Research Square

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Shorter Leukocyte Telomere Length as a Marker of Biological Aging in Relapsing-Remitting Multiple Sclerosis

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Abstract

Background

Multiple sclerosis (MS) is increasingly recognized not only as an immune-mediated demyelinating disease but also as a disorder characterized by accelerated biological aging. Leukocyte telomere length (LTL) serves as a hallmark biomarker of cellular senescence, yet its predictive role in early-stage MS and its modulation by shelterin complex genetics remain to be fully elucidated.

Methods

In this case-control study, relative LTL was measured via qPCR in a highly characterized, young cohort of patients with relapsing-remitting MS (RRMS; n = 40, age ≤ 40) and age- and sex-matched healthy controls (n = 39). High-Resolution Melting (HRM) analysis was utilized to genotype key shelterin complex polymorphisms: *TERF1* (rs10107605, rs1545827) and *TERF2* (rs251796). Comprehensive genetic association testing across codominant, dominant, recessive, and additive models was conducted alongside clinical/imaging phenotype correlations.

Results

LTL was significantly shorter in RRMS patients than in healthy controls (p = 0.005), suggesting evidence of accelerated biological aging even in this relatively young cohort. ROC analysis demonstrated modest discriminatory performance (AUC = 0.698 (95% CI: 0.60–0.79)). Notably, across all inheritance models, *TERF1* and *TERF2* SNPs exhibited no significant association with LTL. Furthermore, subgroup analyses revealed that LTL attrition was independent of chronological age, sex, smoking status, or disease duration, indicating that telomere erosion is driven primarily by intrinsic disease-related systemic stress rather than host shelterin genetic predisposition.

Conclusions

Our findings demonstrate that leukocyte telomere shortening represents a distinct molecular signature of premature biological aging in young MS patients. By decoupling telomere depletion from primary shelterin genetic variability, this work highlights disease-driven immunosenescence as a key pathophysiological feature of MS. In long-standing, heterogeneous disorders like MS, LTL emerges as a promising prognostic biomarker for capturing biological decline prior to irreversible neurodegeneration. This study provides a foundational framework and strategic catalyst for future longitudinal multi-omics investigations exploring telomere dynamics in chronic neuroinflammation.

Introduction

Multiple sclerosis (MS) is a chronic inflammatory and neurodegenerative disease affecting the central nervous system (CNS), characterized by immune mediated demyelination and progressive axonal damage. The disease usually appears in young adulthood (aged 20 to 40) and has a prevalence approximately three times higher in females than in males (Jakimovski et al., 2024). The disease has shown a noticeable increase worldwide, with approximately 2.9 million people diagnosed with MS [1]. The prevalence of MS is highest in Europe and North America and varies depending on geographic region, genetic susceptibility, and environmental factors [2]. Although the epidemiology of MS is not yet fully understood, studies suggest that low vitamin D levels, smoking, and Epstein-Barr virus (EBV) infection may increase the risk of developing the disease [3, 4]. These environmental factors are thought to contribute to disease development through immune dysregulation and chronic inflammation within the central nervous system, and further increase the risk of the disease when combined with genetic susceptibility. The strongest genetic risk factor for MS is the HLA-DRB1*15:01 allele, which is located within the Major Histocompatibility Complex (MHC) region on chromosome 6 [5].

The clinical presentation and disease course vary substantially among individuals, reflecting the heterogeneity of pathological processes. MS most commonly presents with acute neurological episodes resulting from focal inflammatory demyelinating lesions within the CNS. In the majority of patients, the disease initially follows a relapsing-remitting course, characterized by attacks accompanied by partial or complete clinical recovery. This phase represents an early, immunologically active stage of the disease, predominantly driven by inflammatory mechanisms. Over time, a substantial proportion of patients transition to secondary progressive MS, marked by gradual neurological deterioration and relative decline in overt inflammatory activity, while a smaller subset exhibits a primary progressive disease course from disease onset. These distinct clinical phenotypes reflect changes in the balance between inflammatory and neurodegenerative processes throughout the disease course, underscoring the importance of investigating early biological mechanisms that may influence long term disease trajectories.

