



**HAL**  
open science

## The crustacean *Armadillidium vulgare* (Latreille, 1804) (Isopoda: Oniscoidea), a new promising model for the study of cellular senescence

Charlotte Depeux, Ascel Samba-Louaka, Thomas Becking, Christine Braquart-Varnier, Jérôme Moreau, Jean-François Lemaître Lemaître, Tiffany Laverre, Hélène Paulhac, François-Xavier Dechaume-Moncharmont, Jean-Michel Gaillard, et al.

### ► To cite this version:

Charlotte Depeux, Ascel Samba-Louaka, Thomas Becking, Christine Braquart-Varnier, Jérôme Moreau, et al.. The crustacean *Armadillidium vulgare* (Latreille, 1804) (Isopoda: Oniscoidea), a new promising model for the study of cellular senescence. *Journal of Crustacean Biology*, 2020, 40 (2), pp.194-199. 10.1093/jcbiol/ruaa004 . hal-03060295

**HAL Id: hal-03060295**

**<https://hal.science/hal-03060295>**

Submitted on 14 Dec 2020

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

1 Running head: DEPEUX *ET AL.*: *ARMADILLIDIUM VULAGARE* AS A MODEL FOR  
2 CELLULAR SENESCENCE

3

4 **The crustacean *Armadillidium vulgare* (Latreille, 1804) (Isopoda:**  
5 **Oniscoidea), a new promising model for the study of cellular**  
6 **senescence**

7

8 Charlotte Depeux<sup>1, 2</sup>, Ascel Samba-Louaka<sup>1</sup>, Thomas Becking<sup>1</sup>, Christine  
9 Braquart-Varnier<sup>1</sup>, Jérôme Moreau<sup>3</sup>, Jean-François Lemaître<sup>2</sup>, Tiffany Laverre<sup>1</sup>,  
10 Hélène Paulhac<sup>1</sup>, François-Xavier Dechaume-Moncharmont, Jean-Michel  
11 Gaillard<sup>2</sup> and Sophie Beltran-Bech<sup>1</sup>

12

13 <sup>1</sup>*Université de Poitiers, Laboratoire Écologie et Biologie des Interactions UMR CNRS 7267,*  
14 *5 rue Albert Turpin, TSA 51106 86073 Poitiers Cedex 9, France;*

15 <sup>2</sup>*Université de Lyon, Université Lyon 1, CNRS, Laboratoire de Biométrie et Biologie*  
16 *Évolutive UMR 5558, F-69622 Villeurbanne, France;*

17 <sup>3</sup>*Biogéosciences UMR 6282 CNRS, Université Bourgogne Franche-Comté, 6 Boulevard*  
18 *Gabriel, 21000 Dijon, France; and*

19 <sup>4</sup>*Université de Lyon, Université Lyon 1, CNRS, Lehna, UMR 5023, 6 rue Raphaël Dubois,*  
20 *69622 Villeurbanne Cedex, France*

21

22 *Corresponding author: C. Depeux; e-mail: charlotte.depeux@gmail.com*

23

24

25

## ABSTRACT

26 Senescence, the decline of physiological parameters with increasing age, is a quasi-ubiquitous

27 phenomenon in the living world. The observed patterns of senescence, however, can markedly

28 differ across species and populations, between sexes, and even among individuals. To identify

29 the drivers of this variation in senescence, experimental approaches are essential and involve

30 the development of tools and new study models. Current knowledge of the senescence process

31 is mostly based on studies on vertebrates and main information about senescence in

32 invertebrates is mostly limited to model organisms such as *Caenorhabditis elegans* or

33 *Drosophila melanogaster*. In this context, we tested whether biomarkers of vertebrate aging

34 could be used to study senescence in a new invertebrate model: the common woodlouse

35 *Armadillidium vulgare* (Latreille, 1804). More specifically, we looked for the effect of age in

36 woodlouse on three well-established physiological biomarkers of aging in vertebrates:

37 immune cells (cell size, density, and viability),  $\beta$ -galactosidase activity, and the gene

38 expression of telomerase reverse transcriptase (TERT), an essential subunit of telomerase

39 protein. We found that the size of immune cells was higher in older individuals, whereas their

40 density and viability decreased, and that the  $\beta$ -galactosidase activity increased with age,

41 whereas the TERT gene expression decreased. These findings demonstrate that woodlouse

42 display age-related changes in biomarkers of vertebrate senescence, with different patterns

43 depending on gender. The tools used in studies of vertebrate senescence can thus be

44 successfully used in studies of senescence of invertebrates such as the woodlouse. The

45 application of commonly used tools to new biological models offers a promising approach to  
46 assess the diversity of senescence patterns across the tree of life.

47

48 **Key Words:** immunosenescence, telomerase reverse transcriptase (TERT),  $\beta$ -galactosidase  
49 activity

50

51

## INTRODUCTION

52 Many hypotheses have tried to explain why senescence is a quasi-ubiquitous phenomenon in  
53 the living organisms. For instance, the disposable soma theory proposed the senescence  
54 process as a result of damages accumulation over time (Kirkwood, 1977). These damages are  
55 strongly influenced by the environment, leading to trade-offs between the different functions  
56 (e.g., between reproduction and somatic maintenance) and shaping a high diversity of  
57 senescence patterns across species and populations, among individuals, and between sexes.  
58 One current challenge is to understand the selective forces and mechanisms driving this  
59 diversity of senescence patterns.

