



## Human longevity and variation in GH/IGF-1/insulin signaling, DNA damage signaling and repair and pro/antioxidant pathway genes: Cross sectional and longitudinal studies

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### ABSTRACT

Here we explore association with human longevity of common genetic variation in three major candidate pathways: GH/IGF-1/insulin signaling, DNA damage signaling and repair and pro/antioxidants by investigating 1273 tagging SNPs in 148 genes composing these pathways.

In a case–control study of 1089 oldest-old (age 92–93) and 736 middle-aged Danes we found 1 pro/antioxidant SNP (rs1002149 (*GSR*)), 5 GH/IGF-1/INS SNPs (rs1207362 (*KL*), rs2267723 (*GHRHR*), rs3842755 (*INS*), rs572169 (*GHSR*), rs9456497 (*IGF2R*)) and 5 DNA repair SNPs (rs11571461 (*RAD52*), rs13251813 (*WRN*), rs1805329 (*RAD23B*), rs2953983 (*POLB*), rs3211994 (*NTHL1*)) to be associated with longevity after correction for multiple testing.

In a longitudinal study with 11 years of follow-up on survival in the oldest-old Danes we found 2 pro/antioxidant SNPs (rs10047589 (*TNFRD1*), rs207444 (*XDH*)), 1 GH/IGF-1/INS SNP (rs26802 (*GHRL*)) and 3 DNA repair SNPs (rs13320360 (*MLH1*), rs2509049 (*H2AFX*) and rs705649 (*XRCC5*)) to be associated with mortality in late life after correction for multiple testing.

When examining the 11 SNPs from the case–control study in the longitudinal data, rs3842755 (*INS*), rs13251813 (*WRN*) and rs3211994 (*NTHL1*) demonstrated the same directions of effect ( $p < 0.05$ ), while rs9456497 (*IGF2R*) and rs1157146 (*RAD52*) showed non-significant tendencies, indicative of effects also in late life survival. In addition, rs207444 (*XDH*) presented the same direction of effect when inspecting the 6 SNPs from the longitudinal study in the case–control data, hence, suggesting an effect also in survival from middle age to old age.

No formal replications were observed when investigating the 11 SNPs from the case–control study in 1613 oldest-old (age 95–110) and 1104 middle-aged Germans, although rs11571461 (*RAD52*) did show a supportive non-significant tendency (OR = 1.162, 95% CI = 0.927–1.457). The same was true for rs10047589 (*TNFRD1*) (HR = 0.758, 95% CI = 0.543–1.058) when examining the 6 SNPs from the longitudinal study in a Dutch longitudinal cohort of oldest-old (age 85+, N = 563).

In conclusion, the present candidate gene based association study, the largest to date applying a pathway approach, not only points to potential new longevity loci, but also underlines the difficulties of replicating association findings in independent study populations and thus the difficulties in identifying universal longevity polymorphisms.

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### 1. Introduction

Genetic factors contribute approximately 25% to variation in human life span (Herskind et al., 1996), an effect thought to be

minimal before age 60 years and most profound from age 85 years and onwards (Hjelmborg et al., 2006). Candidate longevity genes encode proteins involved in several biological processes including lipid-protein metabolism (*APOE* being by far the most validated longevity gene to date), growth hormone 1/insulin-like growth factor 1/insulin (*GH/IGF-1/INS*) signaling, DNA damage signaling, and repair and pro/antioxidant pathways (Christensen et al., 2006). The genes composing the latter three pathways encode proteins involved in processes such as energy metabolism, growth and differentiation, and the maintenance of genetic stability (including telomere stability), and protection against free radicals produced by the general metabolism. These are all processes believed to be of key importance for aging and longevity from nematodes to humans (reviewed in e.g. Burtner and Kennedy, 2010; Cluett and Melzer, 2009; Harman, 1973; Kenyon, 2010; Kuningas et al., 2008). Studies using various animal models have found that either depletion or over-expression of some of these candidate genes affect the life span of the organism (e.g. *GH*, *GPX1*, *FOXO*, *KL*, *GHRHR*, *POLB*, *RAD52*, *INS* and *TP53* (Bartke, 2005; Cabelof et al., 2006; Flurkey et al., 2001; Giannakou et al., 2004; Holzenberger et al., 2003; Kawano et al., 2000; Kuro-o et al., 1997; Kurosu et al., 2005; Park et al., 1999; Tyner et al., 2002; Mockett et al., 1999)), whereas manipulating other genes leads to aging-like phenotypes (e.g. *PON1* and *CSB* (Shih et al., 1998; van der Horst et al., 1997)).

In humans rare mutations that severely affect the function of some of these genes (*WRN*, *CSB* and *RECQL4*) can cause segmental progeroid premature aging syndromes such as Werner's, Cockayne's and Rothmund–Thomson syndromes (reviewed in Burtner and Kennedy, 2010)), whereas more common genetic variation has been reported to be associated with human lifespan. Examples from the *GH/IGF-1/INS* pathway include *IGF1R*, *GHR* and *FOXO3A*, from the DNA damage signaling and repair pathway *WRN*, *MLH1* and *TP53* and from the pro/antioxidant pathway *SOD1*, *SOD2* and *PON1* (Bonafe et al., 2003; Castro et al., 2000; Christiansen et al., 2004; Flachsbarth et al., 2009a; Kim et al., 2006; van Heemst et al., 2005a; van Heemst et al., 2005b; Willcox et al., 2008a; Yashin et al., 2000).

The vast majority of the candidate genetic association studies published so far focus on a single or a few single nucleotide polymorphisms (SNPs) or candidate genes, although recently a few studies have initiated the investigation of SNPs in groups of candidate genes and pathways based on the functional roles of the gene products (Deelen et al., 2011; Flachsbarth et al., 2010; Nebel et al., 2009; Pawlikowska et al., 2009a). In addition, previous studies have generally applied a case–control study design, thus raising concerns of bias introduced by differences in characteristics of cases and controls, for example cohort effects.

