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- 1 Molecular and biological characterization of vascular endothelial growth
- 2 factor of parapoxviruses isolated from wild Japanese serows (*Capricornis*
- 3 crispus)
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- 15
- 16

16 Abstract

17	Contagious dermatitis in domestic and wild ruminants caused by
18	parapoxvirus (PPV) occurs worldwide. Although PPV infections appear in
19	cattle, sheep and goats, the papular, nodular, pustular and ulcerated skin
20	lesions of wild Japanese serows (<i>Capricornis crispus</i>) are significantly more
21	severe than those of other animals. To determine the factors involved in the
22	severity of these skin lesions, we compared the molecular characteristics of 4
23	PPV isolates from Japanese serows and 2 isolates from sheep in Japan, and
24	also investigated the biological properties of primary endothelial cells from
25	different host species. All of the 6 Japanese isolates harbored a vascular
26	endothelial growth factor (VEGF) gene, which is known as one of the
27	virulence factors of PPVs. Three different amino acid sequences of viral
28	VEGF were identified and the sequence was identical among the 4 isolates
29	from the Japanese serows. The temporal expression pattern of viral VEGF
30	mRNA was almost the same among 3 isolates encoding the 3 different
31	VEGFs in infected cells from different host species. Recombinant forms of
32	the 3 different VEGFs showed the ability to induce vascular permeability
33	and endothelial cell-proliferation. Primary endothelial cells from Japanese
34	serows were most responsive to recombinant viral VEGF compared to cells

 $\mathbf{2}$

- 35 from cattle, sheep, and goats. These results suggest that not only the
- 36 biological activity of viral VEGF but also the high responsiveness to viral
- 37 VEGF of endothelial cells might be involved in the severe proliferative skin
- 38 lesions induced by PPV infection in Japanese serows.
- 39
- 40 Keywords:
- 41 Dermatitis
- 42 Endothelial cells
- 43 Japanese serow
- 44 Parapoxvirus
- 45 VEGF
- 46

46 **1. Introduction**

47

48	Parapoxviruses (PPVs) are the etiological agents of papular
49	stomatitis and pseudocowpox in cattle, and contagious pustular dermatitis in
50	sheep and goats (Damon, 2007; Robinson and Lyttle, 1992). PPV infections in
51	sheep have been known as scabby disease or "orf" among shepherds since the
52	1780s (Robinson and Lyttle, 1992) and the infections are now widespread in
53	both domestic and wild ruminants worldwide. PPV infection of wild
54	Japanese serows (<i>Capricornis crispus</i>) has been common knowledge in Japan
55	since the first outbreak was observed in 1976 (Kumagai et al., 1979). The
56	histopathological features are similar to those of domestic animals (Okada et
57	al., 1984a, b; Suzuki et al., 1986); however, the skin lesions tend to be much
58	more severe. Weakened or dead Japanese serows are frequently found in
59	their natural territories, as they were unable to eat due to such lesions.
60	Generally, the level of severity of the skin lesions is greatest in Japanese
61	serows, moderate in sheep and goats, and low in cattle (Fig. 1). Although
62	PPVs from Japanese serows experimentally infect sheep, goats and cattle,
63	the highly proliferative skin lesions seen in Japanese serows is not
64	reproduced (Masegi et al., 2002; Ogino et al., 1996; Okada et al., 1986). The

65	factors involved in these clinical differences are still unspecified for both the
66	pathogen and host.

67	Previous studies revealed that orf virus, one of the members of PPV,
68	encodes an apparent homologue of the vascular endothelial growth factor
69	(VEGF) gene (Lyttle et al., 1994; Mercer et al., 2002; Rziha et al., 1999), and
70	recent studies have shown that other members of PPV, including
71	pseudocowpoxvirus, bovine papular stomatitis virus and parapoxvirus of red
72	deer in New Zealand, also encode a VEGF gene (Delhon et al., 2004; Ueda et
73	al., 2003, 2007). Cellular VEGF is a potent mitogen for vascular endothelial
74	cells and essential for embryonic vasculogenesis and angiogenesis. VEGF
75	also activates vascular permeability and plays a role in pathological
76	angiogenesis including tumor growth and inflammation (Ferrara, 1999,
77	2005; Ferrara and Davis-Smyth, 1997; Robinson and Stringer, 2001; Stacker
78	and Achen, 1999). The histological characteristics of the lesions of PPV
79	infection, such as extensive vascularization, cell proliferation and vacuolar
80	degeneration of epithelial cells, are thought to be the result of viral VEGF
81	activity. Recent studies have demonstrated that PPV lacking functional
82	VEGF causes relatively reduced skin lesions and histopathological changes
83	(Savory et al., 2000; Wise et al., 2007).