60 At the cellular level, senescence corresponds to the cellular deterioration leading to  
61 stop the cellular cycle (Campisi & d'Adda di Fagagna, 2007). As ageing is associated with  
62 cellular senescence (Herbig *et al.*, 2006; Wang *et al.*, 2009; Lawless *et al.*, 2010), many  
63 biomolecular parameters potentially inform about senescence and can therefore be valuable  
64 tools for studying this process (Bernardez de Jesus & Blasco, 2012). For example, the

65 evolution of the integrity and efficiency of immune cells is particularly relevant to study  
66 cellular senescence because a diminution of the number of effective immune cells with  
67 increasing age takes place in both vertebrates (e.g., Cheynel *et al.*, 2017) and invertebrates  
68 (e.g., Park *et al.*, 2011). Another marker used to study cellular senescence is the enzymatic  
69 activity of the  $\beta$ -galactosidase. This enzyme is a hydrolase that transforms polysaccharides  
70 into monosaccharides. The lysosomal activity of this enzyme is increased when the cell enters  
71 in senescence (Dimri *et al.*, 1995; Itahana *et al.*, 2007). This phenomenon occurs in senescent  
72 cells of many organisms ranging from humans (Gary & Kindell, 2005) to honeybees (Hsieh &  
73 Hsu, 2011). Another protein linked to the cellular senescence process is the telomerase, a  
74 ribonucleoprotein complex composed by two essential components, the telomerase reverse  
75 transcriptase (TERT) and the telomerase RNA (TR) and other accessory proteins (Podlevsky  
76 *et al.*, 2007). Telomerase lengthens the ends of telomeres (i.e., DNA sequences located at the  
77 end of chromosomes that protect chromosome integrity and shorten after each cell division).  
78 Cell senescence arises when the telomere length becomes critically short (Chiu & Harley,  
79 1997; Shay & Wright, 2005). Telomerase activity depends on the species, age, as well as the  
80 type of tissue (e.g., Gomes *et al.*, 2010). For instance, telomerase is active during the  
81 development before birth and after only in stem and germ cells in humans (Liu *et al.*, 2007;  
82 Morgan, 2013) whereas in *Daphnia pulicaria* Forbes, 1893 the telomerase activity in all  
83 tissues of the body decreases with increasing age (Schumpert *et al.*, 2015). The TERT is  
84 essential in the telomerase protein complex and has been shown to be related to cell survival

85 in humans (Cao *et al.*, 2002). The TERT has also been detected in numerous species including  
86 vertebrates, fungi, ciliates, and insects (Robertson & Gordon, 2006; Podlevsky *et al.*, 2007).

87         Because the patterns of senescence are strongly diversified within the living world, it  
88 seems essential to study organisms displaying markedly different life histories strategies to  
89 understand the causes and mechanisms underlying this diversity. Thus, invertebrates are  
90 increasingly used in experimental studies of senescence (Stanley, 2012; Ram & Costa, 2018).  
91 In addition to share similarities with vertebrates in terms of senescence, they can be  
92 manipulated experimentally and they are easier to monitor throughout their entire lifetime  
93 (Ram & Costa, 2018). These advantages make them models of choice for studying  
94 senescence. Here, we propose the common woodlouse *Armadillidium vulgare* Latreille, 1804  
95 as a promising new model for studying senescence. Woodlouse can live beyond three years  
96 and display sex-specific senescence patterns in natural populations (Paris & Pitelka, 1962). In  
97 addition, one study has already reported evidence of immune-senescence in this species  
98 (Sicard *et al.*, 2010).

99         In this context, we tested the suitability of  $\beta$ -galactosidase activity, immune cell  
100 parameters, and the TERT gene expression to cause age-specific responses in *A. vulgare*.  
101 According to reports in the literature, we expected an increase in  $\beta$ -galactosidase activity, and  
102 a decrease of both TERT gene expression and immune cell viability and density in *A. vulgare*.  
103 As males have higher adult survival than females (Paris & Pitelka, 1962), cellular senescence  
104 patterns are also expected to be sex-specific in this species.

105

106

## MATERIALS AND METHODS

107 *Biological model*

108 Individuals of *A. vulgare* used in the experiments were obtained from a wild population  
109 collected in Denmark in 1982. These individuals have been maintained on moistened soil  
110 under the natural photoperiod of Poitiers, France (46.58°N, 0.34°E) at 20 °C, and fed *ad*  
111 *libitum* with dried linden leaves and carrots. Crosses were monitored to control and promote  
112 genetic diversity. For each clutch obtained, individuals were sexed, and brothers and sisters  
113 were separated to ensure virginity. Woodlice are promiscuous and only breed when they are  
114 one-year old during their first breeding season in the spring. Females carry their offspring in a  
115 ventral pouch (marsupium) and can produce up to three clutches per season. In the common  
116 woodlouse, individuals molt throughout their lifetimes, with approximate one molt per month.  
117 During this process all the cells of the concerned tissues are renewed at 20 °C (Steel, 1980).  
118 The brain, the nerve cord, and gonads, however, are not renewed during molting and are  
119 therefore relevant candidates for tissue-specific study of senescence in this species. Woodlice  
120 were classified in three different age categories: juvenile (before first reproduction, birth to  
121 one-year old), young (one-year old, first year of reproduction), and old (up to two-year old),  
122 which are very rare in natural populations (Paris & Pitelka, 1962). As the woodlouse is  
123 continuous grower, juveniles and small individuals could not be used for certain experiments,  
124 especially when they required protein extraction or hemolymph collection. Thus, we were

