

TITLE:

BMI is negatively associated with telomere length; a collaborative cross-sectional meta-analysis of 87 observational studies

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RUNNING HEAD:

BMI and telomere length: a meta-analysis

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ABBREVIATIONS

BMI= body-mass index

TL= Telomere length

BP= base pairs

T/S ratio= Telomere to Single Copy Gene ratio

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Cockcroft

Wilkinson

Erusalimsky

McEniery

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1 **ABSTRACT**

2 **Background**

3 Even before the onset of age-related diseases obesity might be a contributing factor to the
4 cumulative burden of oxidative stress and chronic inflammation throughout the life course and
5 obesity may therefore contribute to accelerated shortening of telomeres.

6 Obese persons are expected to have shorter telomeres, but the association between body-mass index
7 (BMI) and leucocyte telomere length (TL) might differ across the lifespan, ethnicities and sexes.

8 **Objective**

9 A collaborative cross-sectional meta-analysis of observational studies was conducted to investigate
10 the associations between BMI and TL across life span.

11 **Design**

12 Eighty-seven distinct study samples were included in the meta-analysis capturing data from
13 146,114 individuals. Study-specific age and sex adjusted regression coefficients were combined
14 using a random-effects model in which absolute (base pairs [bp]) and relative (T/S ratio) TLs
15 were regressed against BMI. Stratified analysis was performed by three age categories (“young”
16 ≥ 18 and ≤ 60 years, “middle” > 60 and ≤ 75 , “old” > 75 years), sex, and ethnicity.

17 **Results**

18 Each unit increase in BMI corresponded to a -3.99 bp (95% C.I. -5.17, -2.81) difference in TL in
19 the total pooled sample; among young adults each unit increase in BMI corresponded to a -7.67
20 bp (95% C.I. -10.03, -5.31). Each unit increase in BMI corresponded to a -1.58×10^{-3} units T/S
21 ratio (-0.16%) (95% C.I. -2.14×10^{-3} , -1.01×10^{-3}) difference in age and sex adjusted relative
22 telomere length in the total pooled sample; among young adults each unit increase in BMI
23 corresponded to a -2.58×10^{-3} units T/S ratio (-0.26%) (95% C.I. -3.92×10^{-3} , -1.25×10^{-3}). The

24 associations were predominantly for the white pooled population. No sex differences were
25 observed.

26 **Conclusions**

27 Higher BMI is associated with shorter telomeres, especially in younger individuals. The presently
28 observed difference is not negligible. Meta-analyses of longitudinal studies evaluating change in
29 body weight alongside change in TL are warranted.

30

31 **KEY WORDS:**

32 BMI, telomere length, obesity, low grade inflammation, meta-analysis, observational studies

33 INTRODUCTION

34

35 Telomeres, the nucleoprotein structures at the ends of chromosomes, shorten with each cell
36 division in somatic cells (1). When telomere length reaches a critical value, cells either enter a
37 state of senescence or undergo apoptosis (2). Oxidative stress and chronic inflammation are
38 suggested to play a role in accelerated telomere attrition (3-5). Even before the onset of age-
39 related diseases obesity might be a contributing factor to the cumulative burden of oxidative
40 stress and chronic inflammation throughout the life course and obesity may therefore contribute
41 to accelerated shortening of telomeres.

42 Obesity is a growing health problem and worldwide its prevalence has more than doubled
43 since 1980 (6). In addition, the burden of diabetes and cardiovascular disease is partly attributable
44 to being overweight and obese (6). Tackling obesity might be a starting point to delay telomere
45 shortening and the onset of age-related diseases. Although obesity is associated with shorter
46 telomeres (7), studies in the elderly found no relation between telomere length and obesity and no
47 relation between telomere length and mortality (8, 9). We hypothesize that obese persons will
48 have shorter telomeres, compared to those of normal weight of the same chronological age, but
49 that the association between obesity and telomere length will differ across the lifespan.

50 Sex and ethnicity may influence the association between BMI and telomere length. On
51 average, women have longer telomeres than men (10-12). However, published results on sex
52 differences in association between BMI and telomere length are inconsistent (13-15). African
53 Americans and Native Americans have higher rates of obesity (16), and also racial differences in
54 telomere length have frequently been reported with adult African Americans having longer
55 telomeres than white individuals (17-21), but evidence is lacking whether the association between
56 BMI and telomere length differs between ethnicities.

57 Two recent meta-analyses reported the negative association between BMI and telomere length
58 on reported summary statistics in the literature, but could not examine sex differences nor the
59 influence of age and ethnicity (7, 22). To further evaluate whether BMI is associated with
60 telomere length, a large-scale collaborative cross-sectional meta-analysis was conducted across
61 observational studies that collected information on BMI and telomere length of adult individuals.
62 To avoid publication bias and maximize the data in the analyses, a consistent standardized
63 analysis plan across studies was used and principal investigators (PIs) of published studies were
64 contacted and asked to participate in the TELOMAAS group. As the relationship between
65 telomere length and BMI could be moderated by age, sex, and ethnicity we completed additional
66 analyses stratifying by these factors.

67

68

69 **METHODS**

70

71 **Search strategy**

72 We performed a broad literature search up till the end of November 10th 2017 using PUBMED,
73 EMBASE and the Cochrane database without restrictions. Numerous studies have measured BMI
74 and telomere length for purposes other than the association between telomere length and BMI as
75 an outcome. Therefore, the search was rather broad and not narrowed to telomere length or BMI.
76 Based on the existing relation between obesity, diabetes and cardiovascular diseases, and because
77 telomere length is related to aging we completed a search in which terms related to these
78 conditions were entered. Additionally, search items related to study design were entered. The
79 complete search criteria are listed in Supplemental Methods. Citation and reference tracking were
80 performed until no new studies were found. One author (MG) performed the literature search and

81 selected potentially relevant publications. Titles and abstracts of potentially relevant studies were
82 screened. In addition, when the abstract indicated that the article was reporting a study of diabetes
83 and/or cardiovascular disease, the full text was screened. No restrictions for study design or
84 language were applied.