 $\mathbf{5}$

84	The aim of this study was to determine the factors involved in the
85	severe proliferative skin lesions of PPV infection in Japanese serows. Here,
86	we described the molecular and biological characterization of the VEGF of
87	PPVs from Japanese serows and the responsiveness to VEGF of serow
88	endothelial cells compared with Japanese PPVs from sheep.
89	
90	2. Materials and methods
91	
92	2.1. Viruses and cells
93	Four PPV isolates from Japanese serows and 2 isolates from sheep in
94	Japan were used in this study (Table 1). All isolates were propagated in
95	primary fetal bovine muscle (FBM) cells. Primary FBM, fetal lamb lung
96	(FLL), and vascular smooth muscle cells of Japanese serow (SeSM) were
97	maintained in Eagle's minimum essential medium (Nissui, Tokyo, Japan)
98	supplemented with 0.3% tryptose phosphate broth (Difco, Detroit, MI, USA),
99	10% fetal bovine serum (FBS), 100 $\mu g/ml$ of streptomycin, and 100 U/ml of
100	penicillin. Human umbilical vein endothelial cells (HUVEC) were purchased
101	from Lonza (Walkersville, MO, USA) or Cell Applications (San Diego, CA,
102	USA). Primary aortic endothelial cells of cattle (BAEC), sheep (OAEC), goats

103	(CAEC) and Japanese serows (SeAEC) were isolated from aortic vessels.
104	Endothelial cells were maintained in endothelial cell growth medium-2
105	(EGM-2, Lonza) containing supplements as per the manufacturer's
106	instructions and 10% FBS. Primary skeletal muscle cells of Japanese serow
107	were kindly provided by Dr. T. Ishida (Graduate School of Science, The
108	University of Tokyo, Tokyo, Japan) and were maintained in RPMI 1640
109	(Wako, Osaka, Japan) supplemented with 10% FBS, 100 µg/ml of
110	streptomycin, and 100 U/ml of penicillin.
111	

112 2.2. Polymerase chain reaction (PCR) and sequencing

113	For PCR, DNA was extracted from FBM cells infected with each of
114	the isolates using a DNeasy Tissue Kit (Qiagen, Hilden, Germany). PCR for
115	the viral envelope gene using the primers PPP-1 and PPP-4 (Supplementary
116	Table S1) was carried out for identification of PPV species as described
117	previously (Inoshima et al., 2000, 2001a). PCR primers (D27F, 11R and D2R;
118	Supplementary Table S1) were designed for the flanking regions of the viral
119	VEGF gene of the orf virus strains, NZ2 (DDBJ/EMBL/GenBank accession
120	no. S67520) (Lyttle et al., 1994), NZ7 (S67522) (Lyttle et al., 1994), D1701
121	(AY186732) (Rziha et al., 2003), and orf-11 (AY236150). PCR consisted of 9

122	min at 95°C followed by 40 cycles of 94°C for 1 min, 40°C for 1 min and 72°C
123	for 1 min, with a final extension at 72°C for 5 min. Nucleotide sequences of
124	the viral VEGF gene were determined by direct sequencing of the PCR
125	products. Sequences were obtained from both strands for verification.
126	
127	2.3. Reverse transcription-PCR (RT-PCR)

FBM, FLL and SeSM cells were infected with virus at a titer of 10^3 128TCID₅₀/ml. Total RNA was extracted from cells at various intervals after 129virus infection (0, 1, 2, 4, 8, 12, 24, and 36 h) using an RNeasy Mini Kit 130 (Qiagen), and the temporal expression pattern of viral VEGF mRNAs was 131determined by RT-PCR using the primers VEGF orf-11F, VEGF cons340R, 132VEGF HISF, and VEGF HISR (Supplementary Table S1). After treatment of 133RNA samples with DNase I (Invitrogen, Carlsbad, CA, USA), RT-PCR was 134carried out using 0.5 µg of DNase I-treated RNA and a Titan One Tube 135RT-PCR Kit (Roche Applied Science, Mannheim, Germany) according to the 136manufacturer's instructions. 137