125 only able to test in them the telomerase expression. Old individuals were sampled according  
126 to the number of individuals available in our breeding; sometimes we had two-year-old  
127 individuals and sometimes three-year-old ones. Moreover, males and females were tested  
128 separately to assess the impact of sex.

129

### 130 *Measurement of $\beta$ -galactosidase activity*

131 To test the impact of age on  $\beta$ -galactosidase activity, 180 individuals were used: 90 young  
132 (i.e., six-month old, 45 males, and 45 females) and 90 old (two-year old, 45 males, and 45  
133 females).

134 Individuals were dissected separately in Ringer solution (sodium chloride (NaCl) 394  
135 mM, potassium chloride (KCl) 2 mM, calcium chloride (CaCl<sub>2</sub>) 2 mM, sodium bicarbonate  
136 (NaHCO<sub>3</sub>) 2 mM) and nerve cord was removed. To obtain a sufficient amount of protein, we  
137 made pools of five nerve cords from five different individuals of the same age. The five nerve  
138 cords were filed in 500  $\mu$ l of Lyse buffer 1X (Chaps detergent ((3-((3-cholamidopropyl)  
139 dimethylammonio)-1-propanesulfonate) 5 mM, citric acid (C<sub>6</sub>H<sub>8</sub>O<sub>7</sub>) 40 mM, sodium  
140 phosphate (Na<sub>3</sub>PO<sub>4</sub>) 40 mM, benzamidine (C<sub>7</sub>H<sub>8</sub>N<sub>2</sub>) 0.5 mM, and PMSF  
141 (phenylmethylsulfonyl (C<sub>7</sub>H<sub>7</sub>FO<sub>2</sub>S) 0.25 mM, pH 6) (Gary & Kindell, 2005), and then  
142 centrifuged at 15,000g at 4 °C for 30 min. The supernatant was taken and kept at -80°C until  
143 its utilization. The protein concentration was determined by the BCA (bicinchoninic acid  
144 assay) assay (Thermo Fisher Scientific, Waltham, MA, USA) and homogenized at 0.1 mg ml



145 <sup>-1</sup>. The  $\beta$ -galactosidase activity was measured as described by Gary & Kindell (2005). Briefly,  
146 100  $\mu$ l of extracted protein at the concentration of 0.1 mg ml<sup>-1</sup> were added to 100  $\mu$ l of  
147 reactive 4-methylumbelliferyl-D-galactopyranoside (MUG) solution in a 96-well microplate.  
148 The MUG reactive, in contact to  $\beta$ -galactosidase, leads by hydrolysis to the synthesis of 4-  
149 methylumbelliferone (4-MU), which is detectable using fluorescent measurements. Measures  
150 were performed by the multimode Mithrax microplate reader (LB940 HTS III, excitation  
151 filter: 120 nm, emission filter 460 nm; Berthold Technologies, Bad Wildbad, Germany) for  
152 120 min. Two technical replicates were measured for each nerve pool.

153

#### 154 *Measurement of immune cell parameters*

155 To test the impact of age on the immune cell parameters (i.e., density, viability, and size), we  
156 were able to undertake individual tests because of our previous experience. It was therefore  
157 not necessary to carry out pools of hemolymph unlike proteins or DNA to make the  
158 measurements. Sixty mature individuals were used: 30 young (i.e., one-year old, 15 males,  
159 and 15 females) and 30 old (three-year old, 15 males, and 15 females) individuals.

160 To study the impact of age on the immune parameters, a hole was bored in the middle  
161 of the sixth segment and 3  $\mu$ l of haemolymph were collected per individual with an  
162 eyedropper and deposited promptly in 15  $\mu$ l of anticoagulant solution (MAS-EDTA (EDTA  
163 (ethylenediaminetetraacetic (C<sub>10</sub>H<sub>16</sub>N<sub>2</sub>O<sub>8</sub>)) 9 mM, trisodium citrate (Na<sub>3</sub>C<sub>6</sub>H<sub>5</sub>O<sub>7</sub>) 27 mM,  
164 sodium chloride (NaCl) 336 mM, glucose (C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>) 115 mM, pH 7 (Rodriguez *et al.*, 1995)).

165 Then, 6  $\mu$ l of trypan blue at 0.4% (Invitrogen, Carlsbad, CA, USA) were added to color the  
166 dead cells. Thereafter, 10  $\mu$ l of this solution were deposited in a counting slide (Invitrogen  
167 Countess®; Thermo Fisher Scientific). The immune cell density, the immune cell viability,  
168 and the immune cell size were evaluated using an automated cell counter (Invitrogen  
169 Countess®).