85

86 **Eligibility criteria**

87 Studies were included if height and weight or BMI was collected. The corresponding author was
88 invited to participate in the meta-analysis and identified additional unpublished studies. PIs of
89 these unpublished studies were also invited to participate. Cohort studies with healthy individuals
90 at baseline were included and if the study design was a case-control study, only controls were
91 included in the meta-analysis. In compiling the database care was taken to exclude overlapping
92 study cohorts. The study sample (abbreviated as study) was taken as the unit for this meta-
93 analysis.

94

95 **Data extraction**

96 The detailed study protocol can be found in Supplemental Material: Study Protocol for
97 Participating PIs. The PI of each study completed a questionnaire and additional information was
98 extracted from the manuscript. The following data were collected: study name, study design
99 (cohort or case-control), sample size (cohort size or control group size), presence of the variables
100 age, sex, ethnicity (when at least 70% of the individuals of a sample was of a single ethnicity
101 (e.g. white, African American, Native American, Asian, Hispanic) the sample was classified as a
102 sample of a particular ethnicity, when no ethnicity constitutes 70% of the sample, the sample was
103 classified as a mixed sample), leucocyte telomere length, and BMI (kg/m^2), whether BMI was
104 measured or self-reported, white blood cell types from which DNA was extracted for telomere

105 measurements, method of telomere length measurement, and of DNA storage (Supplemental
106 Material: Study Protocol for Participating PIs). Absolute telomere length in base pairs (bp) was
107 distinguished from relative telomere length based on Telomere to Single Copy Gene ratio (T/S
108 ratio) (23). For example, a T/S ratio of 0.8 indicates a relative telomere length which is 80% of
109 the reference used (100%).

110 The PI was free to provide the de-identified raw data or to perform analyses and provide
111 summary statistics. If the PI provided raw data, MG conducted the linear regression analyses to
112 obtain the summary statistics. The linear regression analyses were a combination of one of the
113 following sex and age groups: men and women analyzed together and separately; all age groups
114 together and analyzed in three a priori chosen subgroups (“young” ≥ 18 and ≤ 60 years, “middle”
115 > 60 and ≤ 75 , “old” > 75 years). When appropriate, i.e. men and women analyzed together
116 and/or all age groups together, the analyses were corrected for sex and/or for age. If the T/S ratio
117 was used to estimate absolute telomere length, the PI was asked to provide new analyses with the
118 T/S ratio as the outcome. If the PI did not respond to this request absolute telomere length based
119 on the T/S ratio was used for analyses and included in the analysis. The regression coefficients
120 (beta estimates) and standard errors (SE) were then used in the meta-analyses. In the case of
121 longitudinal data one randomly selected telomere length measurement along with the
122 corresponding measurements (e.g. BMI, age) for that time point was used in the analysis. The
123 summary statistics thus included the results of twelve linear regression analyses with telomere
124 length (bp or T/S ratio) as the outcome and BMI as the independent variable.

125

126 **Assessment of small study effects**

127 To examine the potential presence of publication bias, visual inspection of funnel plots for
128 asymmetry was performed, followed by the Egger and Begg's linear regression test for small
129 study effects (24) and the Duval and Tweedie nonparametric "trim and fill" method (25).

130

131 **Statistical analysis**

132 Statistical pooling

133 The primary outcome of the meta-analysis was a pooled estimation of the difference in absolute
134 telomere length in bp or relative telomere length (T/S ratio) per unit increase in BMI. Study
135 specific regression coefficients (beta estimates) and standard errors (SE) were combined using
136 random-effects pooling in twelve meta-analyses. The assumption of a linear association between
137 BMI and telomere length was verified using the raw data provided by the PIs (Supplemental
138 Methods and Results).

139 Assessment of heterogeneity

140 Details are given in Supplemental Methods.

141 Statistical heterogeneity was estimated by Q and I^2 statistics (26, 27) for each of the twelve meta-analyses.

142 Low heterogeneity was indicated by I^2 up to 25%, medium heterogeneity by 25-50%, and high
143 heterogeneity by > 50% (27). To confirm the expected differences in association for age and sex, meta-
144 regression analysis was performed with age and sex as sources of heterogeneity. Age was therefore
145 categorized into three age categories ("young" ≥ 18 and ≤ 60 years, "middle" > 60 and ≤ 75 , "old" > 75
146 years) and also in two ("young" ≥ 18 and ≤ 60 years vs. "middle and old" > 60 years) age categories.

147 Also other potential sources of heterogeneity at study level were investigated by meta-regression
148 analysis (Supplemental Methods).

149 Sensitivity analyses

150 The following sensitivity analyses were performed: (1) outlier analyses by omitting one study at a
151 time, (2) omitting studies that used the relative telomere length to estimate the absolute telomere

152 length, (3) stratification by method of measurement of telomere length (Southern blot vs. q-PCR),
153 (4) using a cut off value of 90% for defining ethnicity. Details are given in Supplemental
154 Methods.

155 Statistical analyses were performed using Stata software version 12.0 (StataCorp, College
156 Station, TX, USA). All statistical tests were two-sided; p values < 0.05 were considered
157 statistically significant, except where otherwise specified.

158

159 **RESULTS**

160

161 **Search**

162 The search (PUBMED, EMBASE, and Cochrane) yielded 5,021 publications, from which 173
163 potentially relevant publications were identified. Some authors contributed to more than one
164 publication. As a result, 153 corresponding authors were identified and contacted. Sixty one
165 corresponding authors responded positively, 56 authors did not respond, six declined to
166 participate, and three authors did not have the requested data. Since one publication could include
167 multiple studies, the PIs (if not the same as corresponding authors) of the studies were contacted.
168 Eight additional studies were identified by the corresponding authors and the PIs of these
169 additional studies were contacted. We decided to exclude nine studies using techniques other than
170 Southern blots and q-PCR, because the regression coefficients (beta estimates) may not be
171 directly comparable.

172 In total, 87 unique studies were included in the meta-analyses. Twenty-nine studies measured
173 absolute telomere length and 58 studies used the T/S ratio. A flow chart of the inclusion
174 procedure is presented Figure 1.