The pathophysiological features of MS tend to progress with age. Among the key determinants of disease course, biological aging is thought to contribute to disease activity and progression (Hecker et al., 2021). Biological aging is a process that arises from the accumulation of molecular and cellular damage in cells and tissues over time, leading to a gradual loss of function in the organism in the context of chronic inflammatory diseases. In particular, inflammatory processes driven by cellular aging of immune cells, especially T and B cells, may impair immune response, thereby influencing MS activity (Iribarren-Lopez et al., 2025). The age-related changes in MS highlight the importance of using biological aging biomarkers in clinical studies, particularly in RRMS, where individual variability in immune activity is pronounced. Telomere length is a well-known biomarker of aging, and in recent years, the impact of MS on telomere length has become an important area of research [6].

Telomeres are structures localized at the ends of chromosomes, composed of (TTAGGG)n tandem repeat DNA sequences (5–15 kb in humans), and they play a protective role in maintaining genomic stability. As it is known telomeres shorten with each cell division, providing insight into the age of the cell

[7]. Although telomere shortening is normal consequence of cellular replication, it has also been associated with a wide range of pathological conditions including cardiovascular diseases, cancer, diabetes, rheumatoid arthritis, and neurological disorders such as MS [8, 9]. Studies have shown that peripheral blood leukocytes from patients with MS exhibit shorter telomeres compared to healthy controls [10]. Therefore, in MS, persistent immune cell turnover and inflammatory stress may contribute to alterations in telomere dynamics beyond chronological ageing and results in impaired immune function and chronic inflammation.

Telomere synthesis is maintained by the telomerase enzyme; however, most human somatic cells have lower levels of telomerase. Telomeric repeat binding factor 1 (*TERF1*) and telomeric repeat binding factor 2 (*TERF2*) regulate telomere structure and length partly by modulating telomerase access. Increased expression of these genes has been associated with accelerated telomere shortening. In a study published in 2024 by Duseikaite et al., the relationship between leukocyte telomere length and single nucleotide polymorphisms (SNPs) in the *TERF1* and *TERF2* genes was investigated in patients with optic neuritis, which is closely associated to MS, also taking into account age and sex factors. While no significant differences were found in the overall analyses, the study reported that in males, the *TERF2* rs251796 variant may have a potential protective effect against telomere shortening [11].

Given the pivotal role of telomere dynamics in MS, various methodological approaches have been developed to accurately measure telomere length. Among these methods, quantitative polymerase chain reaction (qPCR), terminal restriction fragment (TRF) analysis, quantitative fluorescence in situ hybridization (Q-FISH), single telomere length analysis (STELA), and telomere shortest length assay (TeSLA) are prominent [12–14]. The selection of the most suitable method requires careful consideration of the strengths and limitations of each approach, as with any experimental technique.

In this study, we aimed to investigate the association between telomere length and MS, focusing on the potential role of telomere dynamics as a biological aging biomarker and its relationship with disease activity and clinical characteristics. While telomere attrition has been reported across various chronic conditions, its evaluation in diseases with extended clinical courses—such as MS—holds strategic clinical value. Beyond merely reflecting past cellular turnover, leukocyte telomere length possesses potential as a predictive biomarker for monitoring biological decline and stratifying patient trajectories early in the disease course.

Patients and Methods

Patients

A total of 79 individuals were enrolled in this case–control study, comprising 40 patients diagnosed with RRMS and 39 healthy controls (Table 1). Patients were consecutively recruited from the Basaksehir Cam and Sakura City Hospital, Department of Neurology between 2024 October-2025 March and all fulfilled the 2017 McDonald diagnostic criteria for MS [15]. Eligible participants were between 18 and 40 years of

age. Exclusion criteria for both groups included a history of other neurological, autoimmune, or systemic disorders, malignancy, or chronic infections. None of the participants reported a family history of telomere-related syndromes or other genetic disorders known to affect telomere biology. Clinical and demographic data, including age, sex, body mass index (BMI), smoking status, disease duration, Expanded Disability Status Scale (EDSS) score at sampling, MRI lesion count, brain volumetric measures, immunological parameters (e.g., IgG index), serum vitamin D levels, and treatment status, were obtained. Clinical relapse history within the last year was also documented. The control group consisted of age- and sex-matched healthy volunteers without neurological or systemic diseases, recruited from the same geographic region as the patient cohort.

