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Adenoviruses and Encephalitozoon pogonae in Samples from Bearded Dragons
(Pogona spp.) in Europe
 --Manuscript Draft--

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Abstract:	Adenoviruses (AdVs) and the microsporidium Encephalitozoon pogonae have been repeatedly detected in bearded dragons (Pogona spp.). The majority of adenoviruses found in these animals have been characterized as agamid adenovirus 1 (AgAdV1) in the species Lizard adenovirus B, although other adenoviruses have also been described sporadically. Infection with AgAdV1 has been hypothesized to increase susceptibility to other pathogens, and co-infections with microsporidia and AdVs have been described in individual cases. In a retrospective study, samples from bearded dragons submitted to a commercial laboratory (Laboklin GmbH & Co. KG, Bad Kissingen, Germany) for the detection of AdVs by PCR, were also screened for the presence of E. pogonae. Samples from 144 animals, mostly cloacal swabs as well as feces and tissue samples, were included in the study. The AdV PCR was positive for 35 (24.3%) samples, the E. pogonae PCR was positive for 28 (19.4%). Sequencing of the products from the AdV PCRs showed that 30 of the viruses detected (85.7%) were identifiable as AgAdV1, and 3 (8.6%) belonged to the species Lizard adenovirus A. The remaining 2 (5.7%) AdV PCR products were not sequenced. Evaluation of co-infections showed no correlation between infection with an AdV and E. pogonae when all AdV PCR positive samples were included in the analysis (P = 0.1168), and the correlation remained insignificant when only AgAdV1-like viruses were included (P = 0.0557). Adenoviruses and microsporidia are commonly found in swabs and feces of captive bearded dragons in Europe. Understanding their clinical significance for these animals requires further study.

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1 **Adenoviruses and *Encephalitozoon pogonae* in Samples from Bearded**
2 **Dragons (*Pogona* spp.) in Europe**

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9
10 **Abstract:** Adenoviruses (AdVs) and the microsporidium *Encephalitozoon pogonae*
11 have been repeatedly detected in bearded dragons (*Pogona* spp.). The majority of
12 adenoviruses found in these animals have been characterized as agamid
13 atadenovirus 1 (AgAdV1) in the species *Lizard atadenovirus B*, although other
14 adenoviruses have also been described sporadically. Infection with AgAdV1 has
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17 retrospective study, samples from bearded dragons submitted to a commercial
18 laboratory (Laboklin GmbH & Co. KG, Bad Kissingen, Germany) for the detection of
19 AdVs by PCR, were also screened for the presence of *E. pogonae*. Samples from
20 144 animals, mostly cloacal swabs as well as feces and tissue samples, were
21 included in the study. The AdV PCR was positive for 35 (24.3%) samples, the *E.*
22 *pogonae* PCR was positive for 28 (19.4%). Sequencing of the products from the AdV
23 PCRs showed that 30 of the viruses detected (85.7%) were identifiable as AgAdV1,
24 and 3 (8.6%) belonged to the species *Lizard atadenovirus A*. The remaining 2 (5.7%)
25 AdV PCR products were not sequenced. Evaluation of co-infections showed no
26 correlation between infection with an AdV and *E. pogonae* when all AdV PCR
27 positive samples were included in the analysis ($P = 0.1168$), and the correlation
28 remained insignificant when only AgAdV1-like viruses were included ($P = 0.0557$).
29 Adenoviruses and microsporidia are commonly found in swabs and feces of captive
30 bearded dragons in Europe. Understanding their clinical significance for these
31 animals requires further study.

32

33 **Key Words:** Adenovirus, bearded dragon, *Encephalitozoon pogonae*, microsporidia,
34 *Pogona*