170

#### 171 *Measurement of TERT gene expression*

172 The identification of the telomerase reverse transcriptase (TERT) gene was first performed  
173 from the *A. vulgare* genome (Chebbi *et al.*, 2019). In order to test whether this gene was  
174 present and preserved in crustaceans, phylogenetic analyses were undertaken upstream (see  
175 Supplementary material S1–S4). This gene has been found in crustacean transcriptomes and  
176 the topology of the TERT-gene tree follows the phylogenetic relationships between the  
177 involved species (Supplementary S3), suggesting a conserved role of the TERT gene.

178

#### 179 *Gene expression*

180 We tested the effect of age on the expression of TERT gene within four different age groups:  
181 1) four-month old, 2) one-year old, 3) two-year old, and 4) three-year old. Females and males  
182 were tested separately by pools of five individuals in one-, two-, and three-year-old groups  
183 and by pools of seven individuals in a four-month-old group as smaller individuals provide  
184 less biological material. All conditions required four replicates for each sex. A total of 176

185 individuals were used for this experiment. For each group we tested the expression level of  
186 the TERT gene in two different tissues: the nerve cord (somatic line) and gonads (germinal  
187 line).

188         Animals were washed by immersion for 30 sec in a 30% sodium hypochlorite solution  
189 (NaClO) followed by two 30-sec immersions in distilled water. Tissues were dissected in  
190 Ringer solution (sodium chloride 394 mM, potassium chloride (KCl) 2 mM, calcium chloride  
191 (CaCl<sub>2</sub>) 2 mM, sodium bicarbonate (NaHCO<sub>3</sub>) 2 mM) and deposited by pools of five units for  
192 each tissues on TRIzol reagent (Invitrogen) to extract RNA according to the manufacturer's  
193 protocol after a cell disintegration using a Vibra Cell 75,185 sonicator (amplitude of 30%).  
194 Total RNA was quantified by NanoDrop technology and stored at -80 °C until use. Reverse  
195 transcriptions (RT) were made from 500 ng of RNA previously extracted and using the  
196 SuperScript™ IV Reverse Transcriptase kit (Thermo Fisher Scientific) according to the  
197 manufacturer's instructions. Primers were designed using the identified gene: primer  
198 TERT\_F: 5'-AGGGAAAACGATGCACAACC-3' and primer TERT\_R: 5'-  
199 GTTCGCCAAATGTTCGCAAC- 3' (see Supplementary material S1). Quantitative RT-PCR  
200 was performed using 0.6 µl of each primer (10 µM), 2.4 µl of nuclease-free water, and 1.5 µl  
201 of cDNA template and the LightCycler LC480 system (Roche, Pleasanton, CA, USA ) as  
202 follows: 10 min at 95 °C, 45 cycles of 10 s at 95 °C, 10 s at 60 °C, and 20 s at 72 °C.  
203 Expression levels of target genes were normalized based on the expression level of two

204 reference genes previously established: the ribosomal protein L8 (RbL8) and the Elongation  
205 Factor 2 (EF2) (Chevalier *et al.*, 2011).

206

207 *Statistical analyses.*

208 All statistical analyses were performed using the R software v.3.5.2 (R. Core Team, 2018).

209 The  $\beta$ -galactosidase activity was analyzed with linear mixed effect models using the package

210 lme4 (Bates *et al.*, 2014). As two technical replicates were measured for each pool, the model

211 included the pools fitted as a random effect, age and sex and their two-way interaction as fixed

212 factors.

213 Concerning the immune parameters, linear models with Gaussian distribution were

214 fitted to analyze variation in the cell size and viability. A linear model of the cell number (log-

215 transformed; (Ives, 2015) was fitted for the cell density.

216 The level of TERT expression according to age in the two different tissues were

217 compared by a Kruskal-Wallis rank sum test in combination with Nemenyi's post hoc

218 multiple comparison test with the Tuckey correction using R package PMCMR (Pohlert,

219 2014).

220

## RESULTS

221  *$\beta$ -galactosidase activity*

222 The  $\beta$ -galactosidase activity was higher in old (i.e., two-year old) than in young (i.e., six-

223 month old) individuals ( $\chi^2_1 = 6.15$ ,  $P = 0.013$ ; Fig. 1). We also detected a higher  $\beta$ -

224 galactosidase activity in females than in males ( $\chi^2_1 = 7.26$ ,  $P = 0.007$ ; Fig. 1).

225

<Fig. 1>

226 *Immune cells parameters*

227 Cell size was higher in three-year-old than in one-year-old individuals ( $F_{1,58} = 8.54$ ,  $P =$   
228  $0.005$ ; Fig. 2A). Conversely, the cell density was higher in one-year-old than in three-year-old  
229 individuals ( $F_{1,58} = 4.33$ ,  $P = 0.01$ ; Fig. 2B). Concerning the immune cell viability, a  
230 statistically significant interaction occurred between age and sex, with a relatively lower  
231 immune cell viability in three-year-old females ( $F_{3,56} = 6.85$ ,  $P = 0.01$ ; Fig. 2C). No sex effect  
232 was detected on cell size ( $F_{2,57} = 0.76$ ,  $P = 0.38$ ; Fig. 2A) or cell density ( $F_{2,57} = 0.32$ ,  $P =$   
233  $0.57$ , Fig. 2B).