Table 1
Patient demographic and clinical characteristics

Age at sampling (years)	**N (%)**	**Mean ± SD**	**Median (range)**
	40	**29.5 ± 5.6**	**27 (18–40)**
Sex			
Male	9 (23)		
Female	31 (77)		
BMI	40 (100)	25.7 ± 4.3	25,4 (18.2–37.8)
Smoking status			
Current	6 (15)		
Former	5 (13)		
Never	27 (68)		
Age of onset (years)	40 (100)	26.11 ± 5.81	25.35 (15–39)
Disease duration (months)	40 (100)	40.74 ± 38.27	22.07 (1.30–145.00)
EDSS at sampling	40 (100)	1.7 ± 1.2	1 (0.5–6)
Lesion count	37 (93)	45.5 ± 24.4	41 (12–121)
Whole brain volume (mm^3)	37 (93)	1433.9 ± 130.1	1452 (1057–1632)
Grey matter volume (mm^3)	37 (93)	822.2 ± 80.1	836 (583–952)
Lesion volume (mm^3)	37 (93)	5.92 ± 5.7	4.59 (0.67–22.56)
IgG index	28 (70)	1.0 ± 0.7	0.76 (0.54–3.65)
Vit-D (pg/dL)	38 (95)	23.1 ± 17.2	22 (4–96)
Attack in last one year			
Yes	14 (35)		
No	26 (65)		

DNA Extraction and Genetic Analyses

Peripheral blood leukocytes were isolated and stored at − 80°C until use. Genomic DNA was subsequently extracted using the QIAamp DNA Mini Kit (Qiagen, Germany) according to the manufacturer's protocol. DNA concentration and purity were assessed with a NanoDrop

spectrophotometer (Thermo Fisher Scientific, USA). DNA samples were diluted to a final concentration of 20 ng/µl and stored at − 20°C for further experiments.

Relative telomere length measurement was performed according to the protocol described previously by Joglekar et al. [16]. Briefly, telomeric repeats (T) and the single-copy reference gene β-globin (S) were amplified in separate quantitative PCR reactions using PowerUp™ SYBR™ Green Master Mix (Applied Biosystems, Waltham, MA, USA). Reactions were carried out on a CFX96 Real-Time PCR Detection System (Bio-Rad, USA) in a final volume of 10 µl, containing 20 ng of genomic DNA. The primer sequences used were as follows: Telomere forward (TelA), 5'-CGGTTTGTTTGGGTTTGGGTTTGGGTTTGGGTTTGGGTT-3'; Telomere reverse (TelB), 5'-GGCTTGCCTTACCCTTACCCTTACCCTTACCCTTACCCT-3'; β-globin forward (hbg1), 5'-GCTTCTGACACAACTGTGTTCACTAGC-3'; β-globin reverse (hbg2), 5'-CACCAACTTCATCCACGTTCACC-3'. Each sample was analyzed in duplicate together with no-template controls and inter-plate calibrators. Relative telomere length was expressed as the ratio of telomere repeat copy to single gene (β-globin) copy number (T/S ratio), calculated by the comparative Ct (2^ΔCt) method.

We applied High Resolution Melting (HRM) analysis, a post-PCR technique that enables the detection of single nucleotide polymorphisms (SNPs). This method was used to genotype rs10107605 (*TERF1*), rs1545827 (*TERF1*), and rs251796 (*TERF2*) polymorphisms, which have been previously associated with telomere length shortening [11]. These SNPs belong to Class I and II variants and can be reliably distinguished in genomic DNA based on differences in their HRM profiles, enabling accurate and efficient genotyping. Specific primers were designed for each SNP as follows: rs10107605 forward 5'-AGTGCCGTAGAAGAGTTTTTGA-3' and reverse 5'-ACCTTGGTAACATCGGGACA-3' (161 bp); rs1545827 forward 5'-AGAGCTGTTCCACTTGCCTT-3' and reverse 5'-AGGAGTACAGGGCCAAGAGT-3' (122 bp); rs251796 forward 5'-TGAAGTGCTGGAGAATTTCTTGT-3' and reverse 5'-AATTACTGATACTTGGCATTTGC-3' (132 bp). PCR reactions were prepared in a final volume of 15 µl, containing 7.5 µl of AccuMelt HRM SuperMix (Quantabio, USA), 0.75 µl of each primer (2.5 µM), 1 µL of genomic DNA template (20 ng/µl), and 5 µl of nuclease-free water. The amplification program consisted of an initial denaturation at 95°C for 5 minutes, followed by 40 cycles of denaturation at 95°C for 10 seconds, and annealing/extension at 60°C for 30 seconds. HRM analysis was subsequently performed over a range of 65–95°C, with a temperature increment of 0.2°C/s. HRM data were analyzed using uAnalyze software (version 2.1) to determine genotypes of each sample.