35

36 **Introduction**

37 The family *Adenoviridae* contains non-enveloped double-stranded DNA
38 viruses currently divided into the genera *Atadenovirus*, *Aviadenovirus*,
39 *Ichtadenovirus*, *Mastadenovirus*, *Siadenovirus*, and *Testadenovirus*. Adenoviruses
40 (AdVs) are commonly found in squamate reptiles and the viruses found in these
41 animals have overwhelmingly been atadenoviruses (Marschang *et al.*, 2021). Among
42 squamate reptiles, AdVs appear to be particularly common in bearded dragons
43 (*Pogona* spp.). The AdVs most often found in these lizards belong to the species
44 *Lizard atadenovirus B*, strain agamid atadenovirus 1 (AgAdV1). This virus has been
45 detected in bearded dragons in human care in North America, Europe, Asia, and
46 Australia (Akabane *et al.*, 2020; Marschang *et al.*, 2021) and has also been detected
47 in free-ranging bearded dragons in Australia (Hyndman *et al.*, 2019). The virus strain
48 lizard atadenovirus 2 (LiAdV2) (also referred to as helodermatid adenovirus 2) in the
49 species *Lizard atadenovirus A* was originally detected and isolated from Mexican
50 bearded lizards (*Heloderma horridum*) in Europe (Papp *et al.*, 2009). It has since also
51 been detected in bearded dragons in human care in North America (Crossland *et al.*,
52 2018; Bengé *et al.*, 2019) as well as in a free-ranging central bearded dragon
53 (*Pogona vitticeps*) from western New South Wales, Australia (Hyndman *et al.*, 2019).
54 Although AdVs are generally considered one of the most common pathogens found
55 in bearded dragons, there are limited studies evaluating prevalence of these viruses
56 in managed populations. Detection rates of between 4.5 and >50% have been
57 reported in various countries and groups of animals (Kim *et al.*; 2002, Abbas *et al.*,
58 2012; Kubiak, 2013; Akabane *et al.*, 2020). In a study screening free-ranging
59 bearded dragons in Australia, 18.75% (9/48) of the animals were positive for AdVs
60 (Hyndman *et al.*, 2019).

61 The pathogenicity of AdVs in bearded dragons is not well understood. Infected
62 animals have presented with pneumonia, gastrointestinal disease, and CNS signs,
63 but AdVs have also been detected in clinically healthy animals (Marschang *et al.*,

64 2021). Clinical signs of disease appear to be more frequent in juvenile bearded
65 dragons than in adults (Jacobson *et al.*, 1996; Moormann *et al.*, 2009; Doneley *et al.*,
66 2014).

67 Microsporidia are obligate intracellular fungi. They are a genetically diverse
68 group of microorganisms. Infection is often subclinical in immunocompetent
69 mammals and birds, while they can cause serious disease in immunocompromised
70 hosts (Paré and Conley, 2021). *Encephalitozoon pogonae* was recognized as a
71 pathogen in bearded dragons by Sokolova *et al.* (2016), although previous
72 descriptions of microsporidiosis in bearded dragons are available (Richter *et al.*,
73 2013). *E. pogonae* is closely related to *E. cuniculi*. It has been detected in
74 association with granulomas and necrosis in various tissues (Shibasaki *et al.*, 2017;
75 Wünschmann *et al.*, 2019; Llinas *et al.*, 2021). It has been suggested that it may be
76 associated with aneurysms in bearded dragons in some cases, as it has been shown
77 to cause vascular damage (Wünschmann *et al.*, 2019; Kaiser *et al.*, 2021).

78 Co-infections with multiple pathogens have been frequently reported in reptiles
79 in human care, and the effects of individual pathogens, stress, inadequate
80 husbandry, and other factors in infection prevalence and disease development are
81 generally not well understood. Adenoviruses are often detected together with other
82 potential pathogens in infected bearded dragons. These include dependoviruses
83 (family *Parvoviridae*) (Jacobson *et al.*, 1996; Kim *et al.*, 2002; Péntzes *et al.*, 2015),
84 coccidia (Kim *et al.*, 2002; Schilliger *et al.*, 2016), mycoplasma (Crossland *et al.*,
85 2018), ferlaviruses (Abbas *et al.*, 2012), invertebrate iridoviruses (Papp *et al.*, 2009),
86 and ranaviruses (Stöhr *et al.*, 2013). There are two reports of co-infections with AdVs
87 and *E. pogonae* in bearded dragons (Schilliger *et al.*, 2016; Llinas *et al.*, 2021). In a
88 report from Europe, a juvenile bearded dragon was co-infected with an atadenovirus,
89 coccidia, and *E. pogonae* (Schilliger *et al.*, 2016). In a report on captive bearded
90 dragons in Australia, *E. pogonae* and a virus in the species *Lizard atadenovirus B*
91 were detected in several animals in a collection experiencing granulomatous disease
92 (Llinas *et al.*, 2021).

93 The aim of this study was to screen samples submitted to a veterinary
94 diagnostic laboratory for both AdVs and *E. pogonae*. We hypothesized that all of the
95 AdVs detected would belong to the species *Lizard atadenovirus B* and that there
96 would be a correlation between infection with AdVs and *E. pogonae*.