175

176 **Description of studies**

177 The characteristics of the 87 studies included in this meta-analysis are provided in Table 1.

178 Absolute telomere lengths were obtained from 29 studies (3, 5, 13, 14, 17, 28-61) (and the
179 unpublished data of the HyperGEN study), of which four studies estimated absolute telomere
180 length based on the T/S ratio (19, 22, 62-68). In 17 studies Southern blots were used (3, 5, 13, 14,
181 17, 28-40, 44, 45, 48-52, 55, 56, 59, 61). Fifty-eight studies presented the relative telomere
182 length (T/S ratio) (4, 15, 69-133) (and the unpublished data of Utah Pedigree study). One PI
183 provided the data stratified by cell type (104). One PI provided longitudinal data (55).

184 The total pooled sample of this meta-analysis consisted of 146,114 adults (40% men), the
185 young pooled sample (≥ 18 and ≤ 60 years) consisted of 81,446 adults (51% men), the middle
186 aged pooled sample (> 60 and ≤ 75 years) consisted of 42,991 adults (41% men), and the old
187 pooled sample (> 75 years) consisted of 8,495 adults (65% men). Overall, the majority of the
188 adults were white (including Arab; 83%), followed by Asian (7%), African American (4%),
189 Hispanic, and Native Americans (both 3%). Six studies provided data of mixed study populations
190 stratified by ethnicity (17, 71, 72, 101, 132, 133) (and the unpublished data of the HyperGEN
191 study). Sixty-five studies consisted of $> 70\%$ white individuals (of which 60 had at least 90%
192 white individuals) (3, 5, 13-15, 17, 22, 28-34, 36-45, 48-59, 63-65, 68, 71-95, 98, 100-103, 105,
193 108-114, 116-118, 120-129, 131) (and unpublished data of the HyperGEN, and Utah Pedigree
194 studies). Four studies consisted only of African Americans (17, 71, 72, 101) (and the unpublished
195 data of the HyperGEN study); five only of Asians (35, 61, 100, 115, 130), one study only of
196 Native Americans (96, 97, 106, 107), and four studies comprised only Hispanics (60, 71, 72, 83,
197 84, 101). One study could not provide information about ethnicity (119).

198

199 **Assessment of small study effects**

200 Visual inspection of the funnel plots for absolute telomere length and for relative telomere length
201 yielded symmetric plots (Supplemental Figure 1 Funnel Plots). No publication bias was detected
202 using Egger's test or Begg's test. The "trim and fill" method added one hypothetical study to the
203 meta-analysis for absolute telomere length. However, the recalculated summary estimate did not
204 change and was still significant with their inclusion (beta= -3.99 (95% C.I. -5.16, -2.84); $p <$
205 0.001).

206

207 **Meta-analyses**

208 A summary of the beta estimates of the meta-analysis is shown in Table 2. An overall overview
209 of the meta-analysis is shown Supplemental Tables 2 and 3 in which the beta estimates of all
210 meta-analyses for absolute telomere length as the outcome (Supplemental Table 2) and of all
211 meta-analyses for relative telomere length as the outcome (Supplemental Table 3) are presented.
212 The accompanying forest plots are presented in the Supplemental Figures 2 and 3: Forest Plots.

213 Overall meta-analysis

214 Overall, sex- and age-adjusted absolute telomere length was significantly associated with
215 BMI. Each unit increase in BMI corresponded to a -3.99 bp (95% C.I. -5.17, -2.81; $I^2 = 0.6\%$)
216 difference in absolute telomere length (Table 2 and Figure 2 Forest plot). For example, an
217 estimated difference in telomere length between a normal weight individual with a BMI of 25
218 kg/m^2 and an obese individual with a BMI $> 30 \text{ kg/m}^2$ is (rounded) 20.0 bp, and, if a larger
219 difference is used (BMI 20 kg/m^2 vs. BMI $> 30 \text{ kg/m}^2$), 39.9 bp. The estimated difference
220 between normal weight and morbid obesity (BMI $> 40 \text{ kg/m}^2$) is at least 59.9 bp. Each unit
221 increase in BMI corresponded to a -1.58×10^{-3} units T/S ratio (-0.16%) (95% C.I. -2.14×10^{-3} , -
222 1.01×10^{-3} ; $I^2 = 41.1\%$) difference in age- and sex-adjusted relative telomere length. An estimated
223 difference in relative telomere length between normal weight and obesity is at least 7.9×10^{-3} units

224 (0.79%) T/S ratio (Table 2 and Figure 3 Forest plot) and between normal weight and morbid
225 obesity at least 23.7×10^{-3} units T/S ratio (2.37%). The associations between BMI and telomere
226 length did not differ significantly between men and women (see below).

227 *Age*

228 Analysis stratified by age category revealed that in young adults (≥ 18 and ≤ 60 years) a unit
229 increase of BMI corresponded to a -7.67 bp (95% C.I. -10.03 , -5.31 ; $I^2=31.2\%$) difference in
230 absolute telomere length (Table 2 and Figure 4).

231 In middle age adults (> 60 and ≤ 75) the overall association between BMI and telomere length
232 was -1.65 bp (95% C.I. -4.41 , 1.11 ; $I^2= 19.7$) per unit increase in BMI.

233 In old adults (> 75 years) the overall association between BMI and telomere length was -5.89
234 bp (95% C.I. -10.41 , -1.37 ; $I^2= 5.3$) per unit increase in BMI.

235 For relative telomere length, each unit increase in BMI corresponded to a -2.58×10^{-3} units T/S
236 ratio (-0.26%) (95% C.I. -3.92×10^{-3} , -1.25×10^{-3} ; $I^2= 80.0\%$) difference in relative telomere in
237 young adults (Table 2 and Figure 5).

238 In middle age adults, the overall association between BMI and relative telomere length was
239 found (-1.08×10^{-3} units T/S ratio (-0.1%) (95% C.I. -1.76×10^{-3} , -0.39×10^{-3} ; $I^2= 0.0$)) per unit
240 increase in BMI. For old adults no statistically significant association (0.20×10^{-3} units T/S ratio
241 (0.02%) (95% C.I. -1.40×10^{-3} , 1.80×10^{-3} ; $I^2= 0.0$)) was found between BMI and relative telomere
242 length.