Here we investigate the association of common genetic variation in 148 genes composing the *GH/IGF-1/INS* signaling, DNA damage signaling and DNA repair and pro/antioxidant pathways with human longevity. The study populations are a cohort of Danes born in 1905 and followed from age 93 years until death, as well as a group of middle-aged controls. This provides a unique opportunity to investigate these variations in key candidate genes of human longevity using both case–control and longitudinal designs. Further, the SNPs identified in the case–control study are explored in the longitudinal data in order to investigate whether these SNPs also pose effects on survival during old age, and the SNPs identified in the longitudinal study are examined in the case–control data to investigate whether these SNPs also pose effects on survival from middle age to old age.

Finally, considering the importance of replicating initial results in genetic association studies, the SNPs found to be significant in the case–control study are tested for association in a German case–control sample (1613 long-lived individuals and 1104 controls), while the findings from the Danish longitudinal study are tested in the prospective Dutch Leiden 85-plus Study (563 individuals).

## 2. Material and methods

### 2.1. Subjects

#### 2.1.1. Discovery cohorts

The study population of oldest-old was 1200 participants from The Danish 1905 Birth Cohort Study (1905 cohort) (Nybo et al., 2001). The study was initiated in 1998, when participants were 92.2–93.8 years of age (mean age 93.2). Survivors were re-assessed in 2000, 2003 and 2005. Vital status was followed until death or January 1st 2010, whichever came first, resulting in a mean follow-up time for survivors of 11.4 years (range: 11.2–11.6). Survival status information was retrieved from the Danish Central Person Register, which is continuously updated (Pedersen et al., 2006). The younger control group (46.0–55.0 years of age, mean age 50.5) was 800 individuals from The Study of Middle Aged Danish Twins (MADT) (Skytthe et al., 2002). MADT was initiated in 1998 by random selection of 2640 intact twin pairs from 22 consecutive birth years (1931–1952) via the Danish Central Person Register. Only one twin from each twin pair was included in the present study. Permission to collect blood samples and usage of register based information was granted by The Danish National Committee on Biomedical Research Ethics for both surveys. All participants gave their informed consent.

After data cleaning, the final sample size for data analysis was 1089 oldest-old and 736 middle-aged individuals. Of these 1089 oldest-old, 14 were alive by January 1st 2010, hence, for the longitudinal analysis their remaining life expectancies were imputed using [www.mortality.org](http://www.mortality.org), which, by appliance of data from the Statistics Denmark, contains cohort mortality data for the Danish population. Of the 736 MADT individuals, 35 had died since 1998. Based on period life table data for the Danish population ([www.mortality.org](http://www.mortality.org)) it is anticipated that only approximately 9% of the remaining 701 individuals will become 93 years of age.

#### 2.1.2. Replication samples

For replication of findings from the Danish case–control study, two German samples of 1613 unrelated long-lived individuals (age 95–110) and 1104 middle-aged controls (mean age 67.2) were used. The participants were identified via the local registry offices and the Federal Administrative Office. They were recruited from different geographic regions of Germany and were all of German ancestry (Nebel et al., 2005). Approval was received from the Ethics Committee of the University Hospital Schleswig-Holstein and from local data protection authorities. All participants gave their informed consent.

For replication of findings from the Danish longitudinal study, the Dutch Leiden 85-plus Study was used. This prospective cohort was initiated in 1997, when all 85-year-old inhabitants of the city of Leiden in The Netherlands were invited to participate. The sample used here consists of 563 participants, all Caucasians and members of the 1912–1914 birth cohort recruited from 1997 to 1999 (Bootsma-van der Wiel et al., 2002). Mean follow up time for survivors is 10.35 years (range 9–11 years). The Medical Ethical Committee of the Leiden University Medical Centre approved the study. All participants gave their informed consent.

### 2.2. Selection of candidate genes

A comprehensive literature and data base search was conducted for the identification of longevity candidate genes in the *GH/IGF-1/INS* signaling, DNA damage signaling and repair and pro/antioxidant pathways. The following databases were used: [www.ncbi.nlm.nih.gov \(/sites/entrez/OMIM/sites/entrez?Db=gap\)](http://www.ncbi.nlm.nih.gov/sites/entrez/OMIM/sites/entrez?Db=gap), [www.genecards.org](http://www.genecards.org), [www.hgvsbaseg2p.org](http://www.hgvsbaseg2p.org), [genomics.senescence.info](http://genomics.senescence.info) and [geneticassociationdb.nih.gov](http://geneticassociationdb.nih.gov) using the search terms 'human longevity',

'human aging', 'age related disease' (including specific diseases e.g. myocardial infarction) and 'premature aging syndromes'. Additionally, genes previously identified through animal models were considered. In order to cover the core biological functions of the three candidate pathways, the needed genes were chosen using the [www.ncbi.nlm.nih.gov/sites/entrez](http://www.ncbi.nlm.nih.gov/sites/entrez), [www.biocarta.com](http://www.biocarta.com), [www.reactome.org](http://www.reactome.org), [www.genome.utah.edu/genesnps](http://www.genome.utah.edu/genesnps) and the [www.genome.jp/kegg/pathway.html](http://www.genome.jp/kegg/pathway.html) databases. In total 152 genes composing the three candidate pathways were identified, 148 of which remained after cleaning of the GoldenGate genotyping data (see below). The 148 genes, divided by pathway, are listed in Supplementary Table 1.