234

<Fig. 2>

235 *TERT gene expression*

236 The TERT gene expression decreased with increasing age in nerve cords ( $\chi^2_3 = 23.30$ ,  $P <$   
237  $0.001$ ; Fig. 3A). TERT expression was higher in four-month-old individuals compared to two-  
238 year-old and three-year-old individuals ( $P = 0.001$  in both cases) and in one-year-old  
239 individuals compared to three-year-old individuals ( $P = 0.038$ ), without any detectable sex  
240 effect ( $\chi^2_1 = 0.14$ ,  $P = 0.70$ ; Fig. 3A). In gonads, the TERT gene expression was much higher  
241 in females ( $\chi^2_1 = 17.81$ ,  $P < 0.001$ ; Fig. 3B) and tended to decrease with increasing age ( $\chi^2_3 =$   
242  $7.5$ ,  $P = 0.057$ ; Fig., 3B) as the TERT gene expression tended to be higher in four-month-old  
243 females compared to three-year-old females ( $P = 0.054$ ). A general tendency was also  
244 observed in males ( $\chi^2_1 = 7.34$ ,  $P = 0.061$ ; Fig. 3B), the TERT gene expression tending to be

245 higher in two-year-old individuals compared to one-year-old and three-year-old individuals ( $P$   
246 = 0.14 and  $P = 0.12$ , respectively; Fig. 3B).

247 <Fig. 3>

## 248 DISCUSSION

249 We tested several effective physiological biomarkers of vertebrate senescence to assess  
250 whether they could also be used in invertebrates such as the common woodlouse. Immune  
251 cells showed an increase in their size and a decrease in their density and viability with  
252 increasing age. The activity of the  $\beta$ -galactosidase enzyme in nerve cords increased. The  
253 TERT gene expression decreased with increasing age in nerve cords of males and females and  
254 in the gonads of females. In contrast, the TERT gene expression was very low in the male  
255 gonads to suggest a role on the cellular senescence status in this tissue. The difference  
256 regarding the expression of TERT in the nerve cords and gonads underlies the importance of  
257 organ choice to perform such an analysis.

258 Our study is in line with previous studies that had previously revealed the possibility  
259 of using vertebrate biomarkers in invertebrates (Hsieh & Hsu, 2011; Park *et al.*, 2011;  
260 Schumpert *et al.*, 2015). By testing a set of different physiological biomarkers of vertebrate  
261 senescence, often studied independently, our study supports both ideas that routinely used  
262 biomarkers in vertebrates can be adapted in invertebrates and that the senescence process is  
263 quasi-ubiquitous in the living world and can be expressed in a similar way in very different  
264 organisms.

265 Previous studies have shown that the probabilities to survive decrease with increasing  
266 age in *A. vulgare* (Paris & Pitelka, 1962). The cellular damages accumulated during the life of  
267 the isopod could be the cause of cell senescence and therefore the driving force behind  
268 actuarial senescence (Harman, 1956; Barja, 2000; Barja & Herrero, 2000; Finkel & Holbrook,  
269 2000). In *A. vulgare*, the 2- and 3-year-old individuals could have therefore accumulated more  
270 cellular damages during their lifetime, leading to the cellular senescence we report.

271 Our study also revealed a strong difference between sexes on the response of  
272 biomarkers to age changes. At a given age, females display higher  $\beta$ -galactosidase activity  
273 and lower immune cell viability than males, as if they age faster than males. Between-sex  
274 differences in lifespan have been reported in *A. vulgare* with a longer lifespan in males than in  
275 females (Geiser, 1934; Paris & Pitelka, 1962). Exact differences in actuarial senescence  
276 patterns (i.e., age-specific changes in survival probabilities) remain to be quantified in *A.*  
277 *vulgare* but such differences are quite common both in vertebrates and invertebrates (Tidière  
278 *et al.*, 2015; Marais *et al.*, 2018). One of the main hypotheses proposed to explain sex  
279 differences in longevity or senescence patterns relies on different resource allocation  
280 strategies between sexes (Vinogradov, 1998; Bonduriansky *et al.*, 2008). Females carry their  
281 offspring in their marsupium for one month, giving nutrients and protection, thus, they  
282 allocate more energy to reproduction than males that do not provide any parental care. The  
283 fact that the lifespan of *A. vulgare* is shorter in females (Paris & Pitelka, 1962) thus supports a  
284 role of differential sex allocation in this species. Moreover, the difference between males in

285 TERT expression in gonads also suggest a difference in sex allocation according both to age  
286 and sex. The increased in TERT expression in male gonad in two-years-old individuals should  
287 be the result of a terminal investment in reproduction for males: by increasing their TERT  
288 expression and thus potentially their telomerase activity they should provide a better fitness to  
289 their offspring. This allocation may be lost when males are too old (three-year old).