138

139 2.4. Cloning and expression of viral VEGF

140 For the recombinant expression of viral VEGF, the VEGF gene was

141	amplified from DNA extracted from virus-infected cells by PCR using
142	primers BamConsSigF, EcoConsR and PstConsR (Supplementary Table S1).
143	PCR products were digested with BamHI and EcoRI, or with BamHI and
144	<i>Pst</i> I, and then cloned into the corresponding sites of expression vector
145	pRSET (Invitrogen). Recombinant VEGFs with a hexa-His-tag were
146	expressed in <i>Escherichia coli</i> BL21(DE3)pLysS (Invitrogen) and purified by
147	affinity chromatography on a Ni-chelating column according to the
148	manufacturer's instructions and previous studies (Meyer et al., 1999;
149	Yamamoto et al., 2001). Purified recombinant VEGFs were analyzed by
150	SDS-PAGE followed by Coomassie brilliant blue staining and western blot
151	analysis using anti-His G antibody (R941-25, Invitrogen). The amount of
152	purified recombinant protein was quantified by Lowry's method with DC
153	protein assay reagents (Bio-Rad Laboratories, Hercules, CA, USA).
154	
155	2.5. Miles assay (vascular permeability assay)
156	The vascular permeability activity of recombinant VEGF was
157	detected using guinea pigs according to the Miles assay (Miles and Miles,
158	1952; Ogawa et al., 1998; Wise et al., 1999). Three guinea pigs were used for
159	each recombinant VEGF. Handling of guinea pigs was reviewed and

160	monitored according to the Guidelines for Animal Handling of Gifu
161	University.
162	
163	2.6. Indirect immunofluorescence assay (IFA)
164	Isolated primary cells of cattle, sheep, goats, and Japanese serows
165	(BAEC, OAEC, CAEC, and SeAEC) were confirmed as endothelial cells by
166	IFA and flow cytometry. After fixation by cold acetone, primary cells
167	cultivated on a coverslip were incubated with anti-human von Willebrand
168	factor (vWF) antibody (F 3520, Sigma-Aldrich, St. Louis, MO, USA), washed
169	with phosphate buffered saline (PBS), and then incubated with fluorescein
170	isothiocyanate (FITC)-conjugated goat anti-rabbit IgG antibody (62-6111,
171	Zymed Laboratories, South San Francisco, CA, USA). The same procedure
172	with omission of the primary antibody served as the negative control.
173	
174	2.7. Flow cytometry
175	Primary endothelial cells were incubated with FACS permeabilizing
176	solution 2 (BD Biosciences, San Jose, CA, USA), was hed in sorter buffer (2% $$
177	FBS, 5 mM EDTA and 0.1% sodium azide in PBS), incubated with or without

178 anti-human vWF antibody, washed, and then incubated with

179	FITC-conjugated goat anti-rabbit IgG antibody. After washing,	the cells were
180	analyzed using a FACSCalibur flow cytometer (BD Biosciences).
181		
182	2.8. Proliferation assay	

183	Cell proliferation was determined with a colorimetric assay using the
184	2-(2-methoxy-4-nitrophenyl)-3-(4-nitrophynyl)-5-(2,4-disulfophynyl)-2H-tetr
185	a-zolium, monosodium salt (WST-8), which measures the number of viable
186	cells. HUVEC and primary endothelial cells were seeded in 96-well plates at
187	1,000 cells/well. After 24 h, the supernatant was removed and the cells
188	rinsed in PBS. To starve the cells of supplemental VEGF in the culture
189	medium, the cells were cultivated with human endothelial cell serum-free
190	basal medium (Invitrogen) containing 2% FBS overnight. After changing to
191	fresh medium with or without recombinant VEGF, the cells were incubated
192	at 37°C for 2 days. The supernatant was removed and 100 $\mu l/well$ of fresh
193	medium containing 10% WST-8 solution (Cell Counting Kit-8, Dojindo,
194	Kumamoto, Japan) was added. The cells were incubated for 2 h at 37°C and
195	the absorbance of each well was measured at 450 nm by a plate reader,
196	Multiskan MS-UV (Labsystems, Helsinki, Finland). The proliferation index
197	was determined as the ratio of the absorbance at 450 nm of cells treated with

198	VEGF against the absorbance at 450 nm of untreated cells. Primary skeletal
199	muscle cells of Japanese serow were also treated with recombinant VEGF
200	and used as the control.
201	
202	2.9. Statistical analysis
203	The data were analyzed for statistical significance by parametric
204	non-repeated measures ANOVA and the post hoc test using Dunnett's or
205	SNK tests, and also parametric unpaired Student's <i>t</i> -test.
206	
207	3. Results
208	
209	3.1. Identification and sequences of viral VEGF gene
210	All of the 6 PPV isolates were classified as orf virus by sequence
211	analysis of the viral envelope gene (data not shown). Several PCR primers
212	were first designed to bind outside the viral VEGF gene. However, as already
213	reported by Mercer et al. (2002), these primers were unable to amplify a
214	specific viral VEGF gene (data not shown), indicating sequence variation in
215	the flanking regions of the VEGF gene. The VEGF gene was amplified from
216	all of the 6 PPV isolates using primers D27F and 11R, except for isolate HIS,