### 2.3. Selection of SNPs

The chromosomal regions composing the 152 candidate genes were identified through the [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov) (/gene and /mapview) and [genome.ucsc.edu/databases](http://genome.ucsc.edu/databases), using the same gene ID, Sequence Accession IDs, NCBI Reference Sequence, assembly build 36 and SNP build 129. If more than one isoform of a gene transcript existed, the longest one was chosen. For each gene, 5000 bp upstream and 1000 bp downstream were included. If another gene was located within these regions, only the region until the neighboring gene was included. Due to the size of the genotyping platform, the large intron 2 of *IGF1R* and the large intron 2 of *INSR* were excluded.

Candidate SNPs were identified based on the following criteria: SNPs previously identified in genetic association studies, coding SNPs and SNPs having potential functional impact (coding non-synonymous SNPs, SNPs located in potential splice sites or transcription factor binding sites and SNPs potentially inducing frame shifts or nonsense-mediated mRNA decay). For the identification of potential functional SNPs, the [www.ncbi.nlm.nih.gov/SNP](http://www.ncbi.nlm.nih.gov/SNP), [koreanbio.org/Variome](http://koreanbio.org/Variome), [snpper.chip.org](http://snpper.chip.org), [snps3d.org](http://snps3d.org) and [manticore.niehs.nih.gov](http://manticore.niehs.nih.gov) data bases were used. The identity of each SNP was checked by linking back to the NCBI data base.

In order to cover as much of the common genetic variation within each gene region as possible, a number of tagging SNPs in each gene region were added, obtained through the HapMap consortium database (<http://hapmap.ncbi.nlm.nih.gov/index.html.en>) for the CEU cohort, using the HapMap Data Rel 23a/phase II Mar08, on NCBI B36 assembly, dbSNP build 126 criteria. Genotype data were analyzed using the HaploView software (<http://www.broadinstitute.org/haploview/haploview> and Barrett et al., 2005), by applying the 'pair wise tagging only',  $r^2 > 0.8$ , LOD = 3, minor allele frequency (MAF) > 5%, and a minimum distance between SNPs = 60 bp criteria. Finally, for optimizing the

quality of the genotype data, SNPs known to perform poorly on the Illumina GoldenGate genotyping platform were excluded. In total, 1415 SNPs were chosen and 1273 were successfully genotyped.

### 2.4. Genotyping and data cleaning

DNA was isolated from blood spot cards using the QIAamp DNA Mini and Micro Kits (Qiagen, Düsseldorf, Germany). The genotyping was conducted using the Illumina GoldenGate platform (Illumina Inc, San Diego, CA, USA) and data cleaning was carried out according to the manufacturer's recommendations using the GenomeStudio software ([http://www.illumina.com/software/genomestudio\\_software.ilmn](http://www.illumina.com/software/genomestudio_software.ilmn)); primary exclusion criteria were sample call rate < 90% and SNP call frequency < 90%. Subsequently, SNPs clustering in the following categories were manually evaluated: a call frequency 90–95%, close SNP clusters (score < 2.3), clusters with low intensity (score < 0.2 or > 0.8), cluster having a heterozygote cluster shifting towards a homozygote cluster (score < 0.13), SNPs with excess heterozygosity (score < -0.3 or > 0.2) and SNPs located on the X chromosome (considering male hemizygosity). In total, 142 SNPs and 175 DNA samples were excluded leaving 1825 individuals, 148 candidate genes and 1273 SNPs for data analysis. Furthermore, 24 samples were included twice in order to investigate the intra-plate reproducibility and 48 samples were included twice to test the inter-plate reproducibility. Data showed an intra-plate reproducibility of 99.4% and an inter-plate reproducibility of 96.8%.

Genotyping of the German replication samples were performed using either Sequenom MassARRAY iPLEX®Gold technology (Sequenom®, Inc., CA, USA) with iPLEX primers designed via the MassARRAY Design Software, or via an automated platform using predesigned TaqMan® SNP genotyping assays (Applied Biosystems) (Hampe et al., 2001); PCR was performed using the GeneAmp PCR System 9700 (Applied Biosystems) under standard conditions and the ABI Prism 7900HT Sequence Detection System and the Sequence Detection System Software 2.0 (Applied Biosystems) were used for allelic discrimination.

The Dutch replication samples were genotyped via Sequenom MassARRAY iPLEX®Gold technology (Sequenom®, Inc., CA, USA), using primers designed via the SpectroDESIGNER (Sequenom®, Inc., CA, USA) and the high plex reaction protocol ([www.sequenom.com/plex](http://www.sequenom.com/plex)). Since rs207444 and rs3211994 were not compatible with the iPLEX format, genotyping was conducted using assay-on-demand TaqMan® SNP genotyping assays (Applied Biosystems); PCR was performed on the GeneAmp PCR system 9700 (Applied Biosystems, CA, USA) under universal conditions and the Applied Biosystems 7900HT Fast Real-time PCR System and SDS2.3 Software (Applied Biosystems, CA, USA) were used for allelic discrimination.

### 2.5. Statistical analysis

In the case-control study of the Danish discovery cohorts single-SNP case-control comparisons of allele frequencies (CCA) were performed using the Plink statistical program (<http://pngu.mgh.harvard.edu/purcell/plink>, Purcell et al., 2007) by two-tailed Chi-square test. Replication of the findings from the Danish case-control study was conducted by CCA in the German case-control samples in the same way.

Approximately 1 in 20 members of the 1905 birth cohort in Denmark had survived until 1998 (start of the Danish 1905 Birth Cohort Study) and approximately 1 in 20 of these members survived until 100 years of age, i.e. reaching age 92–93 (the inclusion age of the Danish 1905 Birth Cohort Study participants) is only "halfway to becoming a centenarian" in terms of selection. In the longitudinal survival analysis of the oldest-old from the Danish 1905 Cohort Study, two survival variables were used. First, we wanted to investigate the genetic contribution to surviving for only a short period of time as opposed to surviving for a longer period of time during the ninth

**Table 1**

Characteristics of (A) the Danish discovery cohorts and (B) the German and Dutch replication samples.