290 Sex differences in resource allocation strategies could also be driven by environmental  
291 conditions (Shertzer & Ellner, 2002). Our physiological biomarkers of vertebrate senescence  
292 revealed sex differences, and as supported in Depeux *et al.* (2019), they could constitute  
293 useful tools to identify other factors involved in variations in senescence patterns, such as  
294 environmental stressors. Moreover, if these biomarkers seem to predict better the  
295 physiological age than chronological age, notably in terms of survival and reproduction, they  
296 could correspond to biomarkers of senescence in the woodlouse (Baker & Sprott, 1988; Simm  
297 *et al.*, 2008; Sprott, 2010).

298 The physiological biomarkers of vertebrate senescence thus respond to age changes in  
299 *A. vulgare*, a species that represents a new invertebrate model of aging. The parameters that  
300 predict the chronological age of *A. vulgare* individuals might offer reliable biomarkers,  
301 especially if their measurements are related to both reproductive and survival prospects more  
302 than to the chronological age of individuals. The availability of its genome, the ease of its  
303 breeding, its particularity to continue growing during its lifespan, and its adaptations to



304 terrestrial life as well as the presence of cellular senescence on our senescence biomarkers  
305 make it a promising candidate to study senescence.

306

#### 307 SUPPLEMENTARY MATERIAL

308 Supplementary material is available at *Journal of Crustacean Biology* online.

309 S1. Phylogenetic analysis protocol of the TERT gene in crustaceans.

310 S2. TERT-gene alignment used for the phylogenetic analysis.

311 S3. TERT-gene tree following the phylogenetic relationships between the species involved.

312 S4. TERT-gene tree following the phylogenetic relationships between the species involved  
313 (Newick format).

314

#### 315 ACKNOWLEDGEMENTS

316 We would like to thank Sylvine Durand, Richard Cordaux, Isabelle Giraud, and Bouziane

317 Moumen for our constructive discussions as well as Marius Bredon, Carine Delaunay,

318 Maryline Raimond, and Alexandra Lafitte for technical assistance. The preprint of this work

319 has been deposited in BioRxiv (<https://doi.org/10.1101/583914>). This work was supported by

320 the 2015–2020 State-Region Planning Contract and European Regional Development Fund

321 and intramural funds from the Centre National de la Recherche Scientifique (CNRS) and the

322 University of Poitiers. JFL and JMG were supported by a grant from the Agence Nationale de

323 la Recherche (ANR-15-CE32-0002-01 to JFL). Our research also received funding from the

324 *Appel à projets de recherche collaborative inter-équipes 2016-2017* by the laboratory

325 Ecologie et Biologie des Interactions.

326

327

## REFERENCES

- 328 Baker, G.T. & Sprott, R.L. 1988. Biomarkers of aging. *Experimental Gerontology*, **23**: 223–  
329 239.
- 330 Barja, G. 2000. The flux of free radical attack through mitochondrial DNA is related to aging  
331 rate. *Aging*, **12**: 342–355.
- 332 Barja, G. & Herrero, A. 2000. Oxidative damage to mitochondrial DNA is inversely related to  
333 maximum life span in the heart and brain of mammals. *FASEB Journal*, **14**: 312–318.
- 334 Bates, D., Mächler, M., Bolker, B. & Walker, S. 2014. Fitting linear mixed-effects models  
335 using lme4. *Journal of Statistical Software*, **67**: 1–48.
- 336 Bernardez de Jesus, B. & Blasco, M.A. 2012. Assessing cell and organ senescence  
337 biomarkers. *Circulation Research*, **111**: 97–109.
- 338 Bonduriansky, R., Maklakov, A., Zajitschek, F. & Brooks, R. 2008. Sexual selection, sexual  
339 conflict and the evolution of ageing and life span. *Functional Ecology*, **22**: 443–453.
- 340 Campisi, J. & d’Adda di Fagagna, F. 2007. Cellular senescence: when bad things happen to  
341 good cells. *Nature Reviews. Molecular Cell Biology*, **8**: 729 [doi: 10.1038/nrm2233].
- 342 Cao, Y., Li, H., Deb, S. & Liu, J.-P. 2002. TERT regulates cell survival independent of  
343 telomerase enzymatic activity. *Oncogene*, **21**: 3130–3138.
- 344 Chebbi, M.A., Becking, T., Moumen, B., Giraud, I., Gilbert, C., Peccoud, J. & Cordaux R.  
345 2019. The genome of *Armadillidium vulgare* (Crustacea, Isopoda) provides insights into  
346 sex chromosome evolution in the context of cytoplasmic sex determination. *Molecular*  
347 *Biology and Evolution*, **36**: 727–741.
- 348 Chevalier, F., Herbinière-Gaboreau, J., Bertaux, J., Raimond, M., Morel, F., Bouchon, D.,  
349 Grève, P. & Braquart-Varnier, C. 2011. The immune cellular effectors of terrestrial isopod

350 *Armadillidium vulgare*: Meeting with their invaders, *Wolbachia*. *PLoS ONE*, **6**: e18531  
351 [doi: 10.1371/journal.pone.0018531].

352 Cheynel, L., Lemaître, J.-F., Gaillard, J.-M., Rey, B., Bourgoïn, G., Ferté, H., Jégo, M.,  
353 Débais, F., Pellerin, M., Jacob, L. & Gilot-Fromont, E. 2017. Immunosenescence patterns  
354 differ between populations but not between sexes in a long-lived mammal. *Scientific*  
355 *Reports* **7**: 13700 [doi: 10.1038/s41598-017-13686-5].