Statistical analyses

Statistical analyses were performed using IBM SPSS Statistics (29.0.2). Continuous variables were summarized as mean ± standard deviation (SD) and categorical variables as frequency and percentages. Normality of distributions was assessed using the Shapiro–Wilk test, and homogeneity of variances was evaluated prior to parametric testing. Between-group comparisons of continuous variables (e.g., telomere length) were conducted using independent samples t-tests when assumptions were met. Receiver operating characteristic (ROC) curve analysis was applied to determine the discriminatory

performance of telomere length between patients and controls, and the area under the curve (AUC) was calculated as a measure of performance. The effect of genotype on telomere length was examined using Binary Logistic Regression analysis with the Enter method. Genotype frequencies of single nucleotide polymorphisms (SNPs) were assessed for conformity with Hardy–Weinberg equilibrium (HWE) in the control group using the Chi-square test. Genotype–phenotype associations between SNPs and telomere length were investigated under codominant, dominant, recessive, overdominant, and additive genetic models. Statistical significance was set at $p < 0.05$ for all analyses.

Results

Baseline demographic and clinical features of the study population are summarized in Table 1. Patients and controls were broadly comparable in terms of age and sex distribution, with female comprising the majority in both groups (77%). The mean BMI of patients was in the overweight range, and most patients reported never smoking, with a minority being current or former smokers. Brain volumetric measures, including whole brain and grey matter volumes, showed inter-individual variability but were largely within expected ranges for the studied age group. Immunological and biochemical parameters also demonstrated heterogeneity, particularly in serum vitamin D levels, which ranged from markedly deficient to adequate values. Approximately one-third of the patients experienced a clinical relapse in the previous year, while the majority remained relapse-free.

Telomere length analysis was first conducted to evaluate potential differences between patients and controls. Relative telomere length was quantified by qPCR using the ΔCt method with β-globin as the reference gene. The patient group exhibited a mean ΔCt of 7.53 ± 0.31, whereas the control group had a mean ΔCt of 7.73 ± 0.31 (Table 2). Both groups satisfied the assumptions of parametric testing, showing normal distribution according to the Shapiro–Wilk test ($p > 0.05$) and equal variance across groups. Accordingly, an independent samples t-test was applied, and it revealed a statistically significant difference between the groups ($t = 2.89$, $p = 0.0050$). These results indicate that telomere length was significantly shorter in the patient cohort compared with healthy controls (Fig. 1). To further explore potential modifiers of telomere length, subgroup analyses were performed according to demographic and clinical variables such as age, sex, smoking status, and other relevant clinical characteristics among MS patients. Relative telomere length did not differ significantly across any of these subgroups ($p > 0.05$), suggesting that the observed telomere shortening in patients compared to controls was independent of demographic and clinical characteristics. In addition, disease duration was not associated with telomere length in MS patients ($p = 0.431$), and the association remained non-significant after age adjustment ($p = 0.356$).

Table 2
Telomere length between patient and control groups (ΔCt = $Ct_{\beta-globin}-Ct_{telomere}$, T/S ratio = 2^ΔCt)

	N	ΔCt (mean ± SD)	T/S ratio (mean ± SD)	t (df)	p-value
Patients	40	7.53 ± 0.31	189.28 ± 42.11	2.89(77)	**0,0050**
Controls	39	7.73 ± 0.31	217.18 ± 43.79		

As an additional analysis, the discriminatory capacity of telomere length between patients and controls was evaluated using a ROC curve. The resulting area under the curve (AUC) was 0.698, indicating modest discriminatory ability between patients and controls. (Fig. 2). Despite the statistically significant difference in mean values, there was considerable overlap in telomere length distributions across patients and controls.