97

98 **Materials and Methods**

99 Samples submitted to Laboklin GmbH & Co. KG (Bad Kissingen, Germany)
100 from veterinarians for routine testing for AdVs by PCR were included in the study.
101 Only samples for which the host species was specified to have been a bearded
102 dragon and sample types that included cloacal swabs, feces, and/or tissue were
103 included. No clinical information on the animals tested was provided. DNA was
104 prepared from samples within 24 h of arrival in the laboratory. Prior to nucleic acid
105 extraction, tissue and fecal samples were placed in MagNA Lyser Green Bead-tubes
106 (Roche Diagnostics, Mannheim, Germany). Tissue samples were then incubated in a
107 tissue lysis buffer (Roche Diagnostics) with proteinase K (Carl Roth GmbH & Co. KG,
108 Karlsruhe, Germany). Fecal samples were incubated in STAR Buffer (Roche
109 Diagnostics). Swabs were incubated in tissue lysis buffer (Roche Diagnostics) and
110 proteinase K (Carl Roth GmbH & Co. KG). DNA was prepared using the Roche
111 MagNA Pure 96 system with the MagNA Pure 96 DNA and Viral RNA Small Volume
112 Kit (Roche Diagnostics) according to the manufacturer's instructions. Adenoviruses
113 were detected using a pan-AdV PCR targeting the DNA polymerase gene (Wellehan
114 *et al.*, 2004). *E. pogonae* was detected using a PCR targeting the 18S ribosomal
115 RNA gene (Forward primer: 5' - GTG AGA CCC TTT GAC GGT GT - 3'; Reverse
116 primer: 5' - GCT TCG TCA GCC GCT ATT AC - 3'). Both PCRs used 5 µl of
117 prepared DNA as template. All PCR products of the expected size from both PCRs
118 were sequenced using Sanger sequencing as described previously (Salzmann *et al.*,
119 2021). Sequences were all analyzed by BLAST analysis
120 (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>).

121 Correlations between AdV and *E. pogonae* detection were evaluated using a
122 Chi-squared test. Significance level was set at $P < 0.05$.

123

124 **Results**

125 At least one of the two pathogens included in the study were detected in 53 of
126 the 144 (36.8%) samples tested (Table 1). In the AdV PCR, products of the expected
127 size were obtained from 35 of the 144 samples tested (24.3%). Of the AdV PCR
128 positive samples, 32 were swabs, one was a mixed swab and fecal sample, and two

129 were fecal samples (Table 1). Sequencing identified 30 of the 35 samples (85.7%) as
130 belonging to the species *Lizard atadenovirus B*, three (8.6%) as belonging to the
131 species *Lizard atadenovirus A*, while the sequence data was lost for analysis due to a
132 laboratory error in two cases (5.7%) (Table 1).

133 Positive results for *E. pogonae* were obtained from 28 of the 144 samples
134 tested (19.4%) (Table 1). Of the *E. pogonae* PCR positive samples, 24 were swabs,
135 two were fecal samples, one was a mixed swab and mucous sample, and one was a
136 tissue sample that was not further identified. All PCR products were identified as *E.*
137 *pogonae* specific based on sequencing.

138 Both AdV and *E. pogonae* were detected in 10 animals (6.9%) (Table 1).
139 When all 35 animals that had a positive PCR result for AdVs were included in
140 calculations, there was no significant correlation between AdV and *E. pogonae*
141 detection ($P = 0.1168$). When only those animals in which an AdV in the species
142 *Lizard atadenovirus B* was identified were included, the correlation with *E. pogonae*
143 detection approached significance, but was still above the cut-off ($P = 0.0557$).

144

145 Discussion

146 While AdV infections are well documented in squamates in general and in
147 bearded dragons in particular, there is little data indicating the prevalence of these
148 viruses in bearded dragons in human care around the world. There is also limited
149 data on the specific AdV species found, although the majority of detections in which
150 the virus has been further characterized have been identified as AgAdV1 in the
151 species *Lizard atadenovirus B*. The identification of the majority of the AdVs found in
152 the present study as belonging to this group was therefore expected. The other AdV
153 found in individual samples, clustering in the species *Lizard atadenovirus A*, has also
154 been found previously in bearded dragons, but only in sporadic cases. A virus with
155 the same sequence was found in a pet bearded dragon in Florida, USA (Benge *et al.*,
156 2019). That animal was reported to have been ill, although no specific clinical signs
157 were reported. The same virus was detected in a clinically healthy free-ranging
158 central bearded dragon in New South Wales, Australia (Hyndman *et al.*, 2019). In a
159 study detecting antibodies against various atadenoviruses in a wide range of reptiles,
160 antibodies against AgAdV1 were most commonly found in agamids (mostly bearded

161 dragons) (33.2% positive, n = 223), followed by antibodies against LiAdV2
162 (helodermatid adenovirus 2, in the virus species *Lizard atadenovirus A*) (15.2%
163 positive) (Ball *et al.*, 2014). In the two cases reported here in which the sequence of
164 the AdV PCR product could not be evaluated, this was due to a laboratory error, so
165 that the specificity of the PCR products and the identity of the viruses in these two
166 cases cannot be confirmed.

