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Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

Sta	atistics
For	all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.
n/a	Confirmed
	\square The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
	The statistical test(s) used AND whether they are one- or two-sided Only common tests should be described solely by name; describe more complex techniques in the Methods section.
	A description of all covariates tested
	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
	For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
\boxtimes	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
\boxtimes	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
	Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated
,	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.
So	ftware and code
Poli	cy information about <u>availability of computer code</u>
ata co	llection Not software was used. Data included in this study is available in https://github.com/Al-BrainLat-team/Latam-Aging-Meta-Analysis/tree/main/Data
Data	analysis All models and statistical analyses were run using Python version 3.9.13. Code is avaiable in GitHub at https://github.com/Al-BrainLat-team Latam-Aging-Meta-Analysis
	nanuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and wers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.
Da	ta
Poli	cy information about <u>availability of data</u>

Data included in this study is available in GitHub at https://github.com/Al-BrainLat-team/Latam-Aging-Meta-Analysis/tree/main/Data

- Accession codes, unique identifiers, or web links for publicly available datasets

- For clinical datasets or third party data, please ensure that the statement adheres to our policy

Databases used in this study included MEDLINE; EMBASE; Virtual health library, and Web of science

- A description of any restrictions on data availability

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

Research inv	olving nu	man participants, their data, or biological material
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Seed stocks	N/A
Novel plant genotypes	N/A
Authentication	N/A