimentin mouse monoclonal antibody (both from Sigma-Aldrich, and diluted as 1:1,000) in the primary antibody reaction, and Alexa Fluor 488 goat anti-mouse IgG (diluted to 1 μ g/mL, Thermo Fisher Scientific) in the secondary antibody reaction.

300

301 Analysis of the 5'-flanking region of SERPINH1

The 5000-nucleotide sequence of the 5'-flanking region of the SERPINH1 gene 302 303 (chromosome 15: 54,737,997-54,748,417) was obtained using the online Ensembl Search 304 Genome program (http://www.ensembl.org) against the bovine genome database (April. 305 2018, ARS UCD 1.2/bosTau9). The sequence was analysed using Genetyx software v.13 306 (Genetyx, Tokyo, Japan) for the presence of consensus response element (RE) sequences for oestrogen-i.e., ERE (5'-GGTCANNNTGACC-3'), ERE-like sequence (5'-307 308 TGACCCCTGGGTCA-3') (Gruber et al., 2004), and half ERE (GGTCA, TGACC, or TGACT) (Liu et al., 1995), as well as for progesterone—i.e., PRE (5'-G/A G G/T AC 309 310 A/GTGGTGTTCT-3') (Geserick et al., 2005) and half PRE (5'-TGTTCT-3') (Tsai et al., 3111988).

313 Statistical analysis

314The statistical analyses were performed using StatView version 5.0 for Windows 315(SAS Institute, Inc., Cary, NC, USA). Grubb's test verified the absence of outliers. The 316 Shapiro-Wilk's test and Kolmogorov-Smirnov Lilliefors test verified the normality of 317 distribution of each variable. Two-factor analysis of variance (ANOVA) was used to 318 evaluate the effect of age (young or old), stage (days 2 to 3, 8 to 12, 15 to 17, or 19 to 21), 319 and interaction followed by post-hoc comparisons using Fisher's protected least 320 significant difference (PLSD) test for the data of RT-qPCR or western blotting for HSP47. The statistical significance of differences among stages was assessed by one-factor 321ANOVA followed by post-hoc comparisons using Fisher's PLSD test using a model 322323consisting of variance from the effect of stage and the residual. The level of significance 324was set at P < 0.05. Data are expressed as means \pm standard errors of the mean (SEM). 325

326 Results

327 Picro-sirius red staining showed red or orange colour in almost all parts of the 328 ampullae, isthmuses, CAR, ICAR, and myometria (Fig. 1).

We successfully developed a new *in situ* assay for the detection of denatured collagen 329 (Fig. 2). The non-treated young tissues showed a very subtle signal indicating the 330 331presence of denatured collagen (red). By contrast, the old samples, similar to the heated and enzyme-treated young tissues, showed a strong signal indicating the presence of 332333 denatured collagen in the lamina propria and muscular layer of the ampullae and isthmuses. In addition, the heated young uteri showed strong signals in the luminal 334 epithelia and uterine stroma of CAR as well as in the glandular epithelia and uterine 335 336 stroma of ICAR, and various cells in the uterine myometria.

337 PCR products of a size corresponding to that of HSP47 (470 bp) were obtained from 338 the ampullae, isthmuses, CAR, ICAR, and myometria, as revealed by agarose gel electrophoresis (Fig. 3). Neither the NTC nor any of the NRCs yielded any PCR-amplified 339 340 products. A homology search against gene databases for the sequenced amplified products revealed bovine HSP47 (NM 001046063) as the best match, with a query coverage of 341 342100%, an e-value of 0.0, and a maximum alignment identity of 99%. No other bovine 343 genes displayed homology with the PCR product, indicating that the amplified product was indeed HSP47. 344

We combined the in situ detection method for denatured collagen with 345346 immunofluorescence staining of HSP47 in the ampulla (Fig. 4A), isthmus (Fig. 4B), CAR (Fig. 5A), ICAR (Fig. 5B), and myometrium (Fig. 5C). Robust, high-intensity 347 fluorescence signals of denatured collagen were localised again in the above-mentioned 348 areas of old samples but not in those of young samples. In addition, HSP47 signals were 349 localised in the epithelial layer and superficial stroma very near to the epithelial layer of 350oviducts of old individuals but only weakly in those of young individuals (Fig.6). HSP47 351signals were localised in the epithelia and stroma of the CAR and ICAR of old and young 352353 individuals. HSP47 signals were localised in the myometrium of old individuals but not in those of young individuals. More importantly, HSP47 rich-areas (green) and denatured 354 collagen-rich area (red) were different because there was little colocalisation (yellow) in 355 356 the merged panels. There was no signal indicating that HSP47 had colocalised with 357denatured collagen in the lamina propria and muscular layers of ampullae and isthmuses. Therefore, HSP47-rich and denatured collagen-rich areas were different. 358