(A) The Danish discovery cohorts	MADT	1905	
Number of individuals	736	1089	
Average age in years at intake (range)	50.6 (46.0–55.0)	93.2 (92.2–93.8)	
Male:female ratio (%) at intake	50.4:49.6	28.7:71.3	
Mean follow up time (SD)	–	3.53 (2.5)	
Follow up time (years)	–	11.4	
(B) The replication samples	German case-control study	Dutch longitudinal study	
	Controls	LLI	
	Controls	LLI	
Number of individuals	1104	1613	563
Average age at intake (SD)	67.2 (4.1)	98.4 (2.7)	85.0 (0)
Male:female ratio (%) at intake	25.6:74.3	26.8:73.2	33.4:66.6
Mean follow up time (SD)	–	–	5.49 (3.0)
Follow up time (years)	–	–	10.4

Notes: MADT: the Study of Middle Aged Danish Twins, 1905: the Danish 1905 Birth cohort, LLI: long lived individuals, SD: standard deviation.

decade of life. Since the distribution of survival times was clearly right skewed (data not shown), a cut-off with respect to time of death was made at December 31st 2000, when approximately half of the males and one third of the females in the cohort had died. Consequently, the early/late death variable was defined as: early = death occurred between 1998 (date at intake) and December 31st 2000 (i.e. individuals living to maximum age 95) and late = death occurred after January 1st 2001 (i.e. individuals surviving to age 95+). As the second variable, we used the number-of-days-lived defined as the exact number of days lived from date of intake in 1998 to either death or the imputed date (the latter is described in Section 2.1.1). For this variable, the assumptions of normal distribution and equal variance were tested in the STATA 11.1 statistical program (Stata Corporation, College Station, TX, USA) by Shapiro–Wilk and Breusch–Pagan/Cook–Weisberg tests. Since the variable did not show normal distribution, it was transformed to the square root for a better fit. Association analysis was performed by two-tailed linear (for the number-of-days-lived variable) or logistic (for the early/late death variable) regression in Plink, adjusting for sex and age or stratifying by sex, while adjusting for age.

Replication of the findings from the Danish longitudinal study was performed in Stata 11.1 by analyzing genotype data from the Leiden 85-plus Study using a sex-adjusted Cox proportional hazard model. An additive model was used, and only in cases when inspection of Kaplan–Meier plots indicated a recessive or dominant model, such a model was applied.

In order to obtain a quantitative estimate for the differences in mean survival time between individuals homozygous for the common alleles of a SNP found to be associated with the number-of-days-lived variable and individuals being either heterozygous or homozygous for the rare allele at the same SNP, regression analysis was performed for same sex and same age (93 years) individuals and the regression coefficients were used for estimation. Moreover, the relative risks (RRs) of being alive after age 95 (corresponding to the 1st of January 2001) were calculated for the heterozygotes and homozygotes for the rare allele of each SNP found to be associated to the early/late death variable. The RRs between genotype groups were estimated based on the ORs obtained in the logistic regression analysis. All these analyses were performed in STATA 11.1.

For all the analyses, the nominal significance level was set to 0.05. Correction for multiple testing within each pathway was performed by a permutation approach applying max(T) permutation mode set at 10,000 permutations for the analyses carried out in the Plink software. Correction for multiple testing in analyses performed in the STATA software was done using the Bonferroni approach.

### 3. Results

By conducting a thorough literature and data base search candidate genes, candidate SNPs and tagging SNPs were identified (see Sections 2.2 and 2.3 for details). A total of 148 candidate genes and 1273 SNPs were successfully genotyped and are listed in Supplementary Table 1: these constitute 592 SNPs in 77 genes of the DNA damage signaling and DNA repair pathway, 370 SNPs in 33 genes of the GH/IGF-1/INS signaling pathway and 311 SNPs in 38 pro/antioxidant genes. The characteristics of the Danish discovery cohorts of middle-aged and oldest-old individuals are described in Table 1A, while the German and Dutch replication samples are described in Table 1B.

#### 3.1. Case–control comparison of middle-aged and oldest-old Danes

Exploiting the case–control allele comparisons revealed considerably more nominally significant differences than would be expected by chance (see Supplementary Table 2). After adjusting allelic comparisons for multiple testing by permutation, 10 of the 1273 SNPs remained significant; of these SNPs the minor allele of the GH/IGF-

1/INS-SNPs rs1207362 (*KL*), rs2267723 (*GHRHR*) and rs572169 (*GHSR*), as well as the pro/antioxidant-SNP rs1002149 (*GSR*) and the DNA-repair-SNP rs1805329 (*RAD23B*) decreased in frequency from middle-aged to old-aged ( $OR < 1$ ), whereas the GH/IGF-1/INS-SNPs rs3842755 (*INS*) and rs9456497 (*IGF2R*) and the DNA-repair-SNPs rs11571461 (*RAD52*), rs13251813 (*WRN*) and rs2953983 (*POLB*) increased in frequency ( $OR > 1$ ). As sex-specific differences previously have been suggested for association of SNPs with longevity (Candore et al., 2006; Franceschi et al., 2000; Li et al., 2009; Soerensen et al., 2010) a sex-stratified analysis was also performed; the analysis supported the associations of the 10 SNPs mentioned above for both genders (data not shown), and in addition identified 1 DNA-repair-SNP in males; the minor allele of rs3211994 (*NTHL1*) increased in frequency from middle-aged to old-aged. The data are summarized in Table 2.