243

244 Meta-regression and sources of heterogeneity

245 Age and ethnicity were a source of heterogeneity at study level in the meta-regression analyses.
246 Sex was never a source of heterogeneity (Supplemental Results). Therefore, all analyses were
247 stratified by ethnicity in addition to the originally planned analyses.

248 With absolute telomere length as the outcome, stratified analyses revealed that all estimates were
249 statistically significant for the white pooled sample, whereas none of the other were statistically
250 significant.

251 With relative telomere length as the outcome, stratified analyses revealed that the estimates
252 (except one estimate for the “old” pooled sample) were statistically significant for the white
253 pooled sample. In addition, the estimates of the overall and young pooled sample for the Native
254 Americans and the estimate of the young pooled Asian were statistically significant. None of the
255 estimates for the African American and Hispanic were statistically significant.

256

257 Sensitivity analysis

258 None of the sensitivity analyses resulted in substantial change of the summary estimate
259 (Supplemental Results).

260

261

262 **DISCUSSION**

263

264 This cross-sectional meta-analysis of 87 observational studies of adult pooled population
265 confirmed previous observations that BMI is negatively associated with telomere length. After
266 stratification for age and ethnicity the negative association between BMI and telomere length
267 appeared to be stronger in the “young adult” pooled population (age < 60 years) and in the white
268 pooled population. Differences between men and women could not be confirmed.

269 Based on our estimates for absolute telomere length, a ~5-unit increase in BMI appears to be
270 equivalent to a difference in telomere length of ~20-38 bp or $\sim 7.9 \times 10^{-3}$ - 13×10^{-3} units T/S ratio
271 (0.79-1.3%). Compared to an estimated average yearly decrease (i.e., ~25 bp/year or ~0.01 T/S

272 ratio/per year) of leucocyte telomere length in adults based on cross-sectional data (3, 32, 134-
273 136), the association is not negligible. In addition, compared to accelerated attrition (i.e. 3-5
274 bp/year) due to smoking one pack of cigarettes daily (94, 137) the association reported in this
275 meta-analysis appears relevant and could exceed or at least be in line with the effect of smoking.
276 A major disadvantage of cross-sectional analysis is the impossibility to infer causation. However,
277 the robust association between higher BMI and lower telomere length found in this meta-analysis
278 highlights another potential area of concern for the obesity epidemic.

279 Since obesity, and more specifically an increase in leptin and a decrease in adiponectin have
280 been associated with low-grade inflammation and oxidative stress (138), the observed negative
281 association between BMI and leucocyte telomere length may be due in part to the chronic
282 inflammatory state associated with higher leptin. Recently, a negative association was observed
283 between age-related relative telomere length and serum leptin in seven cohorts of 11,448
284 participants, which remained significant after adjustment for BMI (103). These data suggest that
285 beyond a high BMI, inflammatory conditions, mediated via increase in leptin, likely contribute to
286 telomere shortening. Since a longitudinal study found a tendency for a higher reduction in BMI
287 over a 5 year period in participants who initially had the longest telomeres (98), it is also
288 suggested that a common factor, such as chronic inflammation, is associated both with leptin
289 resistance and with telomere length.

290 The negative association between BMI and telomere length was most apparent in the younger
291 pooled population, in which a stronger association was found for absolute and relative telomere
292 length compared to the other age groups, which highlights the urgency to address the obesity
293 epidemic. Three possible explanations could explain this observation. First, BMI could be a
294 better marker for adiposity in younger individuals aged less than 60 years compared to older
295 individuals (22). Above 65 years of age BMI may less consistently reflect obesity because of

296 potential loss of muscle and bone mass and height (22). The fact that older men weigh less than
297 the middle-aged men at a given height is attributed to older men having less lean tissue, and a
298 lower BMI can actually reflect a higher fat mass (139). Second, selective survival might be one
299 of the causes for the stronger association found in the younger age category. As Manson et al.
300 state “obesity in one’s 40s contributes to the onset of type 2 diabetes in one’s 50s, which leads to
301 myocardial infarction (MI) in one’s 60s, heart failure and weight loss due to debilitation and
302 muscle wasting at age 70, and death at age 75” (140). People who suffered from age-related
303 diseases may have died and those who survived may therefore differ from those who died (141).
304 Third, older people are more likely to have chronic diseases that lead to weight loss and people
305 with chronic diseases are probably less likely to participate in studies (140).

306 The magnitude of the negative association between BMI and leucocyte telomere length was
307 found largest in the white pooled population. One possible explanation could be that telomere
308 length differs between different cell types (142) and that leucocyte cell subpopulations (143)
309 differ between whites and African Americans. However, since only four samples consisted of
310 African Americans, more research is required to resolve whether this observation explains the
311 racial differences in association between telomere length and BMI for white and African
312 Americans. Second, it was recently reported that the estimation of visceral adipose tissue, the
313 most relevant tissue that determines the risk to develop chronic metabolic diseases, was different
314 in white and African American adults (144). At higher BMI or increased waist circumference
315 (WC), white adults had higher levels of visceral adipose tissue than African American adults
316 (138). Since the presence of leptin resistance or markers of inflammation were not included in
317 these studies, it remains to be determined whether the relation between BMI, leptin resistance,
318 inflammation and telomere attrition is different for African Americans from whites. In addition,
319 the one study sample consisting of 3,256 mostly “young” Native Americans showed similar

320 results as found for the white study population (107). The majority of this study sample was
321 centrally obese, and leucocyte telomere length was negatively correlated with C-reactive protein.

322 One of the main strengths of this study is that we did not rely on publications. Instead we
323 contacted PIs, which in turn have pointed us towards important studies we may have missed, to
324 obtain the data used in the meta-analysis. Also we incorporated several potential confounders
325 (age and sex) and sources of heterogeneity (ethnicity and study design). The response rate of the
326 originally contacted PIs was 55% with a final count of 87 unique studies and over 140,000
327 individuals. Although it is impossible to make a direct comparison with the unpublished beta
328 estimates of the non-responders, we assume, also based on the absence of significant publication
329 bias, that the studies in this meta-analysis are a random selection of all studies conducted and that
330 we present a valid representation of the association between BMI and telomere length. Because
331 of the large variation in adult telomere length, as well as biological and measurement variation
332 (q-PCR), large sample sizes are needed, especially in cross-sectional studies, to detect modest
333 effects (30). In this meta-analysis we were able to detect a statistically significant association of -
334 3.99 bp or -1.58×10^{-3} units T/S ratio (0.16%) per unit increase BMI.

