EP20.025

ASSOCIATION BETWEEN LONGEVITY-RELATED SNPS AND REACHING 90.0 YEARS OF AGE AMONG THE ELDERLY CROATIAN POPULATION

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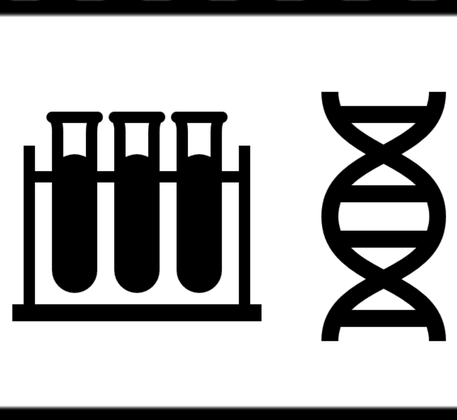
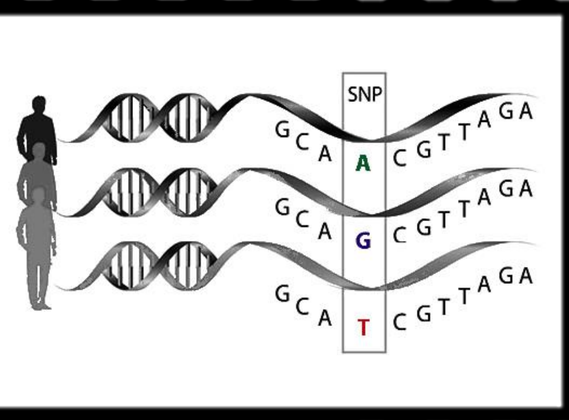
BACKGROUND/OBJECTIVES:

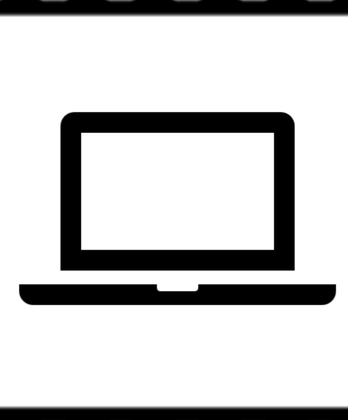
- Human longevity is influenced both by genetic and non-genetic factors, where genetic variability accounts for 25% of human life expectancy variation (1).
- We aimed to elucidate SNPs that are significantly related to longevity as defined by the cut-off age of 90.0 in a sample of elderly persons of European origin.

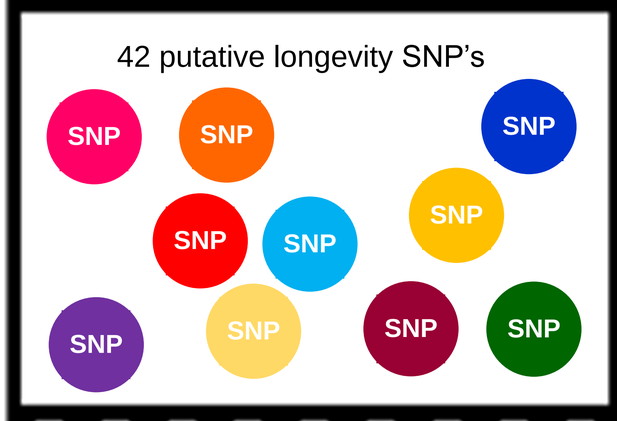
METHODS:

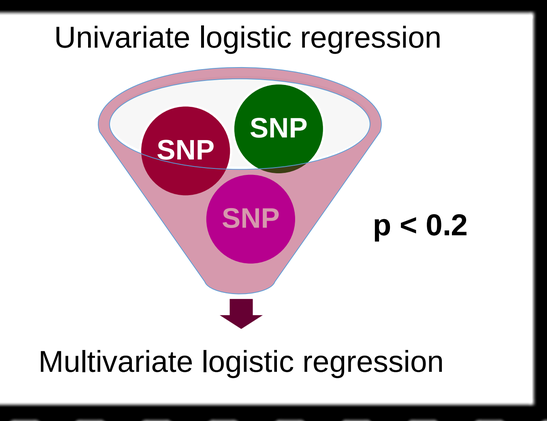
- 42 SNPs – selected due to strong or repeatedly found association with human longevity in other studies – were genotyped in 314 individuals aged 85.0+ from Croatia.
- Univariate and multivariate logistic regressions were performed with genotypic data coded as 2 = longevity allele homozygotes; 1 = heterozygotes; 0 = non-longevity allele homozygotes.