Figure 7 shows the results of western blot and outcomes of two-factor ANOVA. The western blot revealed HSP47 protein in all five specimens obtained from old cows, but

only weak expression in those from young heifers (Fig. 4). Unexpectedly, an extra band 361 362at 25 kDa appeared only in old samples. The ANOVA revealed that the age effect was 363 significant for the 47 kDa or 25 kDa bands in the ampulla, isthmus, CAR, ICAR, and 364 myometrium, and old samples contained a higher amount of HSP47 than the young samples. The effect of stage was significant in almost all samples, except for the 47 kDa 365 366 band in ampulla and isthmus, and 25 kDa band in the myometrium. The interaction 367 between the effects of age and stage was significant only for 47 kDa and 25 kDa bands in the CAR. 368

Figure 8 shows the results of RT-qPCR, and outcomes of two-factor ANOVA. The age effect was significant in the CAR, ICAR, and myometrium, but not in the ampulla and isthmus. The effect of stage was significant in the ampulla, isthmus, and ICAR, but not in CAR and myometrium. The interaction between the effects of age and stage was significant only in the isthmus.

The 5'-flanking region of the bovine SERPINH1 gene was analysed for EREs, PREs, and similar sequences. Although there were no ERE, ERE-like, or PRE sequences, 19 half ERE (7 GGTCA, 7 TGACC, and 5 TGACT) and 3 half PRE sequences were identified.

378

379 Discussion

We developed a new method that uses a denatured collagen detection reagent to identify denatured collagen-rich areas. The picro-sirius red stain showed red or orange colour in almost all parts of oviduct and uterus, including the epithelium. Boos (2000) reported the presence of collagen types I, III, IV, and VI in various parts of the uterus and

the presence of collagen types IV and VI in the epithelium. We did not identify the 384 collagen type in this study, but collagen was present in almost all parts of the oviduct and 385uteri. The results indicated that the levels of denatured collagen in old oviducts and uteri 386 387 were higher than those in the oviducts and uteri of young ones. Thus, it is possible that repeated pregnancy and parturition increase the denatured collagen. Another possible 388 reason for such an increase in the levels of denatured collagen may be infection and 389 390 inflammation because lipopolysaccharides decrease collagen synthesis in myometrial explants from women (Wendremaire et al. 2013). 391

The tunica mucosa of oviducts and epithelia of the endometrium are located adjacent to the lumen, and thus, the structure of these layers may be susceptible to damage or frequent changes. Ovarian steroid hormones drive ECM remodelling in the bovine oviduct (Gonella-Diaza *et al.* 2018). Therefore, even young heifers may require collagen biosynthesis because these layers provide growth factors and nutrients for embryogenesis (Hugentobler *et al.* 2010; Besenfelder *et al.* 2012).

Little is known regarding HSP47 expression in the oviducts and uteri of all species. Therefore, we were unable to compare the data obtained by the current study with those of previous studies. The high HSP47 protein amounts observed in old oviducts and uteri compared with those in the young oviducts and uteri was somewhat unexpected because body weights of heifers were still in the phase of increasing (Inoue *et al.* 2020), and thus, we speculated that increased size of the uteri and oviducts may also play a role in HSP47 404 expression. Little is known regarding postnatal changes associated with the sizes of 405 bovine oviducts and uteri, as growth continues at least until 15 months of age in beef 406 heifers (Honaramooz *et al.* 2004). However, the minimum age at first calving among 407 about 2600 Japanese Black heifers was 21.4 months old (Inoue *et al.* 2020). Therefore, it 408 was possible that the growth of oviducts and uteri of the young group was completed 409 before sampling in this study.