335 Two recently meta-analyses, which relied on published data, also reported negative
336 associations between BMI and telomere length. The first smaller scale meta-analysis reported
337 negative regression coefficients on the association between telomere length and BMI (22), of
338 which five studies were also included in this meta-analysis (13, 14, 19, 82, 145). The larger scale
339 meta-analysis reported a weak negative correlation, a standardized mean differences of 0.84
340 (95%C.I. 0.22, 1.46) between obese individuals and normal weight individuals and an odds ratio
341 of 1.39 (95%C.I. 1.15, 1.69) (7). Of the 45 samples that met our inclusion criteria 33 collaborated
342 in our analysis. This shows that the results between the meta-analyses are consistent and very
343 robust. Although age and ethnicity were taken into account, it should be mentioned that the older

344 study sample was relatively small (~ 8,400 individuals), and that the majority of the individuals
345 were white (83%). Unfortunately, we did not include smoking in the meta-analysis. Smoking is
346 generally associated with a lower BMI and shorter telomere length (3, 137, 140), which may have
347 caused an underestimation of the inverse association between BMI and telomere length. Also
348 inflammation was not directly measured. We were also not able to measure telomere attrition as
349 we did not incorporate longitudinal data and reverse causation cannot be excluded. However,
350 there are very few large scale studies with repeated measures of telomere length.

351 The lengths of telomeres at different ages are highly correlated, and it has been suggested that
352 most of the variation in leucocyte telomere length in adults is a result of telomere length at birth
353 and that therefore the impact of environmental and lifestyle factors is rather small (137, 146).
354 Benetos et al. described that ranking of individuals into deciles according to their telomere length
355 barely changes across adult life. They showed that around half of the individuals stay in the same
356 decile, whereas 17.9% showed a downwards shift and 20.7% showed an upward shift of one
357 decile (137). Our meta-analysis shows that five units increase in BMI corresponds to ~20 bp or
358 even ~38 bp change in the young pooled population, which is equivalent to at least a yearly
359 decrease irrespective of ranking. This could be an additional argument to tackle the obesity
360 epidemic.

361 In summary, a higher BMI is associated with shorter telomeres, especially in the younger
362 pooled population. Although no causal inference can be drawn and residual confounding is
363 always a possibility, the results were robust across a variety of potential confounders. Given this,
364 we could possibly infer that tackling the obesity epidemic might be a starting point to delay
365 telomere shortening and the onset of age-related diseases, thereby contributing to a decreased
366 biological aging of the population. However, meta-analyses of longitudinal studies that can
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368

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526

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528 M.G. wrote the manuscript, researched data and contributed to design and discussion had
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538 **CONFLICT OF INTEREST**

539 The authors declare that they have no conflict of interest.

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Table 1 Characteristics of included Study samples

ref	Study Name	all n	men n	women n	18 - 60 yrs n	> 60 - 75 yrs n	> 75 yrs n	Cell type	telomere length measure	DNA	BMI	data provided	design	Ethnicity (proportion) White/ Black/ Asian/ Hispanic/ Native American
Absolute telomere length measured in base pairs (bp)														
(3, 28-31)	TwinsUK	3236	286	2950	2630	574	32	Leucocytes	Southern Blot RF	stored	measured	summary	cohort	1 / 0 / 0 / 0 / 0
(17, 32-34)	Bogalusa	635	635	0	635	0	0	Leucocytes	Southern Blot RF	unknown	measured	raw data	cohort	0.71 / 0.29 / 0 / 0 / 0
(147)	India CURES Study	40	20	20	37	3	0	Leucocytes	Southern Blot RF	stored	measured	raw data	case-control	0 / 0 / 1 / 0 / 0
(36)	Campania	528	251	277	320	100	108	Leucocytes	Southern Blot RF	stored	measured	raw data	cohort	1 / 0 / 0 / 0 / 0
(14, 37-39)	Asklepios	2509	1218	1291	2509	0	0	Leucocytes	Southern Blot RF	stored	measured	raw data	cohort	1 / 0 / 0 / 0 / 0
(5, 13, 40)	Framingham	1146	557	589	658	444	44	Leucocytes	Southern Blot RF	NA	measured	summary	cohort	1 / 0 / 0 / 0 / 0
(42)	COPD	178	89	89	113	60	5	Leucocytes	Real Time PCR	NA	measured	raw data	case-control	1 / 0 / 0 / 0 / 0
(43)	Crete	109	109	0	0	0	109	Leucocytes	Real Time PCR	NA	measured	raw data	cohort	1 / 0 / 0 / 0 / 0
(41)	Zutphen	189	189	0	0	68	121	Leucocytes	Real Time PCR	NA	measured	raw data	cohort	1 / 0 / 0 / 0 / 0
(17)	Family Heart African American	625	216	409	459	148	18	Leucocytes	Southern Blot RF	NA	measured	summary	cohort	0 / 1 / 0 / 0 / 0
(17)	Family Heart White	2603	1170	1433	1419	997	187	Leucocytes	Southern Blot RF	NA	measured	summary	cohort	1 / 0 / 0 / 0 / 0
Not publ	HyperGEN African American	224	108	116	172	51	1	Leucocytes	Southern Blot RF	NA	measured	summary	cohort	0 / 1 / 0 / 0 / 0
Not publ	HyperGEN White	1240	612	628	799	426	15	Leucocytes	Southern Blot RF	NA	measured	summary	cohort	1 / 0 / 0 / 0 / 0
(44, 45)	LSADT	525	171	354	0	82	443	Leucocytes	Southern Blot RF	NA	measured	summary	cohort	1 / 0 / 0 / 0 / 0
(46, 47)	Heart and Soul	954	777	177	274	451	229	Leucocytes	Real Time PCR	unknown	measured	summary	cohort	0.60 / 0.16 / 0.12 / 0.09 / 0.03
(57, 58)	Lothian	1057	530	527	0	1057	0	Leucocytes	Real Time PCR	stored	measured	summary	cohort	1 / 0 / 0 / 0 / 0
(48, 49)	WarTwins	639	639	0	0	86	553	Leucocytes	Southern Blot RF	stored Buffy coat	reported	raw data	cohort	1 / 0 / 0 / 0 / 0
(55)	Jerusalem LRC	620	413	207	620	0	0	Leucocytes	Southern Blot RF	stored Buffy coat	measured	summary	cohort	1 / 0 / 0 / 0 / 0
(56)	Jerusalem Palestinians	939	498	441	336	306	0	Leucocytes	Southern Blot RF	stored	measured	summary	cross-sectional	1 / 0 / 0 / 0 / 0
(50-52)	Helsinki Businessmen Study (HBS)	487	487	0	0	250	237	Leucocytes	Southern Blot RF	stored	reported	raw data	cohort	1 / 0 / 0 / 0 / 0
(53)	Copenhagen General Population Study	45069	20422	24647	26040	14525	4504	Leucocytes	Real Time PCR	stored	measured	summary	cohort	1 / 0 / 0 / 0 / 0
(54)	SOLVABLE	152	0	152	136	16	0	PBMC	Real Time PCR	stored	measured	summary	case-control	0.70 / 0.22 / 0.03 / 0.05 / 0
(59)	ZTL2008	25	17	8	24	1	0	PBMC	Southern Blot RF	stored	measured	raw data	cohort	1 / 0 / 0 / 0 / 0
(60)	Venado Tuerto 2	401	0	401	325	63	0	Leucocytes	Real Time PCR	stored	measured	raw data	cohort	0 / 0 / 0 / 1 / 0
(61)	NHSC	672	333	339	534	138	0	Leucocytes	Southern Blot RF	stored	measured	summary	cohort	0 / 0 / 1 / 0 / 0