Hardy–Weinberg equilibrium (HWE) analysis was subsequently performed to assess the genetic balance of the control population. All examined SNPs were found to be in HWE, supporting the validity of further association analyses (rs10107605 p = 0.7804, rs251796 p = 0.6028, rs1545827 p = 0.9240). Following confirmation of HWE, genotype–phenotype correlation analyses were performed to examine whether the investigated SNPs influenced telomere length. Multiple inheritance models were applied, including codominant, dominant, recessive, overdominant, and additive models. Across all models, no statistically significant associations were observed (Table 3). These findings collectively indicate that the studied SNPs did not significantly contribute to inter-individual variation in telomere length in this population.

Table 3
Binary logistic regression analysis of rs10107605, rs251796 and rs1545827 in relative telomere length among all participants

Model		OR (%95CI)	p-value	AIC
	rs10107605			
Codominant	AC vs AA	1.222 (0.288–5.222)	0.782	101.935
	CC vs AA	0.459 (0.014–14.845)	0.660	102.005
Dominant	AC + CC vs AA	0.893 (0.270–4.489)	0.893	95.435
Recessive	CC vs AA + AC	2.157 (0.086–54.076)	0.640	103.866
Overdominant	AC vs AA + CC	0.697 (0.162–3.008)	0.629	97.942
Additive	C	0.810 (0.814–1.651)	0.506	101.827
	rs1545827			
Codominant	CT vs CC	1.471 (0.296–7.321)	0.637	89.114
	TT vs CC	1.330 (0.173–10.249)	0.784	91.016
Dominant	CT + TT vs CC	1.436 (0.313–6.580)	0.641	99.082
Recessive	TT vs CC + CT	0.940 (0.148–5.974)	0.947	94.645
Overdominant	CT vs CC + TT	0.767 (0.193–3.055)	0.707	112.754
Additive	T	0.734 (0.088–6.143)	0.785	104.852
	rs251796			
Codominant	AG vs AA	0.386 (0.089–1.670)	0.203	97.328
	GG vs AA	0.352 (0.030–4.145)	0.407	95.419
Dominant	AG + GG vs AA	0.366 (0.086–1.555)	0.173	107.008
Recessive	GG vs AA + AG	0.662 (0.074–5.889)	0.711	99.895
Overdominant	AG vs AA + GG	0.459 (0.113–1.856)	0.275	112.289
Additive	G	2.692 (0.252–28.708)	0.988	108.654

Discussion

In this study, we demonstrated that leukocyte telomere length is significantly shorter in patients with MS compared with age- and sex-matched healthy controls, independent of demographic and clinical factors. Notably, no significant association was observed between telomere length and the investigated *TERF1* (rs10107605, rs1545827) or *TERF2* (rs251796) single nucleotide polymorphisms (SNPs). These findings

suggest that accelerated telomere attrition may represent a molecular signature of biological aging in MS, while the examined genetic variants appear to play a minimal role in modulating inter-individual telomere length in this cohort.

Our results are consistent with prior reports demonstrating shorter telomeres in MS patients relative to healthy individuals [6, 10]. These observations support the hypothesis that MS is associated with accelerated cellular aging, likely driven by chronic immune activation and oxidative stress. Several studies have proposed that chronic inflammation and repeated immune cell proliferation lead to telomere shortening, particularly in T and B lymphocytes, which are central mediators of MS pathophysiology [7, 9]. In contrast, some investigations with smaller sample sizes or heterogeneous patient populations have not identified significant differences, suggesting that cohort characteristics, disease stage, and methodological variability may influence outcomes [17–19].

Telomere attrition in immune cells has functional consequences relevant to MS [20]. Shortened telomeres limit the proliferative capacity of T and B cells, contributing to immunosenescence and impaired immune surveillance [21]. This phenomenon may exacerbate chronic low-grade inflammation and compromise immune regulation, potentially accelerating neurodegenerative processes [8]. The observed telomere shortening may therefore reflect a bidirectional relationship: chronic neuroinflammation drives telomere erosion, which in turn impairs immune competence, creating a feedback loop that could promote disease progression [22].