167 Detection of *E. pogonae* in bearded dragons has so far been limited to
168 individual case reports or case series, and no information on screening of larger
169 numbers of animals or prevalence in specific populations has previously been
170 available. Infections with this pathogen have been reported in pet bearded dragons in
171 Australia (Llinas *et al.*, 2021), the USA (Sokolova *et al.*, 2016; Wünschmann *et al.*,
172 2019), Canada (Kaiser *et al.*, 2021), Japan (Shibasaki *et al.*, 2017), and France
173 (Schilliger *et al.*, 2016). Based on the limited data available, it was somewhat
174 surprising that *E. pogonae* was found in such a relatively high percentage of cases
175 (19.4% of the animals tested).

176 Disease associated with both AdV and microsporidia in bearded dragons has
177 been hypothesized to be dependent on various factors, including co-infections. Co-
178 infections between AdVs and *E. pogonae* have been described in several cases
179 (Schilliger *et al.*, 2016; Llinas *et al.*, 2021). However, the interaction between
180 infection, co-infection, and disease is not yet understood for either group of
181 pathogens. In the dataset presented here, there was no correlation between AdV and
182 *E. pogonae* detection. Regarding the ten cases in which both pathogens were
183 detected, the AdV was identified as an AgAdV1 in eight cases, while the virus could
184 not be identified due to a laboratory error in two cases. Looking at only the co-
185 infections between *E. pogonae* and AgAdV1, the correlation did approach
186 significance but did not fall below the specified significance level of $P = 0.05$. Since
187 both pathogens appear to be relatively common among pet bearded dragons in
188 Europe, it is necessary to screen a larger number of animals for both in order to fully
189 understand whether infection with one pathogen influences the probability of infection
190 with the other. It would also be helpful in future studies to determine the health status
191 of the animals in order to evaluate the role of each pathogen separately and together
192 in disease development.

193 Another factor that might influence infection rate, as well as disease
194 development, is the age of the animals. It would be helpful in future studies to also
195 document the age of the animals to determine whether this is a factor that can
196 influence the prevalence of infection with AdVs and microsporidia as well as whether
197 age influences disease development following infection with one or both pathogens.

198 The majority of samples screened in this study were cloacal swabs. The
199 samples were all submitted to the laboratory for screening for AdVs. Cloacal swabs
200 as sample material are generally recommended for AdV testing in bearded dragons
201 as virus is mostly found in the intestine and liver (Marschang *et al.*, 2021). Samples
202 used for the detection of microsporidia in bearded dragons have included mostly
203 tissues from dead animals (Richter *et al.*, 2013; Schilliger *et al.*, 2016; Sokolova *et*
204 *al.*, 2016; Shibasaki *et al.*, 2017; Wünschmann *et al.*, 2019; Kaiser *et al.*, 2021; Llinas
205 *et al.*, 2021). Only one study reported detection in samples from live bearded
206 dragons, including oral-cloacal swabs and blood (Llinas *et al.*, 2021). Based on the
207 detection rate in the present study, cloacal swabs appear to be a useful sample for
208 the detection of *E. pogonae* in bearded dragons, although phase of infection and
209 disease status could influence detection and require further study.

210 The sample set used for the present study was biased, as samples were
211 submitted by veterinarians to a diagnostic laboratory for testing for AdVs. No
212 information was provided on the reasons for testing, but these likely included both
213 testing to determine possible causes of disease as well as health screenings.
214 Nevertheless, it is interesting to note that both of the pathogens included in this study
215 were found relatively frequently in the animals tested. Based on the results of the
216 present study, screening for both AdVs and microsporidia should be considered in
217 health screening of bearded dragons.

218

219 **Disclaimer:** The authors are employed by a commercial veterinary diagnostic
220 laboratory (Laboklin GmbH & Co., KG, Bad Kissingen, Germany).