Absolute telomere length estimated from Telomere to Single Copy Gene ratio (T/S ratio)

(19, 62, 66, 67)	South Carolina	323	145	178	305	18	0	Leucocytes	Real Time PCR	unknown	measured	summary	cohort	0.57 / 0.41 / 0.01 / 0.01 / 0
(63, 64, 68)	Bruneck	800	395	405	363	315	122	Leucocytes	Real Time PCR	stored	measured	summary	cohort	1 / 0 / 0 / 0 / 0
(65)	RPCI	174	0	174	111	47	16	Leucocytes	Real Time PCR	stored	reported	raw data	case-control	0.93 / 0.05 / 0 / 0 / 0.02
(22)	ESTHER	3559	1583	1976	1432	2127	0	Leucocytes	Real Time PCR	stored	measured	summary	cohort	1* / 0 / 0 / 0 / 0

Telomere length based on Telomere to Single Copy Gene ratio (T/S ratio)

(15)	MONICA	511	183	328	419	92	0	Leucocytes	Real Time PCR	NA	measured	raw data	cohort	1 / 0 / 0 / 0 / 0
(15)	MDCC	476	330	146	199	277	0	granulocytes	Real Time PCR	NA	measured	raw data	cohort	1 / 0 / 0 / 0 / 0
Not publ	Utah Pedigree Study	964	493	471	725	183	56	Leucocytes	Real Time PCR	NA	measured	summary	cohort	1 / 0 / 0 / 0 / 0
(71, 72)	MESA White	182	89	93	80	80	22	Leucocytes	Real Time PCR	stored	measured	summary	cohort	1 / 0 / 0 / 0 / 0
(71, 72)	MESA African American	278	125	153	141	109	28	Leucocytes	Real Time PCR	stored	measured	summary	cohort	0 / 1 / 0 / 0 / 0
(71, 72)	MESA Hispanic	518	252	266	245	231	42	Leucocytes	Real Time PCR	stored	measured	summary	cohort	0 / 0 / 0 / 1 / 0
(73)	EARSII	395	395	0	395	0	0	Leucocytes	Real Time PCR	unknown	measured	raw data	case-control	1 / 0 / 0 / 0 / 0
(74)	UCLA MacArthur	233	115	118	0	144	89	Leucocytes	Real Time PCR	NA	reported	summary	cohort	1 / 0 / 0 / 0 / 0
(75)	Ashkenazi	359	191	168	50	179	130	Leucocytes	Real Time PCR	stored	measured	raw data	cohort	1 / 0 / 0 / 0 / 0
(76)	Warsaw	714	246	468	235	411	68	Leucocytes	Real Time PCR	stored	measured	raw data	case-control	1 / 0 / 0 / 0 / 0
(77)	Finland Health 2000 cohort	938	350	588	754	137	47	Leucocytes	Real Time PCR	stored	unknown	summary	cohort	1 / 0 / 0 / 0 / 0
(78)	Sister Study I (Vanguard sample)	644	0	644	475	169	0	Leucocytes	Real Time PCR	stored	measured	summary	cohort	0.83 / 0.07 / 0.02 / 0.02 / 0.05
(114)	Sister Study II (Genetic Study subcohort)	734	0	734	548	186	0	Leucocytes	Real Time PCR	stored	measured	summary	cohort	0.92 / 0.04 / 0 / 0.02 / 0.02
(79)	CAS	183	96	87	112	53	18	Leucocytes	Real Time PCR	stored	measured	raw data	case-control	1 / 0 / 0 / 0 / 0
(80)	PATH 40	331	151	180	331	0	0	Leucocytes	Real Time PCR	stored	reported	raw data	cohort	0.95 / 0 / 0.03 / 0 / 0.02
(80)	PATH 60	294	157	137	0	294		Leucocytes	Real Time PCR	stored	reported	raw data	cohort	0.97 / 0 / 0.02 / 0 / 0.01
(81)	Italy alcohol controls	258	258	0	255	3	0	Leucocytes	Real Time PCR	stored	reported	raw data	case-control	1 / 0 / 0 / 0 / 0
(82)	Fels Longitudinal Study	257	116	104	196	54	7	Leucocytes	Real Time PCR	stored	measured	summary	cohort	1 / 0 / 0 / 0 / 0
(83, 84)	Ecran	188	38	150	121	41	26	PBMC	Real Time PCR	NA	measured	raw data	cohort	0 / 0 / 0 / 1 / 0
(85, 86)	Heart Scan Study	434	206	228	169	259	0	Leucocytes	Real Time PCR	stored	measured	summary	cohort	1 / 0 / 0 / 0 / 0
(87, 88)	Boiler workers	104	104	0	97	7	0	Leucocytes	Real Time PCR	stored	measured	summary	cohort	0.85 / 0.09 / 0.02 / 0.03
(89, 90)	Mayo	2886	1470	1416	2001	709	176	Leucocytes	Real Time PCR	NA	measured	raw data	case-control	0.98 / 0 / 0.01 / 0.01 / 0
(91, 92, 105, 108-111)	HBCS	1962	911	1051	703	1259	0	Leucocytes	Real Time PCR	NA	measured	raw data	cohort	1 / 0 / 0 / 0 / 0
(93-95)	PREVEND	7991	3994	3997	6094	1897	0	Leucocytes	Real Time PCR	NA	measured	summary	cohort	0.96 / 0.01 / 0.02 / 0 / 0.01