The 11 SNPs were subsequently analyzed in replication samples of 1613 long-lived and 1104 middle-aged Germans. The MAF of the SNPs in the German and Danish case–control samples are listed in Supplementary Table 3. None of the 11 SNPs formally replicated in the German samples (see Table 3), although rs11571461 (*RAD52*) did show a non-significant tendency of association in the same direction (95% CI (OR) = [0.927–1.457]).

#### 3.2. Longitudinal study in the cohort of oldest-old Danes

As for the case–control study, analysis of survival data in the oldest-old Danes revealed more nominally significant associations than would be expected by chance, whether using the categorical early/late death or the numeric number-of-days-lived variables (see Supplementary Table 4). After correcting for multiple testing 2 SNPs were found to be associated with late life survival for both genders combined: carriers of the rare allele of the pro/antioxidant-SNP rs10047589 (*TXNRD1*) displayed a significant increase in survival when categorizing into early/late death, whereas the rare allele of the pro/antioxidant-SNP rs207444 (*XDH*) was found to be significantly associated with increased number of days lived (see Table 4A). When stratifying by sex, these results were supported in both genders (data not shown). Moreover, when applying the early/late death variable, positive effects of the rare alleles of the GH/IGF-1/INS-SNP rs26802 (*GHRL*) and the DNA-repair-SNP rs13320360 (*MLH1*) on survival were observed in males, while the DNA-repair-SNP rs2509049 (*H2AFX*) had a negative effect on survival in females. Using number-of-days-lived as the measure of survival, the rare allele of the DNA-repair-SNP rs705649 (*XRCC5*) positively affected survival in males. The results are summarized in Table 4B.

Since we performed the longitudinal analyses as regression analyses, we were able to estimate the quantitative effects of the 6 SNPs, represented by the risk differences (RD) for the SNPs associated with the early/late death variable, and by the additional survival time for the SNPs associated with the number-of-days-lived variable. These estimates indicated rather substantial effects: a maximum RD was seen for rs26802 (*GHRL*) CC males having a 53% higher chance for being alive after age 95 (corresponding to the 1st of January 2001) as compared to AA homozygotes, while a maximum difference of 1.66 additional years of survival was seen for rs705649 (*XRCC5*) GG males as compared to rs705649-AA males, who obtained a mean survival time of 2.15 years. The data are summarized in Supplementary Tables 5A and B.

Next the 6 SNPs were evaluated in a replication cohort of 563 85+ year old Dutch individuals. The frequency data of the 6 SNPs in the Dutch and Danish longitudinal cohorts are listed in Supplementary Table 6. Applying an additive model, none of the SNP associations was replicated in the Dutch cohort (see Table 5). However, inspection of Kaplan–Meier survival plots for the 6 SNPs suggested a recessive mode of effect for rs10047589 (*TXNRD1*) in the Dutch data (data not shown), with a similar direction of effect as in the Danish

**Table 2**

SNPs significantly associated with longevity after correction for multiple testing in the case–control comparison of middle-aged and oldest-old Danish cohorts. (A) Both genders combined and (B) additional SNP in sex-stratified analyses.

	Gene	SNP	Minor/major allele	Chr./position	Position in gene	MAF MADT/1905	PCCA uncorrected	PCCA corrected	OR (95% CI)
<i>(A) Both genders</i>									
Pro/antioxidants	GSR	rs1002149	A/C	8/30705280	5'	0.183/0.137	$1.47 \cdot 10^{-4}$	0.0335	0.706 (0.589–0.845)
GH/IGF/INS	INS	rs3842755	A/C	11/2137372	3' UTR	0.292/0.424	$8.38 \cdot 10^{-16}$	$1 \cdot 10^{-4}$	1.789 (1.552–2.063)
	KL	rs1207362	A/C	13/32510839	Intronic	0.339/0.245	$2.77 \cdot 10^{-9}$	$1 \cdot 10^{-4}$	0.634 (0.545–0.737)
	GHRHR	rs2267723	G/A	7/30973467	Intronic	0.414/0.330	$2.28 \cdot 10^{-7}$	$1 \cdot 10^{-4}$	0.696 (0.607–0.799)
	GHSR	rs572169	A/G	3/173648421	Coding (syn)	0.342/0.274	$1.65 \cdot 10^{-5}$	0.0045	0.725 (0.626–0.839)
	IGF2R	rs9456497	G/A	6/160363418	Intronic	0.191/0.252	$1.86 \cdot 10^{-5}$	0.0050	1.424 (1.211–1.674)
DNA repair	RAD52	rs11571461	G/A	12/896580	Intronic	0.098/0.195	$5.05 \cdot 10^{-15}$	$1 \cdot 10^{-4}$	2.226 (1.815–2.730)
	WRN	rs13251813	A/G	8/31083753	Intronic	0.077/0.134	$1.72 \cdot 10^{-7}$	$2 \cdot 10^{-4}$	1.840 (1.460–2.318)
	POLB	rs2953983	G/A	8/42332413	Intronic	0.080/0.123	$4.54 \cdot 10^{-5}$	0.0225	1.599 (1.274–2.006)
	RAD23B	rs1805329	A/G	9/109124149	Coding (non-syn)	0.245/0.190	$6.74 \cdot 10^{-5}$	0.0309	0.722 (0.615–0.847)
<i>(B) Males</i>									
DNA repair	NTHL1	rs3211994	A/G	16/2029029	3'	0.112/0.201	$1.38 \cdot 10^{-5}$	0.0056	1.994 (1.455–2.732)

Notes: Chr: chromosome, MAF: minor allele frequency, MADT: the Study of Middle Aged Danish Twins, 1905: the Danish 1905 Birth cohort, PCCA: allelic case–control comparison P-value, OR: odds ratio, 95% CI: 95% confidence interval, UTR: untranslated region, Syn: synonymous, Non-syn: Non-synonymous.

longitudinal study, although the association was not significant; HR = 0.758,  $p = 0.103$ , 95% CI = [0.543–1.058].