410 We must be careful in interpreting the data obtained using the anti-HSP47 antibody for two reasons. First, the antibody is not recommended for 411 412immunohistochemistry in frozen sections by the supplier. However, we observed 413increased denatured collagen in the paraffin section in our preliminary trial using the denatured collagen detection reagent because the steps of paraffin embedding and 414 deparaffinisation increased the denatured collagen. Second, we observed an extra 25 kDa 415band in the western blot. We could not find any paper reporting another size of HSP47. 416 Therefore, we must be careful as the HSP47 signal in the immunohistochemistry results 417may have been caused by another protein. However, we performed western blotting using 418 419 another anti-HSP47 mouse monoclonal antibody, clone M16.10A1 (Enzo Life Sciences, 420 Inc., Farmingdale, New York. USA) and we observed both the 25 kDa and 47 kDa bands 421 (Supplementary Figure 1). We tried to search similar proteins using the amino acid sequence of bovine HSP47 using protein BLAST. However, we could not find any protein 422423with high homology. Therefore, further studies are required to identify the protein that the 25 kDa band corresponds to. 424

Importantly, HSP47 protein amount was increased in areas other than the denatured collagen-rich areas in old cows. These results suggested a possibility that collagen synthesis may not occur in denatured collagen-rich areas, indicating that a damaged structure may remain uncured. This may explain the increased infertilityobserved in older beef cows (Osoro and Wright 1992).

430 However, this brings into question the physiological significance of increased 431HSP47 protein amount observed in other areas with less denatured collagen. Notably, an abnormal increase in collagen synthesis by fibroblasts induced by transforming growth 432433factor (TGF)-\beta1 and its isoforms may lead to adenomyosis and ectopic endometria in 434women (Cheong et al. 2019). TGF-B1 may also exert important pathological effects on fibroblasts during equine endometriosis (Szostek-Mioduchowska et al. 2019). Although 435HSP47 is a key regulator of cell homeostasis, it also plays a role in fibrogenesis and 436 437fibrotic disorders in the liver, kidneys, and lungs. Excess HSP47 expression is an 438important step in collagen-related diseases, including keloids and fibrosis (Ito and Nagata, 2019). In addition, this study showed an increase in the number of fibroblasts in various 439parts of the oviducts and uteri, thereby suggesting fibrosis. Therefore, any increase in 440 HSP47 protein amount may play an important role in inducing infertility in old cows. 441

442The bovine endometrium is thicker on days 19–21 or days 2–3 than on other days (Sugiura et al. 2018). The highest amount of HSP47 mRNA was observed in the ampulla, 443444 isthmus, CAR, and ICAR on either days 19–21 or days 2–3 in this study. Young oviducts and uteri showed a higher amount of HSP47 mRNA than did old ones, whereas young 445oviducts and uteri showed a lower amount of HSP47 protein than did old ones. Based on 446 447 these results, high levels of HSP47 protein may be required only temporarily in oviducts 448 and uteri to avoid excess collagen synthesis, a possible cause for inflexibility. The HSP47 protein is bound to a ubiquitin-like protein, UBIN (Matsuda et al. 2001) and is degraded 449 450via the ubiquitin-proteasome system (Ito and Nagata 2016). Therefore, further studies are required to clarify the possibility that HSP47 protein is degraded via the ubiquitin-451

452 proteasome system shortly after translation in young organs but is not degraded smoothly453 in old organs, resulting in abnormal collagen synthesis.

454HSP47 is induced by cellular stresses, but it is also constitutively expressed, and its expression is always up- or down-regulated concomitantly with changes in the 455expression of various types of collagens, as reviewed by Ito and Nagata (2017). Therefore, 456a possible reason for the lower amount of HSP47 mRNA observed in old organs is the 457increased collagen. We found 19 half ERE and 3 half PRE sequences in the 5'-flanking 458region of the bovine SERPINH1 gene. A caveat here is that half ERE and PRE-like 459460 sequences are only five or six nucleotides long; such short sequence can appear at random at every 1024 (= 4^5) or 2048 (= 4^6) nucleotides. Thus, some of the identified sequences 461may not be involved in the control of gene expression. Detailed studies are required to 462463 clarify the mechanisms regulating HSP47 expression and the roles of oestradiol and 464 progesterone.