356 Chiu, C.-P. & Harley, C.B. 1997. Replicative senescence and cell immortality: The role of  
357 telomeres and telomerase. *Experimental Biology and Medicine*, **214**: 99–106.

358 Depeux, C., Samba-Louaka, A., Braquart-Varnier, C., Moreau, J., Lemaître, J.-F., Laverre, T.,  
359 Pauhac, H., Dechaume-Moncharmont, F.-X., Gaillard, J.-M. & Beltran-Bech, S. 2019.  
360 Impact of temperature and photoperiod impact on survival and biomarkers of senescence  
361 in common woodlouse. *bioRxiv* [doi: 10.1101/433011].

362 Dimri, G.P., Lee, X., Basile, G., Acosta, M., Scott, G., Roskelley, C., *et al.* 1995. A  
363 biomarker that identifies senescent human cells in culture and in aging skin in vivo.  
364 *Proceedings of the National Academy of Sciences of the United States of America*, **92**:  
365 9363–9367.

366 Finkel, T. & Holbrook, N.J. 2000. Oxidants, oxidative stress and the biology of ageing.  
367 *Nature*, **408**: 239–247.

368 Gary, R.K. & Kindell, S.M. 2005. Quantitative assay of senescence-associated  $\beta$ -  
369 galactosidase activity in mammalian cell extracts. *Analytical Biochemistry*, **343**: 329–334.

370 Geiser, S.W. 1934. Further observations on the sex-ratios of terrestrial isopods. *Field and*  
371 *Lab*, **3**: 7–10.

372 Gomes, N.M.V., Shay, J.W. & Wright, W.E. 2010. Telomere biology in Metazoa. *FEBS*  
373 *Letters* **584**: 3741–3751.

374 Harman, D. 1956. Aging: a theory based on free radical and radiation chemistry. *Journal of*  
375 *Gerontology*, **11**: 298–300.

376 Herbig, U., Ferreira, M., Condel, L., Carey, D. & Sedivy, J.M. 2006. Cellular senescence in  
377 aging primates. *Science*, **311**: 1257.

378 Hsieh, Y.-S. & Hsu, C.-Y. 2011. Honeybee trophocytes and fat cells as target cells for cellular  
379 senescence studies. *Experimental Gerontology*, **46**: 233–240.

380 Itahana, K., Campisi, J. & Dimri, G.P. 2007. Methods to detect biomarkers of cellular  
381 senescence: the senescence-associated  $\beta$ -galactosidase assay. *Biological Aging: Methods*  
382 *and Protocols*, **2007**: 21–31.

383 Ives, A.R. 2015. For testing the significance of regression coefficients, go ahead and log-  
384 transform count data. *Methods in Ecology and Evolution*, **6**: 828–835.

385 Kirkwood, T.B. 1977. Evolution of ageing. *Nature*, **270**: 301–304.

386 Latreille, P.A. 1804. Tableau méthodique des Insectes. *Nouveau Dictionnaire d'Histoire*  
387 *Naturelle*. Déterville, Paris.

388 Lawless, C., Wang, C., Jurk, D., Merz, A., Zglinicki, T. von & Passos, J.F. 2010. Quantitative  
389 assessment of markers for cell senescence. *Experimental Gerontology*, **45**: 772–778.

390 Liu, L., Bailey, S.M., Okuka, M., Muñoz, P., Li, C., Zhou, L., *et al.* 2007. Telomere  
391 lengthening early in development. *Nature Cell Biology*, **9**: 1436–1441.

392 Marais, G.A.B., Gaillard, J.-M., Vieira, C., Plotton, I., Sanlaville, D., Gueyffier, F. Wu, C.,  
393 Czerwiec, E., Sandler, L. Seyfang, A., Blasco, M.A. & Keefe, D.L. 2018. Sex gap in  
394 aging and longevity: can sex chromosomes play a role? *Biology of Sex Differences*, **9**:  
395 1436–1441.

396 Morgan, G. 2013. Telomerase regulation and the intimate relationship with aging. *Research*  
397 *and Reports in Biochemistry*, **2013**: 71–78.

398 Paris, O.H. & Pitelka, F.A. 1962. Population characteristics of the terrestrial isopod  
399 *Armadillidium vulgare* in California grassland. *Ecology*, **43**: 229–248.

400 Park, Y., Kim, Y. & Stanley, D. 2011. Cellular immunosenescence in adult male crickets,  
401 *Gryllus assimilis*. *Archives of Insect Biochemistry and Physiology*, **76**: 185–194.

402 Podlevsky, J.D., Bley, C.J., Omana, R.V., Qi, X. & Chen, J.J.-L. 2007. The telomerase  
403 database. *Nucleic Acids Research*, **36**: D339–D343.

404 Pohlert, T. 2014. The pairwise multiple comparison of mean ranks package (PMCMR). *R*  
405 *package* [<http://CRAN.R-project.org/package=PMCMR>].

406 R. Core Team. 2018. *R: A language and environment for statistical computing*. Foundation  
407 for Statistical Computing, Vienna.