### 3.3. Similar directions of effect in the Danish case–control and longitudinal studies

We wanted to explore whether the 11 SNPs identified via the Danish case–control study maintained an effect during old age. Consequently we investigated the 11 SNPs in the longitudinal data on the oldest-old Danes. Similar directions of effects, i.e. positive effects on survival, were noted for 5 SNPs; when applying the number-of-days-lived variable, rs13251813 (*WRN*) and rs3842755 (*INS*) displayed nominally significant associations ( $p < 0.05$ ), the former in the entire group of oldest-old and the latter when restricting to males. Additionally, rs9456497 (*IGF2R*) showed a borderline significant association when restricting to males ( $p = 0.05$ ). For the early/late death variable, rs3211994 (*NTHL1*) displayed nominal significance in both genders combined, while rs1157146 (*RAD52*) showed a non-significant tendency in females only ( $p = 0.10$ ). None of the remaining six SNPs showed similar directions of effect. The data is summarized in Table 6A.

Finally, in order to explore whether the 6 SNPs, identified in the longitudinal study of oldest-old Danes, presented a similar direction of effects on survival from middle age to old age, we investigated the 6 SNPs in the Danish case–control data. Only rs207444 (*XDH*) displayed a nominally significant effect in the same direction as found in the oldest old ( $p = 0.005$ ). The data is summarized in Table 6B.

## 4. Discussion

The vast majority of the candidate genetic association studies of longevity published so far has explored only a small number of

variations and/or genes. The investigation of large collections of candidate variations grouped together based on the functional roles of the gene products is a much more recent strategy (Flachsbart et al., 2010; Nebel et al., 2009; Pawlikowska et al., 2009b). In this study we investigated 592 SNPs in 77 genes of the DNA damage signaling and DNA repair pathway, 370 SNPs in 33 genes of the GH/IGF-1/INS signaling pathway and 311 SNPs in 38 pro/antioxidant genes, making it the most comprehensive study to date following this strategy. Furthermore, in addition to the widely used case–control approach, we also present data from a longitudinal analysis of survival in the oldest-old.

In the analysis of the case–control study of 1089 oldest-old and 736 middle-aged Danes, we found 11 novel SNPs in 11 different genes to be associated with human longevity. The rare allele of variants in *INS*, *IGF2R*, *POLB*, *RAD52*, *WRN* and *NTHL1* was demonstrated to be advantageous, the latter most evident in males, whereas the rare allele of variants in *KL*, *GHRHR*, *GHSR*, *GSR*, and *RAD23B* was disadvantageous for survival.

None of the findings could be formally confirmed in a German replication cohort of comparable size, although rs11571461 (*RAD52*) did show a tendency in the same direction as found in the Danish data. In support of our findings, other variants in *KL*, *WRN* and *NTHL1* have previously been associated with longevity (Arking et al., 2005; Castro et al., 2000; Yashin et al., 2010) and rs687045 (*KL*) which was put forward by Lunetta et al. as a mortality SNP during old age (Lunetta et al., 2007), is in our cohorts in moderate LD ( $R^2 = 0.25$ ) with rs1207362 (*KL*) described in our study as disadvantageous for longevity. Moreover, supportive of an association of *INS*, a very recent publication of gene-based case–control analysis of genes in the IGF-1/Insulin pathway reported gene-based association of *INS* with longevity (Deelen et al., 2011). Additionally, some of the 11 SNPs have been

**Table 3**

Replication of Danish case–control findings in the German case–control samples.

	Gene	SNP	OR (Danish study)	OR (German study)	PCCA Germans	95% CI
Pro/antioxidants	GSR	rs1002149	0.706	1.054	0.470	0.913–1.217
	INS	rs3842755	1.789	0.949	0.434	0.832–1.082
GH/IGF/INS	KL	rs1207362	0.634	0.985	0.804	0.873–1.110
	GHRHR	rs2267723	0.696	1.005	0.934	0.900–1.121
	GHSR	rs572169	0.725	1.106	0.097	0.981–1.247
	IGF2R	rs9456497	1.424	0.962	0.586	0.837–1.105
DNA repair	RAD52	rs11571461	2.226	1.162	0.191	0.927–1.457
	WRN	rs13251813	1.84	0.999	0.998	0.754–1.325
	POLB	rs2953983	1.599	1.046	0.683	0.842–1.299
	RAD23B	rs1805329	0.722	0.955	0.507	0.833–1.094
DNA repair (males)	NTHL1	rs3211994	1.994	0.931	0.627	0.699–1.241

Notes: OR: odds ratio, PCCA: allelic case–control comparison P-value, 95% CI: 95% confidence interval.

**Table 4**  
SNPs significantly associated with longevity after correction for multiple testing in the longitudinal analysis of follow-up survival data from the cohort of oldest-old Danes. (A) Both genders combined and (B) additional SNPs in sex-stratified analyses.