Our analysis of *TERF1* and *TERF2* SNPs did not reveal a significant effect on telomere length. While these genes encode proteins essential for telomere maintenance, the lack of association may be attributable to several factors. First, the examined SNPs may exert only subtle functional effects that are difficult to detect in moderate-sized cohorts. Second, telomere dynamics are influenced by a combination of genetic, epigenetic, and environmental factors, including oxidative stress, vitamin D status, and treatment exposure [11]. Therefore, additional genomic loci or regulatory mechanisms may exert stronger influence on telomere length in MS than the *TERF1*/*TERF2* variants analyzed here. The absence of association between *TERF1*/*TERF2* variants and LTL in our cohort is a critical mechanistic finding. It strongly suggests that telomere shortening in young RRMS patients is not an inherited structural vulnerability dictated by shelterin complex architecture, but rather an acquired biological consequence driven by ongoing systemic inflammation, oxidative stress, and persistent immune cell turnover.

From a clinical perspective, telomere length holds potential as a biomarker of biological aging and disease related biological processes in MS [6, 23]. In our study, the ROC analysis yielded an area under the curve (AUC) of 0.698, indicating moderate discriminatory ability between patients and controls. Although telomere length alone is unlikely to serve as a stand alone diagnostic marker, it may become more informative when integrated into composite panels alongside immunological, neuroimaging, and biochemical parameters. Such multidimensional models could provide a more comprehensive assessment of biological age, disease burden, and treatment response.

The study also provides insight into the independence of telomere shortening from other clinical variables. Subgroup analyses demonstrated that telomere length did not significantly differ across age, sex, smoking status, or disease duration among MS patients. These findings suggest that telomere attrition reflects intrinsic biological aging mechanisms rather than being merely a consequence of disease duration or modifiable lifestyle factors. This is particularly relevant for younger adults with MS, for whom accelerated cellular aging may precede overt clinical progression. In this context, the restriction of the study cohort to patients with RRMS under 40 years of age, in comparison with age-matched healthy controls further strengthens the interpretation of these findings. This design minimizes the confounding effect of chronogical age and suggests that telomere shortening may be detectable even before transition to a progressive disease phase, during an early and immunologically active stage.

Several limitations of the present study warrant consideration. The sample size was moderate, which may limit the statistical power to detect subtle genotype–phenotype relationships. However, although our sample size is moderate, the strict enrollment criteria—focusing exclusively on young adults (age < 40) with RRMS—effectively controlled for the dominant confounding effect of chronological aging, thereby amplifying the biological signal of disease-specific telomere attrition. Additionally, telomere length was measured in peripheral blood leukocytes, which may not fully represent telomere dynamics in CNS resident cells such as microglia or oligodendrocytes [24]. Nevertheless, given the central role of immune cells in MS pathophysiology and their interaction with CNS inflammation, peripheral leukocyte telomere length may still provide meaningful insight into MS related biological aging processes. Future studies incorporating tissue-specific analyses could clarify whether peripheral leukocyte telomere shortening directly mirrors CNS aging. Moreover, cumulative treatment exposure and inflammatory burden were not quantitatively assessed; these factors could influence telomere attrition and may be relevant confounders in longitudinal studies.

Despite these limitations, the study provides robust evidence that telomere shortening is a characteristic feature of MS and may serve as an informative biomarker of biological aging. It underscores the importance of considering cellular aging mechanisms in understanding MS pathophysiology, particularly given the increasing recognition of age-related influences on disease progression. Furthermore, the lack of association with the analyzed *TERF1*/*TERF2* SNPs highlights the need for broader genomic and epigenetic investigations to identify determinants of telomere dynamics in this population.

In conclusion, our findings support the hypothesis that accelerated telomere attrition reflects a component of biological aging in multiple sclerosis. While the studied *TERF1* and *TERF2* variants did not significantly contribute to telomere length variation, the observed telomere shortening reinforces the relevance of cellular aging processes in MS pathogenesis. Future longitudinal and multi-omics studies are warranted to clarify the causal pathways linking telomere biology, immune dysfunction, and neurodegeneration, and to explore the potential utility of telomere length in capturing disease related biological heterogeneity.

Declarations

Conflict of interest

The authors declare that they have no conflict of interest.

Author contributions

The experiments were performed by Ilker Karacan, Seda Susgun, Begum Yigit, Deniz Yozlu, Nur Damla Korkmaz and Omer Faruk Duzenli. Clinical evaluations were performed by Didem Savasci and Azize Esra Basar Gursoy. Statistical analyses were performed Ilker Karacan and Aysegul Yabaci. Azize Esra Basar Gursoy conceptualized and supervised the study with additional guidance from Emrah Yucesan. The original draft with input from all other authors was written by Ilker Karacan. All authors have read and approved the final version of the manuscript.