HSP47 signals were observed in the epithelial layer and superficial stroma very 465466 near to the epithelial layer of oviducts and endometria of old individuals. HSP47 is 467expressed also in the surface epithelial cells of pneumonia (Kakugawa et al. 2005) and 468 desmin-positive glomerular epithelium cells of the kidney (Razzaque and Taguchi 1999). 469 Moreover, HSP47 expression in human nasal mucosa and lacrimal sac (obtained surgically) is associated with surgical outcome (Park et al. 2018). HSP47 induces 470 471mesenchymal phenotypes in mammary epithelial cells for cancer metastasis, and HSP47 472is a hub of the ECM transcription network (Xiong et al. 2020). Therefore, further studies 473are required to clarify the relationship between HSP47expression in the layers and fertility 474in cows.

475

Takita et al. (2019) produced a standard curve based on an enzyme immunoassay

476 (EIA) utilising the denatured collagen detection reagent and heated pure collagen (grade 477for culture dish coating). However, our attempts of immunoassays (HRP-conjugated streptavidin for EIA, fluorochrome-conjugated streptavidin for fluorescent immunoassay, 478479lanthanide-conjugated streptavidin for dissociation-enhanced lanthanide fluorescence immunoassay) failed to obtain a good parallel between the standard curve and serially 480 481diluted bovine oviduct or uterine extracts that were extracted using various methods. This 482was due to the samples showing strong matrix effects unlike pure collagen. Therefore, our comparison could be performed only on photographic images. 483

In conclusion, these findings revealed the specific location and amounts of damaged collagen and HSP47 in the oviducts and uteri of old cows compared to those in heifers.

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495

496 **Conflicts of Interest**

497 The authors declare no conflicts of interest.

499 **References**

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Gene	Primer	Sequence 5'-3'	Position		Size (bp)
			Nucleotide	Exon	
HSP47	Forward	GACAACCGAGGCTTCATGGT	770	4	470
	Reverse	AGCTCCTCACGCCCGTAGAT	1239	6	
C2orf29	Forward	AAGTTTTTTTTTTTCCCAGCTCATG	666–688	2	562
	Reverse	CAGGAAGTTTGGCTGGAGTGA	1207–1227	5	
SUZ12	Forward	GGAAGAGACTGCCTCCATTTGA	1019–1040	10	1169
	Reverse	CCCTGAGACACCATCTGTTTCC	2166–2187	16	
HSP47	Forward	TGTCGGGCAAGAAGGACCTA	1131	5	800
	Reverse	AAAATGGGGAGGAAAGTGGG	1930	6	
HSP47	Forward	ACAAGATGCGAGACGAGTTGT	1347	5	93
	Reverse	CCCTGTTTTCCCACCCATGT	1439	5&6	
C2orf29	Forward	TCAGTGGACCAAAGCCACCTA	928–948	3	170
	Reverse	CTCCACACCGGTGCTGTTCT	1077–1097	4	
SUZ12	Forward	CATCCAAAAGGTGCTAGGATAGATG	1441–1465	13	160
	Reverse	TTGGCCTGCACACAAGAATG	1581–1600	14	

Table 1. Details of the primers used for PCRs.



Fig. 1. Picro-sirius red staining for total collagen in ampulla, isthmus, and caruncular (CAR) and intercaruncular (ICAR) areas of the endometrium and myometrium in healthy postpubertal, growing and young nulliparous heifers (Young), and old multiparous Japanese Black beef cows (Old). The Picro-sirius red staining shows collagen in red, muscle fibres and cytoplasm in yellow, and complex in orange.



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Fig. 2. *In situ* detection of denatured collagen. The no-heated, non-digested young tissues show very subtle signals of denatured collagen (red). In contrast, the old samples, in a manner similar to the heated or enzyme-digested young tissues, show strong signals corresponding to denatured collagen in the lamina propria and muscular layers of ampullae and isthmuses; the stroma of CAR and ICAR; the glandular epithelium of ICAR; and various myometrial cells.



Fig. 3. Expression of heat shock protein (HSP47) detected via RT-PCR analysis. The
electropherogram shows the size (470 bp) expected from PCR products of bovine *HSP47*in the ampulla, isthmus, CAR, ICAR, and myometrium (Myo) in old cows. Bands were
not present in the no template control (NTC) and no reverse transcription control (NRCs)
lanes.