(A) Both genders combined										
Early/late death										
Pathway	Gene	SNP	Minor/major allele	Chr./position	Position in gene	Freq 1905	P-value	P-value corrected	OR	95% CI
Pro/antioxidants	TNFRD1	rs10047589	A/G	12/103268518	3'	0.098/0.445/0.455	0.00018	0.043	1.458	1.143–2.318
Number-of-days-lived										
Pathway	Gene	SNP	Minor/major allele	Chr./position	Position in gene	Freq 1905	P-value	P-value corrected	$\beta$ -coefficient	95% CI
Pro/antioxidants	XDH	rs207444	A/G	2/31417301	Intronic	0.001/0.177/0.820	0.00016	0.046	4.043	1.946–6.141
(B) Stratified by sex										
Early/late death										
Pathway	Gene	SNP	Minor/major allele	Chr./position	Position in gene	Freq 1905	P-value	P-value corrected	OR	95% CI
Males	GH/IGF-1/INS	rs26802	C/A	3/10307365	Intronic	0.076/0.392/0.531	$1.89 \cdot 10^{-5}$	0.032	2.338	1.585–3.451
	DNA repair	rs13320360	G/A	3/37028124	Intronic	0.003/0.311/0.684	$1.66 \cdot 10^{-5}$	0.0036	3.132	1.863–5.267
Females	DNA repair	rs2509049	A/G	11/118471731	5'	0.156/0.527/0.315	$4.77 \cdot 10^{-5}$	0.017	0.625	0.498–0.782
Number-of-days-lived										
Pathway	Gene	SNP	Minor/major allele	Chr./position	Position in gene	Freq 1905	P-value	P-value corrected	$\beta$ -coefficient	95% CI
Males	DNA repair	rs705649	G/A	2/216689431	Intronic	0.175/0.512/0.311	$6.19 \cdot 10^{-5}$	0.029	4.669	2.416–6.921

Notes: Chr: chromosome, Freq: frequency, 1905: the 1905 cohort, 95%CI: 95% confidence interval. The frequencies in the Freq. 1905 column refer to the frequencies of the rare homozygotes/the heterozygotes/the common homozygotes for each SNP.

reported as associated with phenotypes of possible relevance to variation in lifespan; rs572169 (*GHSR*) with obesity (Gueorguiev et al., 2009), and rs2953983 (*POLB*), rs1805329 (*RAD23*), rs11571461 (*RAD52*) and rs13251813 (*WRN*) with different types of cancers (Pan et al., 2009; Schildkraut et al., 2010; Van Ness et al., 2008; Yang et al., 2009).

An interesting question was whether the genetic variants with a proposed effect on survival from middle age to old age would also demonstrate an effect for survival during old age. We therefore tested the 11 SNPs for association to survival in the Danish 1905 cohort using the longitudinal design and found 3 SNPs to display the same nominal significant ( $p < 0.05$ ) direction of effect in the longitudinal data, while 2 SNPs showed similar tendencies ( $0.05 < p < 0.10$ ). Interestingly, all 5 SNPs were apparent longevity SNPs, i.e. SNPs with a positive effect on survival. This is in line with a recent study suggesting that long life is not due to a decreased burden of negatively affecting disease variants but rather due to positively influencing longevity variants (Beekman et al., 2010).

A lack of similar effects in the longitudinal data for the remaining SNPs could indicate that these SNPs may be relevant at different ages, i.e. the influence of genes and gene variants may be of consequence for survival in young elderly, but lose this importance at the highest ages.

When investigating the association of the 1273 SNPs with survival at advanced age using a longitudinal study approach, we identified 6 novel SNPs in 6 genes to be associated with longevity. The rare allele of a variant in *H2AFX* appeared disadvantageous, while the rare variants in *GHRL*, *MLH1*, *TXNRD1*, *XDH* and *XRCC5* were advantageous for longevity. In line with these results an *MLH1* haplotype was previously reported to be associated with longevity in a case-control study (Kim et al., 2006), whereas genetic variants in *GHRL* have been described as associated with phenotypes of possible relevance to variation in lifespan; high HDL-cholesterol levels (Hubacek et al., 2007) and hypertension (Berthold et al., 2010). Finally, the activity of the *XRCC5* protein product Ku80 has been reported to decrease from young to old age in humans (Scarpaci et al., 2003), indicating a biological change with age.

The Danish case-control study supported an advantageous effect of rs207444 (*XDH*) also on survival from middle age to old age, and additionally some support was observed for rs10047589 (*TNFRD1*) in the Dutch replication cohort, indicating a recessive mode of effect for this variant.

Interestingly, the longitudinal study revealed more longevity-associated SNPs in the sex-stratified analysis (4 of 6 SNPs) than the Danish case-control study (1 of 11 SNPs). This observation could indicate that the impact of genetic effect becomes more gender-specific during advanced age than at younger ages, and that the genetic effect in old age might be most pronounced for males. Such a difference between genders was recently suggested by Montesanto et al. (2011) for Italians.

From a pathway perspective a few comments can be made on the genes holding the SNPs suggested here. For the GH/IGF-1/INS pathway the present data suggests that variations in genes whose products take part in growth hormone synthesis and secretion (*GHRHR*, *GHRL* and *GHSR*) or in signaling to and affecting target organs/cells (*INS*, *KL*, *IGF2R*) might pose effects on longevity. With respect to DNA repair, the gene products of the genes holding the significant SNPs take part in different DNA repair activities, though the majority take part in base excision repair (*NTHL1*, *POLB*, and *WRN*) or in DNA double strand break repair (*RAD52*, *H2AFX*, *XRCC5* and *WRN*), thus indicating that variation in the repair of DNA damage induced by for instance reactive oxygen species and ionizing radiation could pose effects on longevity. Lastly, with respect to the pro/antioxidant pathway both antioxidants (*GSR* and *TXNRD1*) and a prooxidant (*XDH*) are observed, indicating that the role of this pathway in longevity appears complex.

**Table 5**  
Replication of findings from the Danish longitudinal study in the longitudinal Dutch Leiden 85-plus Study.

Both genders combined			Danish longitudinal study	Dutch longitudinal study		
Pathway	Gene	SNP	Estimate	HR	P-value	95%CI
Pro/antioxidants	TNFRD1	rs10047589	1.458 (OR)	0.969	0.659	0.844–1.112
Pro/antioxidants	XDH	rs207444	4.043 (β)	0.886	0.404	0.667–1.177
<i>Males</i>						
GH/IGF-1/INS	GHRL	rs26802	2.338 (OR)	0.730	0.962	0.774–1.197
DNA repair	MLH1	rs13320360	3.132 (OR)	1.169	0.827	0.288–4.727
	XRCC5	rs705649	4.669 (β)	1.037	0.749	0.828–1.300
<i>Females</i>						
DNA repair	H2AFX	rs2509049	0.625 (OR)	0.909	0.260	0.769–1.073

Notes: β: Beta coefficient (linear regression using the number-of-days-lived variable), OR: odds ratio (logistic regression using the early/late death variable), HR: hazard ratio, 95%CI: 95% confidence interval.