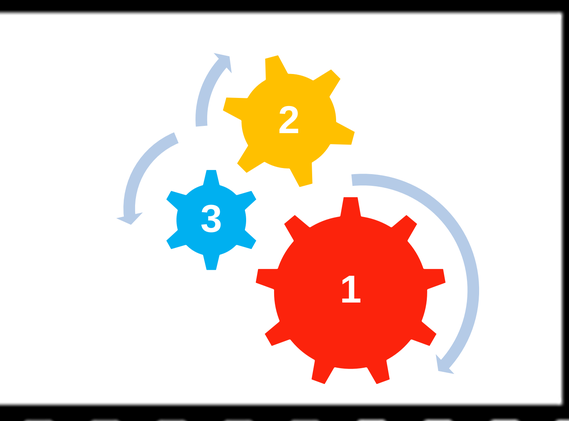












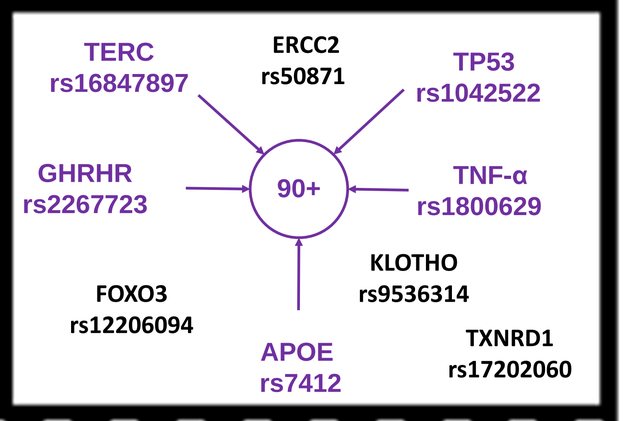


TABLE 1.

Closest gene: SNP	Longevity genotype(s) vs other genotype(s)	B	p	OR	95% C.I. EXP(B)
TERC: rs16847897	GG vs CC GC	0.755	**0.005**	2.128	1.249 - 3.627
GHRHR: rs2267723	AA vs GG, AG	0.824	**0.008**	2.280	1.239 - 4.194
APOE: rs7412	TT, TC vs CC	1.117	**0.016**	3.055	1.230 - 7.587
TNF-α: rs1800629	GG vs AA, GA	0.641	**0.037**	1.898	1.038 - 3.468
TP53: rs1042522	CG vs CC	0.561	**0.046**	1.752	1.010 - 3.040
	GG vs CC	0.833	0.248	2.300	0.559 - 9.456
TXNRD1: rs17202060	TC vs TT	0.705	0.094	2.024	0.887 - 4.621
	CC vs TT	0.292	0.480	1.339	0.595 - 3.012
FOXO3: rs12206094	TC vs CC	-0.363	0.183	0.696	0.408 - 1.187
	TT vs CC	0.847	0.159	2.332	0.717 - 7.583
KLOTHO: rs9536314	GG, TG vs TT	0.454	0.181	1.575	0.809 - 3.065
ERCC2: rs50871	AC vs CC	-0.407	0.229	0.665	0.343 - 1.292
	AA vs CC	0.069	0.856	1.072	0.506 - 2.268

RESULTS & CONCLUSION:

- 16 SNPs that reached inclusion criteria (p < 0.2 in univariate logistic regression) were selected for a series of multivariate logistic regression analyses.
- The best model, explaining 20.5% of variance for survival to the age of 90.0, has 9 SNPs (Table 1).
- Significant association with longevity has been shown for genotypes containing longevity alleles of **TERC rs16847897** and **GHRHR rs2267723** (p<0.01), as well as of **APOE rs7412** and **TNF-α rs1800629** loci (p<0.05), while the same effect was found in **TP53 rs1042522** heterozygotes (p=0.046).
- Loci **FOXO3 rs12206094**, **KLOTHO rs9536314**, **ERCC2 rs50871**, **TXNRD1 rs17202060** although not significant also contribute to the overall quality of the model.
- Our study points to TERC rs16847897 and GHRHR rs2267723 as the most significant genetic predictors for reaching longevity (defined by cut-off age 90.0) in the Croatian elderly population.

REFERENCES

Passarino et al. Human longevity: Genetics or Lifestyle? It takes two to tango. Immun Ageing, 2016;13:12.

ACKNOWLEDGEMENT

Croatian Science Foundation IP-01-2018-2497 (HECUBA)

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