Fig. 4. Comparison of denatured collagen-rich areas (red) and HSP47-rich areas (green) 678 679 in the ampullae or isthmuses (collected on day 3 of the oestrous cycle) of Young and Old 680 groups. Nuclei are counterstained with DAPI (dark blue). Unlike the Young, the Old specimens showed strong signal corresponding to denatured collagen in the lamina 681 682 propria and muscular layers. The Old specimens showed strong signal corresponding to HSP47 in the epithelia of tunica mucosa and superficial stroma. Not many signals 683 684 corresponding to colocalisation (yellow) were present in the Merge panels; scale bars are 68550 µm.

(A) CAR	Denatured Collagen	HSP47	DNA	Merge
Young		per		
OId (Low magnification)		A A		
Old (High magnification)		in the second		
(B) ICAR	Denatured Collagen	HSP47	DNA	Merge
Young				
Old (Low magnification)				
Old (High magnification)		<u>.</u> 6		
(C) Myo	Denatured Collagen	HSP47	DNA	Merge
Young	29,	,80 0	a BA	a de la companya de la
Old (Low magnification)				
Old (High magnification)		4		

Fig. 5. Comparison of denatured collagen-rich areas (red) and HSP47-rich areas (green)

in the CAR, ICAR, or Myo (collected on day 13 of the oestrous cycle) of Young and Old 688 groups. Nuclei are counterstained with DAPI (dark blue). Both the Young and Old 689 specimens showed signals corresponding to both denatured collagen and HSP47 in 690 luminal epithelia, glandular epithelia, and stroma. Unlike the Young, the Old specimens 691 692 also showed strong signals corresponding to both denatured collagen and HSP47 in the 693 stroma and myometria. Particularly, the number of fibroblasts (green dots) increased. However, not many signals corresponding to colocalisation (yellow) were present in the 694 Merge panels; scale bars are 50 µm. The dark patches in old myometria are broken parts. 695696



Fig. 6. Comparison of HSP47-rich areas (green) and cytokeratin- or vimentin-rich areas 699 (red) in the ampullae or isthmuses (collected on day 3 of the oestrous cycle), or the CAR, 700 ICAR, or Myo (collected on day 13 of the oestrous cycle) of Old groups. Nuclei are 701

- counterstained with DAPI (dark blue); scale bars are 50 µm. 702
- 703



Fig. 7. Representative photos of western blotting analysis for HSP47 or anti- β -actin mouse antibodies in extracts from ampulla, isthmus, CAR, ICAR, and myometrium (Myo) in the Young and Old groups (A). Relative HSP47 protein levels normalised to

those of β -actin in the ampulla (B), is thmus (C), CAR (D), ICAR (E), or myometrium (F)

in the Young and Old groups. The header in the upper corner of each graph represents the

results of two-factor ANOVA followed by Fisher's PLSD test, including the effect of age

711 (Young or Old) and effect of stage and interaction. Greek letters (α , β , or χ) above the

grey left-side bars indicate significant between-stage differences in expression in Young

samples; letters (a, b, or c) above the white right-side bars indicate significant between-

stage differences in expression in Old samples (one-factor ANOVA followed by Fisher's

- 715 PLSD test).
- 716 N.S., non-significant.
- 717



Fig. 8. Relative HSP47 mRNA levels (mean \pm SEM) in the ampulla (A), isthmus (B), 720 CAR (C), ICAR (D), or Myo (E) in healthy, post-pubertal growing nulliparous heifers 721722 (Young group) and old multiparous cows (Old group), as determined via RT-qPCR. Data 723 were normalised to the geometric means of C2orf29 and SUZ12 levels. The header in the 724upper corner of each graph represents the results of two-factor ANOVA followed by Fisher's PLSD test, including the effect of age (Young or Old) and effect of stage and 725interaction. Greek letters (α , β , or χ) above the grey left-side bars indicate significant 726 between-stage differences in expression in Young samples; letters (a, b or c) above the 727 white right-side bars indicate significant between-stage differences in expression in Old 728 729 samples (one-factor ANOVA followed by Fisher's PLSD test).

730N.S. is abbreviation of non-significant.



Supplementary Fig. 1. Representative photos of western blotting using another anti-HSP47 mouse monoclonal antibody, clone M16.10A1 (Enzo Life Sciences, Inc., Farmingdale, New York. USA) or anti- β beta-actin mouse antibodies in extracts from ampulla, isthmus, CAR, ICAR, and myometrium (Myo) in the Young and Old groups.