(96, 97, 106, 107)	Strong Heart Family Study	3256	1315	1941	2834	340	82	Leucocytes	Real Time PCR	NA	measured	summary	cohort	0/0/0/0/1
(98)	PREDIMED-NAVARRA	521	236	285	81	401	38	Leucocytes	Real Time PCR	stored	measured	summary	RCT	1/0/0/0/0
(99)	NHANES	7349	3542	3807	5034	1564	751	Leucocytes	Real Time PCR	stored	measured	summary	cohort	0.52/0.18/0/0.30/0
(100)	SWHS	2912	0	2912	1812	1100	0	Leucocytes	Real Time PCR	NA	measured	summary	cohort	0/0/1/0/0
(101)	DHS white	1073	493	580	821	245	7	Leucocytes	Real Time PCR	stored	measured	summary	cohort	1/0/0/0/0
(101)	DHS black	1667	606	1061	1348	317	17	Leucocytes	Real Time PCR	stored	measured	summary	cohort	0/1/0/0/0
(101)	DHS hispanic	464	194	270	412	51	1	Leucocytes	Real Time PCR	stored	measured	summary	cohort case-control	0/0/0/1/0
(102)	DALS	734	401	333	268	366	100	Leucocytes	Real Time PCR	stored	measured	summary	case-control	0.96/0/0/0.03/0
(105, 113)	FinnTwin study Former Athletes Study	2096	1101	995	1589	385	122	Leucocytes	Real Time PCR	NA	measured	summary	cohort	1/0/0/0/0
(112)		586	586	0	1	376	209	Leucocytes	Real Time PCR	stored	measured	summary	cohort case-control	1/0/0/0/0
(104)	USKCS whole blood	765	442	323	395	320	50	Leucocytes	Real Time PCR	stored	measured	summary	case-control	0.61/0.39/0/0/0
(104)	USKCS buffy coat Erasmus Rucphen Study	126	70	56	87	36	3	Leucocytes	Real Time PCR	stored	measured	summary	case-control	0.66/0.34/0/0/0
(103)		2449	1082	1367	1900	499	50	Leucocytes	Real Time PCR	stored	measured	summary	case-control	1/0/0/0/0
	Rotterdam Study	2231	944	1287	556	1272	404	Leucocytes	Real Time PCR	stored	measured	summary	control	1/0/0/0/0
(103)	KORA F3	3113	1509	1604	1768	1051	294	Leucocytes	Real Time PCR	stored	measured	summary	cohort	1/0/0/0/0
(103)	KORA F4	3014	1457	1557	1824	943	247	Leucocytes	Real Time PCR	stored	measured	summary	cohort case-control	1/0/0/0/0
(148)	CAVASIC	315	315		155	160	0	Leucocytes	Real Time PCR	stored	measured	summary	control	1/0/0/0/0
(103, 149)	SAPHIR	1681	1055	626	1586	95	0	Leucocytes	Real Time PCR	stored	measured	summary	cohort	1/0/0/0/0
(115)	Cebu Longitudinal Health and Nutrition Survey (CLHNS) Nutrition and Exercise for Women (NEW) Study	3467	893	2574	3380	87	0	Leucocytes	Real Time PCR	stored	measured	summary	cohort	0/0/1/0/0
(116)		437	0	437	304	131	2	Leucocytes	Real Time PCR	stored	measured	raw data	cohort	0.85/0.08/0.02/0.03/0.02
(117)	NESDO	495	173	322	17	354	124	Leucocytes	Real Time PCR	stored	measured	summary	cohort	0.95/0.01/0.04/0/0
(118)	NESDA	2936	986	1950	2749	187	0	Leucocytes	Real Time PCR	stored	measured	summary	cohort case-control	0.97/0.02/0.01/0/0
(119)	PRT	43	0	43	43	0	0	Leucocytes	Real Time PCR	stored	measured	raw data	control	**
(120, 121)	UMS	67	67	0	65	1	1	Leucocytes	Real Time PCR	stored	measured	raw data	cohort	1/0/0/0/0
(122)	YMCA	1126	1126	0	1126	0	0	Leucocytes	Real Time PCR	stored	measured	raw data	cohort	1/0/0/0/0
(123-125)	BASE II	1894	946	948	441	1409	44	Leucocytes	Real Time PCR	stored	measured	summary	cohort	1**/0/0/0/0
(126)	Kyiv	82	20	62	36	33	13	Leucocytes	Real Time PCR	stored	measured	raw data	cohort	1/0/0/0/0
(127)	GAHR2	133	53	80	128	5	0	Leucocytes	Real Time PCR	stored	measured	raw data	cohort	0.93/0.01/0.01/0.05/0
(128)	UMED telomere trial	28	7	21	26	2	0	PBMC	Real Time PCR	Not stored	measured	raw data	cohort	1/0/0/0/0