Availability of Data and Materials

The datasets used and analysed during the current study are available from the corresponding author on reasonable request.

Ethical approval

This study was approved by the Bezmialem Vakif University, Clinical Research Ethics Committee (Date and number: 09.09.2024-E.164564) and was conducted in accordance with the principles of the Declaration of Helsinki.

Consent to participate

Informed consent was obtained from all individual participants included in the study.

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Figures

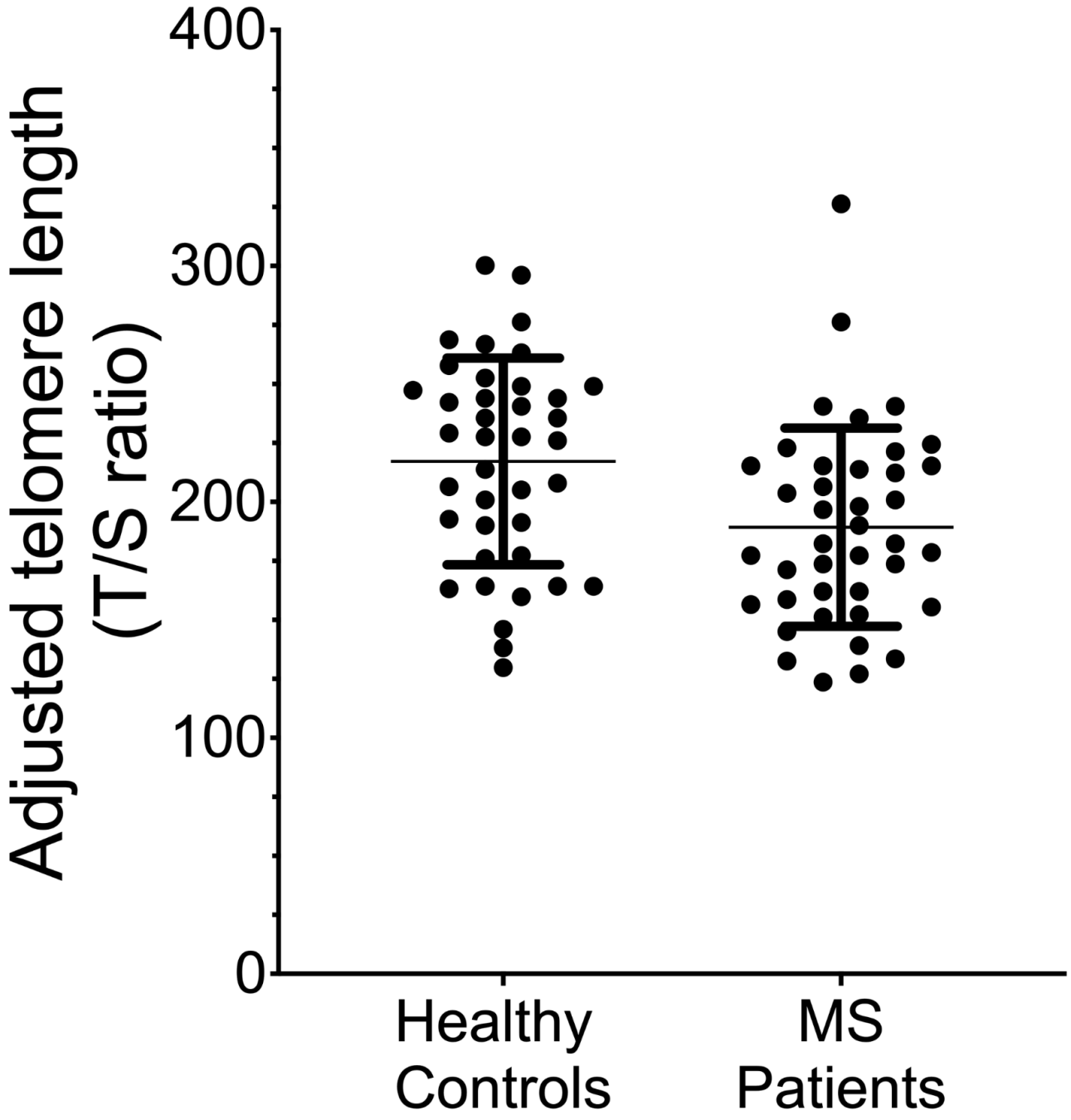

Figure 1

Relative telomere length comparison between patients and healthy controls.