221

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304

305

306 **Table 1:** Samples from bearded dragons (*Pogona* sp.) that tested positive for
 307 adenoviruses (AdVs) and/or *Encephalitozoon pogonae* by PCR. For the AdVs, the
 308 viral species to which the identified virus likely belongs is listed. - = PCR negative.

309

No.	Species	Sample type	AdV PCR and sequencing result	<i>E. pogonae</i> PCR and sequencing result
1	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus A</i>	-
2	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus A</i>	-
3	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus A</i>	-
4	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	-
5	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	-
6	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	-
7	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	-
8	<i>Pogona vitticeps</i>	Swab	<i>Lizard atadenovirus B</i>	-
9	<i>Pogona vitticeps</i>	Swab	<i>Lizard atadenovirus B</i>	-
10	<i>Pogona vitticeps</i>	Swab	<i>Lizard atadenovirus B</i>	-
11	<i>Pogona vitticeps</i>	Swab	<i>Lizard atadenovirus B</i>	-
12	<i>Pogona vitticeps</i>	Swab	<i>Lizard atadenovirus B</i>	-
13	<i>Pogona vitticeps</i>	Swab and feces	<i>Lizard atadenovirus B</i>	-
14	<i>Pogona vitticeps</i>	Feces	<i>Lizard atadenovirus B</i>	-
15	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	-
16	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	-
17	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	-
18	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	-
19	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	-
20	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	-
21	<i>Pogona vitticeps</i>	Swab	<i>Lizard atadenovirus B</i>	-
22	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	-
23	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	-
24	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	-
25	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	-
26	<i>Pogona</i> sp.	Swab	<i>Lizard atadenovirus B</i>	<i>E. pogonae</i>
27	<i>Pogona vitticeps</i>	Swab	<i>Lizard atadenovirus B</i>	<i>E. pogonae</i>
28	<i>Pogona vitticeps</i>	Swab	<i>Lizard atadenovirus B</i>	<i>E. pogonae</i>
29	<i>Pogona vitticeps</i>	Swab	<i>Lizard atadenovirus B</i>	<i>E. pogonae</i>
30	<i>Pogona vitticeps</i>	Swab	<i>Lizard atadenovirus B</i>	<i>E. pogonae</i>
31	<i>Pogona vitticeps</i>	Swab	<i>Lizard atadenovirus B</i>	<i>E. pogonae</i>
32	<i>Pogona vitticeps</i>	Swab	<i>Lizard atadenovirus B</i>	<i>E. pogonae</i>
33	<i>Pogona vitticeps</i>	Swab	<i>Lizard atadenovirus B</i>	<i>E. pogonae</i>
34	<i>Pogona vitticeps</i>	Swab	PCR positive, no sequence available	<i>E. pogonae</i>
35	<i>Pogona</i> sp.	Feces	PCR positive, no sequence available	<i>E. pogonae</i>
36	<i>Pogona</i> sp.	Swab	-	<i>E. pogonae</i>
37	<i>Pogona vitticeps</i>	Swab	-	<i>E. pogonae</i>
38	<i>Pogona</i> sp.	Swab	-	<i>E. pogonae</i>
39	<i>Pogona vitticeps</i>	Tissue	-	<i>E. pogonae</i>
40	<i>Pogona</i> sp.	Swab	-	<i>E. pogonae</i>
41	<i>Pogona</i> sp.	Swab	-	<i>E. pogonae</i>

42	<i>Pogona vitticeps</i>	Swab	-	<i>E. pogonae</i>
43	<i>Pogona</i> sp.	Swab	-	<i>E. pogonae</i>
44	<i>Pogona</i> sp.	Swab	-	<i>E. pogonae</i>
45	<i>Pogona</i> sp.	Swab	-	<i>E. pogonae</i>
46	<i>Pogona</i> sp.	Swab	-	<i>E. pogonae</i>
47	<i>Pogona vitticeps</i>	Swab	-	<i>E. pogonae</i>
48	<i>Pogona</i> sp.	Feces	-	<i>E. pogonae</i>
49	<i>Pogona</i> sp.	Swab	-	<i>E. pogonae</i>
50	<i>Pogona</i> sp.	Swab	-	<i>E. pogonae</i>
51	<i>Pogona</i> sp.	Swab	-	<i>E. pogonae</i>
52	<i>Pogona</i> sp.	Swab	-	<i>E. pogonae</i>
53	<i>Pogona vitticeps</i>	Swab and mucous	-	<i>E. pogonae</i>

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