217	for which primers D27F and D2R were used. The complete nucleotide
218	sequences of the viral VEGFs were successfully determined by direct
219	sequencing. The deduced amino acid sequences were aligned with each other
220	and with those of the NZ2, D1701 and orf-11 strains by Genetyx ver. 8.2.2.
221	software (Genetyx, Tokyo, Japan) (Fig. 2). Interestingly, among the 4 isolates
222	from the Japanese serows, not only the amino acid sequences but also the
223	nucleotide sequences showed 100% identity. Among the 6 Japanese isolates,
224	the amino acid sequences of VEGF were able to be classified into 3 different
225	types, designated Iwate, HIS and S-1 (S-1 was found in all serow isolates).
226	Sequence identity was also determined using the Genetyx software
227	(Supplementary Table S2). The Iwate and S-1 VEGFs were composed of 137
228	amino acids, with 1 amino acid substitution between them (99.3% identity),
229	whereas HIS was shorter at 132 amino acids and included many amino acid
230	substitutions in the sequence. The identity of the amino acid sequence
231	between Iwate and HIS was 69.8%, and between HIS and S-1 was 70.5%.
232	The Iwate and S-1 VEGFs showed high identity with orf-11 VEGF,
233	conversely HIS VEGF showed higher identity with the NZ2 and D1701 $$
234	VEGFs than Iwate and S-1 (Supplementary Table S2). Eight cysteine
235	residues that are conserved in all members of the VEGF family are also

236	conserved in the sequences of the Iwate, HIS and S-1 VEGFs. The orf virus
237	VEGF utilizes the VEGF receptor 2 and neuropilin-1 (Ogawa et al., 1998,
238	Meyer et al., 1999, Wise et al., 1999). An asparagine residue at the 73
239	position (Iwate VEGF) is conserved in Iwate, HIS and S-1 VEGF; this is an
240	accessible residue on the receptor-binding face of VEGF-A that correlates
241	strongly with binding of the VEGF receptor 2 and is also conserved in PPV
242	VEGFs (Mercer et al., 2002, Ueda et al., 2003, 2007, Inder et al., 2007). The
243	specific mutation corresponding to the binding ability to VEGF receptor 1
244	described by Mercer et al. (Mercer et al., 2002) was not observed at any
245	positions among our 3 VEGF sequences. These results suggested that the
246	Iwate, HIS and S-1 VEGFs bind to VEGF receptor 2 but not to receptor 1, as
247	seen in the other orf viruses. The DNA sequences determined in this study
248	were submitted to DDBJ/EMBL/GenBank under accession numbers
249	AB436805 to AB436810.
250	
251	3.2. Expression of viral VEGF mRNA

Expression of VEGF mRNA was detected in the early stage of infection (Fig. 3). No amplicons were found in PCR products without RT (data not shown). In all cells infected with the Iwate and S-1 VEGFs,

255	expression was detected as early as 4 h post-infection. Expression of HIS
256	VEGF mRNA occurred slightly later, appearing first at 8 h after infection.
257	However, no significant difference was observed among the 3 different types
258	of cells and the 3 isolates.
259	
260	3.3. Expression of recombinant VEGF
261	Viral VEGFs were expressed in <i>E.coli</i> as a fusion protein with a
262	hexa-His-tag. The recombinant VEGFs were purified and estimated by
263	SDS-PAGE followed by Coomassie brilliant blue staining and Western blot
264	analysis. As expected from the sequence analysis, recombinant HIS VEGF is
265	smaller in molecular weight than Iwate and S-1 VEGFs. Under reducing
266	conditions with 2-mercaptoehanol, and as estimated using a pre-stained
267	protein marker (P7708, New England Biolabs, Ipswich, MA, USA), the
268	apparent molecular weight of HIS VEGF is about 18 kDa while that of Iwate
269	and S-1 VEGF is about 22 kDa.; under non-reducing conditions the apparent
270	molecular weight of HIS VEGF is about 44 kDa while that of Iwate and S-1
271	VEGF is about 48 kDa (data not shown). These results indicate that
272	recombinant VEGF forms a homodimer, which is consistent with previous
273	studies (Meyer et al., 1999).