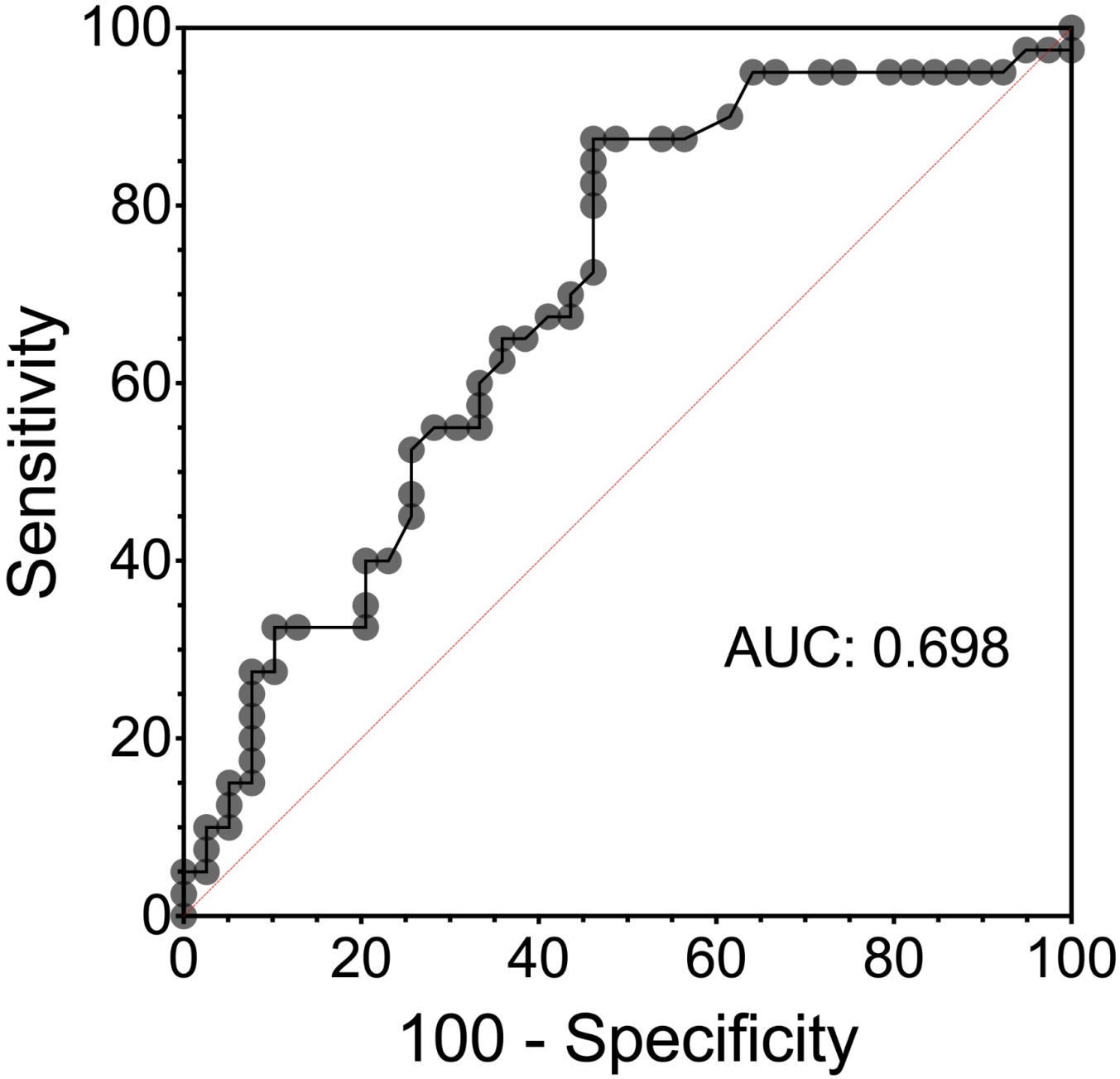

Figure 2

ROC analysis evaluating the discriminative performance of telomere length.