The SNPs suggested here to associate to longevity might induce different functional effects; rs1002149 (*GSR*) and rs2509049 (*H2AFX*) located 5' of genes might affect the level of gene expression, while rs3842755 (*INS*), rs3211994 (*NTHL1*) and rs10047589 (*TNFRD1*) are all located 3' and could thus in principle influence decay of mRNA. The non-synonymous coding SNP rs1805329 (*RAD23B*) could potentially affect protein activity, while the intronic SNPs (rs1207362 (*KL*), rs2267723 (*GHRHR*), rs9456497 (*IGF2R*), rs11571461 (*RAD52*), rs13251813 (*WRN*), rs2953983 (*POLB*), rs207444 (*XDH*), rs26802 (*GHRL*), rs13320360 (*MLH1*) and rs705649 (*XRCC5*)) could possibly induce splicing alterations. Alternatively, the associated SNPs might simply be proxies for other truly causative variants.

How such suggested functional effects might impact aging and/or longevity is an extremely difficult question, especially considering that the role of the three pathways in aging and/or longevity appears very complex. In any case, functional studies of the molecular effects of the associated variants are needed.

Due to the emergence of high throughput techniques facilitating studies of sizeable numbers of variations, the replication of initial findings has become a major issue in genetic epidemiology. In this study we tested our findings from the case-control and the longitudinal study using German samples of 1613 long-lived individuals (95+) and 1104 middle-aged controls, and a cohort of 85+ Dutch elderly, respectively. No formal replication was observed in either case although a few supportive observations were found (see above).

A number of reasons can be given for the lack of true replication. It could be a matter of under-powered replication populations. However, the number of German samples is larger than the Danish discovery cohorts, thus arguing against this explanation. Alternatively it might be due to heterogeneity between samples, for instance differences in enrollment of the participants. As seen in Table 1, the German cases are older than the Danish oldest-old, whereas the members of the Dutch 85+ cohort are somewhat younger at intake than the Danish 1905 cohort members. Hence, if the effects of the variants are not constant throughout old age, they may not replicate well in these study samples. Change in association effects with age has been reported previously (Jacobsen et al., 2010). Finally, it might simply be that the associations are population specific, perhaps mediated through population specific characteristics in environment. Such population specific effects have previously been suggested (Di Bona et al., 2009).

In our study we only performed correction of multiple testing within each pathway, since the selection of genes and SNPs was based on a sound a priori hypothesis. Moreover, due to the design of the statistical software, we corrected for multiple testing within each type of test, and hence, we did not correct for performing the sex-stratified analysis as well as a test for both genders combined, and with respect to the longitudinal study for investigating the 2 survival variables. Such corrections should in principle be included, in order to avoid false positive findings. If correcting the p-values from

**Table 6**  
Similar directions of effect in the Danish case-control and longitudinal studies.

(A) Similar directions of effect in the Danish longitudinal study of SNPs initially identified in the Danish case-control study and (B) Similar direction of effect in the Danish case-control study of a SNP initially identified in the Danish longitudinal study.

(A) Case-control study (initial findings)				Longitudinal study (similar directions of effects)		
Number-of-days-lived variable						
Pathway	Gene	SNP	OR	β-coef.	95% CI	P-value
GH/IGF-1/INS	INS	rs3842755	1.789	2.73♂	0.66–4.80♂	0.01♂
	IGF2R	rs9456497	1.424	2.77♂	–0.01–5.56♂	0.05♂
DNA repair	WRN	rs13251813	1.840	2.23	0.31–4.15	0.02
Early/late death variable						
Pathway	Gene	SNP	OR	OR	95% CI	P-value
DNA repair	RAD52	rs11571461	2.226	1.30♀	0.96–1.78♀	0.10♀
	NTHL1	rs3211994	1.994♂	1.42	1.09–1.86	0.009
(B) Longitudinal study (initial findings)				Case-control study (similar direction of effect)		
Number-of-days-lived variable						
Pathway	Gene	SNP	β-coef.	OR	95% CI	PCCA
Pro/antioxidants	XDH	rs207444	4.043	1.42	1.10–1.83	0.005

Notes: OR: odds ratio, β-coef: beta coefficient, 95% CI: 95% confidence interval, ♂: males separately, ♀: females separately, PCCA: allelic case-control comparison P-value.

each pathway using the overly conservative Bonferroni approach 8 of the 11 SNPs from the case–control study remained significant, while 1 of the 6 SNPs identified in the longitudinal study remained significant. By contrast, correction by the less conservative [Benjamini and Hochberg \(1995\)](#) method, left more associations significant (10 SNPs from the case–control study and 1 SNP from the longitudinal study), thus underscoring the difference in conclusions based on choice of method of correction. In any case, both of these correction methods assume independency between the tests, which is clearly not the case in our study.

In conclusion we here present new candidate variations for human longevity located in the DNA damage signaling and DNA repair, the GH/IGF-1/INS signaling and pro/antioxidant pathways. We find that 4 of the 17 identified SNP associations show significant and similar direction of effect when using the two different study approaches applied to the Danish discovery cohorts, while 2 SNP associations showed similar tendencies. However, none of the 17 SNP associations displayed replication in the independent samples from Germany and the Netherlands, although for 2 SNP associations some support was noticed.

### Conflicts of interest

The authors have no conflicts to declare.

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### Appendix A. Supplementary data

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