274

275 *3.4. Vascular permeability activity*

276	The purified recombinant VEGFs were next investigated for their
277	biological activities. Vascular permeability activity was evaluated using the
278	Miles assay. Dose-dependent permeabilization was induced by all of the viral
279	VEGFs, which was statistically different from the PBS control by parametric
280	non-repeated measures ANOVA and Dunnett's test (Fig. 4a). However,
281	among the 3 VEGFs, no statistically significant difference was observed in
282	each dilution by parametric non-repeated measures ANOVA and the SNK
283	test.
284	

285 3.5. HUVEC-proliferative activity

HUVEC were treated with recombinant VEGF for 2 days. Each VEGF showed mitogenic activity on HUVEC proliferation (Fig. 4b). The proliferation index was determined as the ratio of the absorbance at 450 nm of cells treated with VEGF against the absorbance at 450 nm of untreated cells. When compared at 50 ng/ml of VEGF dilution, the HIS and S-1 VEGFs showed significantly higher activity (P < 0.01) on HUVEC proliferation than the Iwate VEGF (P < 0.05), but no significant difference was observed

293	between the HIS and S-1 VEGFs by parametric non-repeated measures
294	ANOVA and the SNK test (Fig. 4b). Statistically identical results were
295	obtained using 10 ng/ml of VEGF.
296	
297	3.6. Isolation and identification of primary endothelial cells
298	Primary endothelial cells were isolated from the aortas of cattle,
299	sheep, goats, and Japanese serows. Isolated endothelial cells were
300	sometimes retrieved with smooth muscle cells. To purify endothelial cells,
301	several possible antibodies for surface markers to endothelial cells, ovine and
302	human CD31, VEGF receptors and plasmalemmal vesicle associated
303	protein-1 were used in a magnetic activated cell sorting (MACS) assay.
304	However, no antibody was successful in the purification of endothelial cells
305	by MACS (data not shown), suggesting that cross-reactivity of commercially
306	available antibodies seems to be weak against animal endothelial cells, or
307	that the expression patterns are different in ruminants or changed by
308	trypsinization. Thus the purity of the primary endothelial cells was
309	estimated using an antibody to vWF by IFA and flow cytometry. Primary
310	endothelial cells were positive for the presence of vWF in the cytoplasm by
311	IFA, whereas serow skeletal muscle cells were negative (Fig. 5a). Endothelial

cells showing over 80% purity by flow cytometry (Fig. 5a) were used for the 312proliferation assay. 3133143.7. Comparison of responsiveness to VEGF 315Primary endothelial cells from different host species (BAEC, OAEC, 316 CAEC, and SeAEC) were treated with recombinant S-1 VEGF (S-1 was 317found in all serow isolates) for 2 days. The responsiveness to VEGF was 318estimated by cell proliferation and was significantly different among the cell 319types (Fig. 5b). The proliferation index was the lowest in BAECs and the 320 greatest in SeAECs, suggesting that the SeAECs are the most responsive to 321322S-1 VEGF. 3234. Discussion 324325Japanese serows are a protected ruminant species in Japan. PPV 326

327 infection among wild Japanese serows has been continuously observed in

- various areas since the 1970s (Inoshima et al., 1999, 2001b; Kumagai et al.,
- 329 1979). Proliferative severe skin lesions by PPV infection in Japanese serows
- are frequently observed in serows in their natural territories, and most of the

331	affected animals die from debilitation (Okada et al., 1984b; Suzuki et al.,
332	1986, 1997). In cattle, the mortality due to PPV infection is significantly
333	lower and the lesions are considerably milder. Previously we isolated several
334	PPVs from affected Japanese serows and revealed that the PPVs circulating
335	among wild Japanese serows are mainly orf virus and accidentally bovine
336	papular stomatitis virus (Inoshima et al., 2001a, 2002). To define the factors
337	responsible for the severity of PPV-induced lesions in Japanese serows, we
338	characterized the molecular and biological characteristics of viral VEGF
339	using 6 Japanese PPV isolates.
340	At first, we determined the sequence of the VEGF gene from the 6
341	Japanese PPV isolates. Surprisingly, the amino acid sequences of VEGF
342	were identical among the 4 isolates (S-1 type) from the Japanese serows.
343	Next, mRNA expression was compared temporally among the 3 VEGF types
344	(Iwate, HIS and S-1). No significant temporal difference in mRNA expression
345	was observed among the 3 PPVs. Our results are consistent with previous
346	observations. Lyttle et al. (1994) demonstrated that RNA transcripts from
347	the viral VEGF gene can be detected as early as 6 h post-infection in cells.
348	Moreover, Scagliarini et al. (2006) used 4 different PPVs, including an isolate
349	IT 01 from a severe fatal outbreak in sheep, and showed that the expression