408 Ram, J.L. & Costa, A.J. 2018. Invertebrates as model organisms for research on aging  
409 biology. In: *Conn's handbook of models for human aging* (J. Ram & P.M. Conn, eds.), pp.  
410 445–452. Academic Press, London.

411 Robertson, H.M. & Gordon, K.H.J. 2006. Canonical TTAGG-repeat telomeres and telomerase  
412 in the honey bee, *Apis mellifera*. *Genome Research*, **16**: 1345–1351.

413 Rodriguez, J., Boulo, V., Mialhe, E. & Bachere, E. 1995. Characterisation of shrimp  
414 haemocytes and plasma components by monoclonal antibodies. *Journal of Cell Science*,  
415 **108**: 1043–1050.

416 Schumpert, C., Nelson, J., Kim, E., Dudycha, J.L. & Patel, R.C. 2015. Telomerase activity  
417 and telomere length in *Daphnia*. *PLoS ONE*, **10**: e0127196 [doi:  
418 [org/10.1371/journal.pone.0127196](https://doi.org/10.1371/journal.pone.0127196)].

419 Shay, J.W. & Wright, W.E. 2005. Senescence and immortalization: role of telomeres and  
420 telomerase. *Carcinogenesis*, **26**: 867–874.

421 Shertzer, K.W. & Ellner, S.P. 2002. State-dependent energy allocation in variable  
422 environments: life history evolution of a rotifer. *Ecology*, **83**: 2181–2193.

- 423 Sicard, M., Chevalier, F., Vlechouver, M.D., Bouchon, D., Grève, P. & Braquart-Varnier, C.  
424 2010. Variations of immune parameters in terrestrial isopods: a matter of gender, aging  
425 and *Wolbachia*. *Naturwissenschaften*, **97**: 819–826.
- 426 Simm, A., Nass, N., Bartling, B., Hofmann, B., Silber, R.-E. & Navarrete Santos, A. 2008.  
427 Potential biomarkers of ageing. *Biological Chemistry*, **389**: 257–265.
- 428 Sprott, R.L. 2010. Biomarkers of aging and disease: Introduction and definitions.  
429 *Experimental Gerontology*, **45**: 2–4.
- 430 Stanley, D. 2012. Aging and immunosenescence in invertebrates. *Invertebrate Survival*  
431 *Journal*, **9**: 102–109.
- 432 Steel, C.G.H. 1980. Mechanisms of coordination between moulting and reproduction in  
433 terrestrial isopod crustacea. *Biological Bulletin*, **159**: 206–218.
- 434 Tidière, M., Gaillard, J.-M., Müller, D.W.H., Lackey, L.B., Gimenez, O., Clauss, M.  
435 & Lemaître, J.F. 2015. Does sexual selection shape sex differences in longevity and  
436 senescence patterns across vertebrates? A review and new insights from captive  
437 ruminants: *Evolution*, **69**: 3123–3140.
- 438 Vinogradov, A.E. 1998. Male reproductive strategy and decreased longevity. *Acta*  
439 *Biotheoretica*, **46**: 157–160.
- 440 Wang, C., Jurk, D., Maddick, M., Nelson, G., Martin-Ruiz, C. & von Zglinicki, T. 2009.  
441 DNA damage response and cellular senescence in tissues of aging mice. *Aging Cell*, **8**:  
442 311–323.

443

#### 444 **Figure captions**

445 **Figure 1.** Boxplot of  $\beta$ -galactosidase activity in *Armadillum vulgare* according to age and sex  
446 (F, females, M, males). The thick line represents the median, the box the interquartile range,  
447 and the whisker the most extreme data point within 1.5 of the interquartile range. The outliers

448 outside this range are shown as open circles. N = 24 pools of 5 individuals; \*  $P < 0.05$ , \*\*  
449  $P < 0.01$ .

450

451 **Figure 1.** Immune cell size (A), density (B), and viability (C) according to age and sex in  
452 *Armadillum vulgare* (F, females; M, males). The thick line represents the median, the box the  
453 interquartile range, and the whisker the most extreme data point within 1.5 of the interquartile  
454 range. The outliers outside this range are shown as open circles. N = 60 individuals: 15 one-  
455 year-old females, 15 one-year-old males, 15 three-years-old females, and 15 three-years-old  
456 males; \*  $P < 0.05$ , \*\*  $P < 0.01$ .

457

458 **Figure 2.** Relative expression level of TERT expression in nerve cords (A) and in gonads (B)  
459 in *Armadillum vulgare* (F, females; M, males). Expression of each gene was normalized based  
460 on the expression of ribosomal protein L8 (RbL8) and elongation factor 2 (EF2) as reference  
461 genes. The thick line represents the median, the box the interquartile range, and the whisker the  
462 most extreme data point within 1.5 the interquartile range. N = 176 individuals: 28 four-month-  
463 old females, 28 four-month-old males, 20 one-year-old females, 20 one-year-old males, 20 two-  
464 year-old females, 20 two-year-old males, 20 three-year-old females, 20 three-year-old males; #  
465  $P < 0.10$ , \*\*  $P < 0.01$

466

467

468