(129)	ACCT	904	454	450	469	361	74	Leucocytes	Real Time PCR	stored	measured	summary	cohort	0.98 / 0.01 / 0.01 / 0 / 0
(130)	RPE	975	466	509	975	0	0	Leucocytes	Real Time PCR	stored	reported	raw data	cohort	0 / 0 / 1 / 0 / 0
(131)	Sweden Mindfulness Study	172	21	151	167	5	0	Leucocytes	Real Time PCR	stored	reported	raw data	RCT	1 / 0 / 0 / 0 / 0
(132)	EpiDREAM	4205	1565	2640	3363	770	72	Leucocytes	Real Time PCR	stored	reported	summary		0.61 / 0.08 / 0.21 / 0.09 / 0
(133)	INTERHEART	3306	2601	705	2092	997	217	Leucocytes	Real Time PCR	stored	reported	summary	case-control	0.27 / 0.08 / 0.44 / 0.21 / 0

NA=not available; data provided by PI: summary=summary statistics

*= not measured, but all Eurasian descent. ** not measured

Table 2 Summary of the beta estimates (regression coefficients) from the meta-analysis of the association between BMI and telomere length

	All together (total pooled sample, adjusted for age)				“Young” pooled sample (age ≥18 and ≤ 60 years)				“Middle ” pooled sample (60 < age ≤ 75 years)				“Old” pooled sample (age > 75 years)			
	N	estimate	95%C.I.	I ² (%)	N	estimate	95%C.I.	I ² (%)	N	estimate	95%C.I.	I ² (%)	N	estimate	95%C.I.	I ² (%)
Absolute telomere length (base pairs (bp)) as outcome																
Overall	29	-3.99	-5.17, -2.81	0.6	23	-7.67	-10.03, -5.31	31.2	22	-1.65	-4.41, 1.11	19.7	16	-5.89	-10.41, -1.37	5.3
White	21	-4.36	-5.87, -2.85	11.3	15	-8.77	-10.42, -7.12	0.0	15	-2.06	-4.06, -0.06	0.0	13	-6.97	-12.29, -1.64	15.4
African Am.	2	0.86	-4.75, 6.46	0.0	2	0.960	-5.51, 7.43	1.2	2	4.36	-7.25, 15.97	0.0	1	74.70	-76.02, 225.42	
Hispanic	1	5.97	-149.97, 161.91		1	-45.64	-216.24, 124.95		1	212.68	-169.98, 595.34		1			
Asian	2	-7.65	-27.20, 11.91	0.0	2	-48.70	-130.38, 32.99	10.8	1	90.00	27.28, 152.72		0			
Native Am.	0				0				0				0			
Relative telomere length (Telomere to Single Copy Gene ratio (T/S ratio*10⁻³)) as outcome																
Overall	58	-1.58	-2.14, -1.01	32.7	55	-2.58	-3.92, -1.25	80.0	50	-1.08	-1.76, -0.39	0.0	29	0.20	-1.40, 1.80	0.0
white	43	-1.87	-2.44, -1.31	8.1	40	-2.80	-4.77, -0.82	84.1	37	-1.65	-2.45, -0.86	0.0	21	-0.28	-2.29, 1.73	0.0
African Am.	2	5.66	-6.60, 17.92	80.0	2	5.21	-5.67, 16.08	68.7	2	0.08	-6.20, 6.36	0.0	1	-0.74	-12.62, 11.14	
Hispanic	3	2.53	-5.18, 10.25	17.7	3	-0.42	-4.19, 3.34	0.0	3	2.31	-2.35, 6.97	0.0	2	27.29	-40.32, 94.61	77.7
Asian	3	-1.11	-4.23, 2.02	60.4	3	-4.50	-5.75, -3.25	0.0	2	2.18	-2.90, 7.27	0.0	0			
Native Am.	1	-2.64	-3.60, -1.68		1	-4.14	-5.28, -3.00		1	2.23	-1.00, 5.46		1	4.68	-2.35, 11.71	

N= number of studies; Am. = American; The unit of the **estimates and 95%C.I. of T/S ratio is 10⁻³**; Random effect model was used and adjusted for age if analyzed all together (the total study population) and adjusted for sex; Statistical heterogeneity was estimated by Q and I² statistics for each of the twelve meta-analyses; Bold: p< 0.05 or I²>50%

LEGEND OF FIGURES

Figure 1

Inclusion flow chart

Figure 2

Title

Forest plot of the beta estimates (regression coefficients) from the meta-analysis of the association between BMI and absolute telomere length (bp) as outcome in the total pooled population

Legend

ES= estimate; Random effect model was used and adjusted for age and sex; Statistical heterogeneity was estimated by Q and I^2 statistics for each of the twelve meta-analyses; The shaded boxes indicate the inverse variance weighing of each estimate and the size of the box indicates the weight. In case no shaded box is visible, weight is very small.

Figure 3

Title

Forest plot of the beta estimates (regression coefficients) from the meta-analysis of the association between BMI and relative telomere length (T/S ratio) (B) as outcome in the total pooled population

Legend

The **unit of the estimates and 95% C.I. is 10^{-3}** ; ES= estimate; Random effect model was used and adjusted for age and sex; Statistical heterogeneity was estimated by Q and I^2 statistics for each of the twelve meta-analyses; The shaded boxes indicate the inverse variance weighing of each estimate and the size of the box indicates the weight. In case no shaded box is visible, weight is very small.

Figure 4

Title

Forest plot of the beta estimates (regression coefficients) from the meta-analysis of the association between BMI and absolute telomere length (bp) as outcome in the “young” pooled population (age ≥ 18 and ≤ 60 years)

Legend

ES= estimate; Random effect model was used and adjusted for sex; Statistical heterogeneity was estimated by Q and I^2 statistics for each of the twelve meta-analyses; The shaded boxes indicate the inverse variance weighing of each estimate and the size of the box indicates the weight. In case no shaded box is visible, weight is very small.

Figure 5

Title

Forest plot of the beta estimates (regression coefficients) from the meta-analysis of the association between BMI and relative telomere length (T/S ratio) (B) as outcome in the “young” pooled population (age ≥ 18 and ≤ 60 years)

Legend

The **unit of the estimates and 95% C.I. is 10^{-3}** ; ES= estimate; Random effect model was used and adjusted for sex; Statistical heterogeneity was estimated by Q and I^2 statistics for each of the twelve meta-analyses; The shaded boxes indicate the inverse variance weighing of each estimate and the size of the box indicates the weight. In case no shaded box is visible, weight is very small.