350	of VEGF mRNA in cells did not differ chronologically, as estimated by
351	real-time PCR. The current findings revealed that the expression of S-1
352	VEGF mRNA is temporally similar to that of the other types of VEGF, not
353	only in cells from Japanese serows but also in cells from cattle and sheep.
354	Next, the biological activities of the 3 viral VEGFs were compared.
355	Although all 3 VEGFs induced vascular permeabilization, no significant
356	difference was observed at each dilution. In HUVEC-proliferative activity, a
357	significant difference was observed between the S-1 and Iwate VEGFs.
358	Unexpectedly, no significant difference either in vascular permeability or
359	HUVEC-proliferative activity was observed between the S-1 and HIS VEGFs.
360	Although we are unsure of the exact mechanisms involved, there are some
361	possible explanations for these findings. 1) A proline residue at amino acid
362	position 128 of Iwate VEGF is involved in the decrease in
363	HUVEC-proliferation, since the HIS and S-1 VEGFs and previously reported
364	VEGFs from 21 isolates of orf virus except orf-11 (Mercer et al., 2002) have a
365	threonine residue at this position. Amino acid 128 is located in the
366	C-terminal region, which has a threonine/proline-rich unique sequence
367	contributing to the binding of VEGF to cellular co-receptors, neuropilin-1
368	and heparin (Tokunaga et al., 2006). 2) The sequence of the loop 1 region is

369	conserved among the 3 VEGFs, whereas loop 3 of HIS differs from that of the
370	Iwate and S-1 VEGFs. Kiba et al. (2003) demonstrated that the set of the
371	loop 1 and 3 regions is crucial for the formation of the three-dimensional
372	structure important for the high-affinity binding to VEGF receptor 2.
373	Moreover, an arginine residue at amino acid position 115 in the C-terminal
374	region of NZ2 VEGF, which correlates with binding of VEGF to neuropilin-1
375	and heparin (Tokunaga et al., 2006), is glutamine in the Iwate and S-1
376	VEGFs but lysine in the HIS VEGF (Fig. 2). It is conceivable that these
377	differences at loop 3 and the arginine residue, together with other sequence
378	difference between the Iwate and HIS VEGFs, influence the receptor-binding
379	ability and biological activity of HUVEC-proliferation. However, the
380	combined effect of the complex of differences in the loop region, residue and
381	other sequences should be that HUVEC-proliferative activity is not
382	significantly different between the Iwate and HIS VEGFs. Further
383	comparative analyses using other viral and mutated VEGFs are required to
384	clarify the situation. Wise et al. (2003) reported that PPV VEGFs varied in
385	receptor-binding ability and vascular permeability. VEGF has angiogenic
386	activity and Scagliarini et al. (2006) demonstrated that an isolate, IT 01,
387	from a severe fatal outbreak in sheep, produced a higher number of vessels.

388	Moreover it is reported that, despite extreme variation in sequence, the
389	biological activities of viral VEGF including vascular permeability,
390	proliferation of endothelial cells, and angiogenicity, are conserved (Mercer et
391	al., 2002, 2006; Scagliarini et al., 2006; Wise et al., 2003, 2007). These results
392	suggest that the biological activity to stimulate vascular permeability and
393	HUVEC proliferation should be conserved among the Iwate, HIS and S-1
394	VEGFs despite sequence variations.
395	Next, we speculated that Japanese serows are more sensitive to PPV
396	or viral VEGF than the other host species and may be involved in the
397	pathogenesis. Since it was difficult to obtain microvascular endothelial cells
398	from each species involved under the natural conditions of infection, aortic
399	endothelial cells were used in our experiments. A proliferation assay using
400	primary endothelial cells from cattle, sheep, goats and Japanese serows
401	indicated different proliferation properties, in which endothelial cells from
402	Japanese serows showed the greatest response to S-1 VEGF. These results
403	suggest that the high responsiveness of endothelial cells to the viral VEGF
404	may be one of the factors in the severity of skin lesions in Japanese serows.
405	However, the effects on serow cells were not much greater than that on ovine
406	cells. Thus, the severe proliferative skin lesions in Japanese serow most

407	likely result from the combined effects of viral VEGF, other
408	virulence/immune modulator genes such as the genes for viral IL-10
409	(Fleming et al., 2007), viral interferon resistance, and
410	granulocyte/monocytes-colony stimulating factor inhibitory factor (Haig and
411	McInnes, 2002), and host factors such as immune conditions and
412	species-specific factors. It is possible that the orf viruses infecting Japanese
413	serows are much more adapted to Japanese serows than to sheep and cattle,
414	that Japanese serows may have a poorer defense against the infection than
415	sheep and cattle, or that some cellular proteins of serows may interact more
416	efficiently with the viral VEGF promoter or the production of VEGF protein.
417	Taken together, our findings suggest that the biological activities of
418	the viral VEGFs and the responsiveness of endothelial cells to the VEGFs,
419	appear to be factors involved in the severe proliferative skin lesions seen in
420	infected Japanese serows. In addition, other viral and host factors may be
421	involved. Further analyses are required to determine other associated
422	factors, including receptor/co-receptor usage, genetic mutation of immune
423	modulator genes (Rziha et al., 2000), and behavior in, and
424	environmental/physiological conditions of, Japanese serows. Moreover, both
425	in vitro and in vivo analyses using VEGF-deleted recombinant viruses or

426 VEGF-exchanged viruses are required for further interpretation of the role427 of viral VEGF.

428

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110		800 0000 00	10 100100101011	or princip	011010011011011	00110 00110 0011

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- 449
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618	
619	Figure legends
620	Fig. 1. Representative lesions of naturally infected PPV animals. (a) Papules
621	and nodules in the gingiva and lip of an affected cow. (b) Scabby papules and
622	nodules around the mouth of an affected goat. (c) Highly proliferative scabby
623	papules, nodules, pustules and ulcers on the lips, muzzle and eye regions of
624	an affected Japanese serow.
625	Fig. 2. Alignment of the deduced amino acid sequences of the viral VEGFs.
626	The sequences of isolates Iwate and HIS from sheep in Japan and isolate S-1
627	from a Japanese serow were aligned with the published sequences as follows:
628	NZ2 (DDBJ/EMBL/GenBank accession nos. BD320268 and S67520), D1701
629	(AF106020) and orf-11 (AY236150). The sequences of the 4 PPV isolates from
630	Japanese serows were identical and denoted as S-1. The eight cysteine
631	residues that are conserved in all members of the VEGF family are indicated
632	above the Iwate sequence as C. The asterisk indicates the accessible
633	asparagine residue on the receptor-binding face of VEGF-A, which correlates
634	strongly with the binding of VEGF receptor 2 and is conserved in the

635	sequences of PPV VEGFs (Mercer et al., 2002, Ueda et al., 2003, 2007, Inder
636	et al., 2007). The arginine residues that correlate with the binding of
637	co-receptors, neuropilin-1 and heparin, in NZ2 VEGF (Tokunaga et al., 2006),
638	are indicated as R. The bars above the Iwate sequence indicate the loop 1
639	and loop 3 regions of the conformational structure of VEGF; these loops are
640	essential for the binding and activation of VEGF receptor 2 (Kiba et al.,
641	2003).
642	Fig. 3. Comparison of the temporal pattern of mRNA expression <i>in vitro</i> .
643	FBM (fetal bovine muscle), FLL (fetal lamb lung) and SeSM (serow smooth
644	muscle) cells were infected with PPV isolates Iwate, HIS, or S-1. RNA
645	samples were collected 0, 1, 2, 4, 8, 12, 24 and 36 h after virus-inoculation. As
646	a control for the reaction, mRNA of the housekeeping gene cellular
647	glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was also amplified
648	using primers as described previously (Mohan et al., 2001; Palmarini et al.,
649	1996). Distilled water (DW) was used as the negative control.
650	Fig. 4. Comparison of the biological activities of the viral VEGFs. (a)
651	Vascular permeability activity of the viral VEGFs by the Miles assay. VEGF
652	was serially diluted in PBS and intradermally injected into the shaved backs
653	of guinea pigs. Dose-dependent vascular permeabilization was observed for

654	all 3 viral VEGFs. No significant difference was observed among the 3
655	VEGFs at each dilution, as determined by parametric non-repeated
656	measures ANOVA and the SNK test. Data represents the mean \pm SD of 3
657	guinea pigs. (b) HUVEC-proliferative activity of viral VEGFs. HUVECs were
658	treated with the viral VEGFs. The proliferation index was determined as the
659	ratio of the absorbance at 450 nm of cells treated with VEGF against the
660	absorbance at 450 nm of untreated cells. Data represents the mean \pm SD of 6
661	evaluations. The HIS and S-1 VEGFs showed significantly higher activity on
662	HUVEC proliferation than the Iwate VEGF at a concentration of 50 ng/ml
663	(* P < 0.05, ** P < 0.01). No significant difference was observed between the
664	HIS and S-1 VEGFs by parametric non-repeated measures ANOVA and the
665	SNK test. No statistically significant differences were observed at a VEGF
666	concentration of 10 ng/ml.
667	Fig. 5. Comparison of the responsiveness of endothelial cells to viral VEGF
668	among different host species. (a) Isolation of primary endothelial cells.
669	Endothelial cells from animals were stained positively for vWF by IFA. Over
670	80% of cells were positive when counted by flow cytometry; these are shown
671	as a dotted line in the flow cytometry panels. BAEC, bovine aortic
672	endothelial cells; OAEC, ovine aortic endothelial cells; CAEC, caprine aortic

673	endothelial cells; SeAEC, Japanese serow aortic endothelial cells; SeMC,
674	Japanese serow skeletal muscle cells. SeMC were used as control
675	non-endothelial cells. (b) Comparison of the responsiveness to viral VEGF of
676	primary endothelial cells from different host species. Primary endothelial
677	cells were treated with 50 ng/ml of S-1 VEGF for 2 days. The proliferation
678	index was determined as the ratio of the absorbance at 450 nm of cells
679	treated with VEGF against the absorbance at 450 nm of untreated cells.
680	Although no significant difference between OAEC and SeAEC among the 4
681	cells was observed by parametric non-repeated measures ANOVA and the
682	SNK test, a significant difference (* $P < 0.05$) was observed between OAEC
683	and SeAEC analyzed by parametric unpaired Student's <i>t</i> -test. Data
684	represents the mean \pm SD of 6 evaluations. BAEC, bovine aortic endothelial
685	cells: SoAEC, ovine aortic endothelial cells; CAEC, caprine aortic endothelial
687	skeletal muscle cells. ** $P < 0.01$
688	Skeletal indscie cens. $T < 0.01$.
689	
500	

690 Table 1. Parapoxvirus isolates used in this study

691 Isolate Original host Prefecture Year of isolation

692		References		
693	Iwate	sheep	Iwate	1970
694		Kumagai et al., 1971		
695	HIS	sheep	Hokkaido	2004
696		Kanou et al., 2005		
697	S-1	Japanese serow	Gifu	1985
698		Suzuki et al., 1993		
699	GHF	Japanese serow	Gifu	1999
700		Inoshima et al., 2002		
701	R-1	Japanese serow	Toyama	1999
702		Inoshima et al., 2002		
703	Aichi	Japanese serow	Aichi	2000
704		Inoshima et al., 2002		
705				
706				
707				
708				
709	Supplei	mentary data		
710				

	bequeilee (8 to 8)
PPP-1	GTCGTCCACGATGAGCAGCT
PPP-4	TACGTGGGAAGCGCCTCGCT
D27F	AATGTAAATWMTAACGCC
11R	AACCCAGAAACGTCCCGCTAC
D2R	CGTTTGGATMTGCGGTCC
VEGF orf-11F	ATGAGGTTGCTCGTCTGC
VEGF cons340R	CGCACTTTGTATGCTCCACGA
VEGF HISF	ATGAGGTTGCTCGTCGGCATACTG
VEGF HISR	CTAGCGGCGTCTTCTGGGCGGCCT
BamConsSigF	CTGCTG <u>GGATCC</u> GACAGCAGCACAAAAAAA
EcoConsR	CAAAAA <u>GAATTC</u> CTAATAAGCCCTTCGGCG
PstConsR	CAAAAA <u>CTGCAG</u> CTAATAAGCCCTTCGGCG

732		Iwate		HIS		S-1	NZ2(BD)
733		NZ2(S)	D1701		orf-11		
734	Iwate			70.8		99.3	70.8
735		70.1	69.3		99.3		
736	HIS			_		70.8	84.2
737		83.5	89.4		71.3		
738	S-1					- , C	70.8
739		70.1	69.3		98.5		
740	NZ2(BI))					_
741		99.2	83.5		71.3		
742	NZ2(S)						
743		_	82.7		70.6		
744	D1701						
745		_		69.9			
746	orf-11						
747			R	_			
748	* NZ2(]	BD), data from	accessi	on no. l	BD3202	68. NZ2(S), dat	a from accession

731 Table S2. Identity of VEGF amino acid sequence (%)*

749 no. S67520.



		С	Loop	1 C	С	
Iwate	1:MRLLVCILVVVCLLHQHLLNADS	STKKWPEVLEGSKCK	PRPTVLSVNGEHPELT	SQRFNPPCVTL	MRCGG 7	0
HIS	1:GAY	T.SF.S	VP.GEA	v	· 6	8
S-1	1:				7	0
NZ2 (BD320268)	1:.KGAY	NG.SKE	I.VP.SET		6	9
NZ2 (S67520)	1:.KGAY	NG.SKE	I.VP.SET		6	9
D1701	1:.KFGAY	T.SF.N.G	M.FR.HD		6	8
orf-11	1:				6	9
	CC* C	Loop 3	C CR		RR	
Iwate	71: CCNDESLECVPTEEANVTMEFMG	VGVSSTGSSVSTQHL	EFVEHTKCDCQPRG	GQQTTPPPRRR	RRAY 1	.37
HIS	69:QL	A.VSGGNGM	IKKLTT	TPPTR.P	1	.32
S-1	71:			T	1	.37
NZ2 (BD320268)	70:LL.	A.GSG.NGM.R.	SKRFTT	TPPTR.P	1	.33
NZ2 (S67520)	70:VSLL.	A.GSG.NGM.R.	SKRFTT	TPPTR.P	1	.33
D1701	69:QL	A.VSGGNGM	SKK.PLTT	TPPTR.P	1	.32
orf-11	70:				1	.36





Fig. 4. Inoshima et al.



Fig. 5. Inoshima et al.