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Caglayan, A.B., Beker, M.C., Felix-Ilemhenbho, F. et al. (2026) Intergenerational conditioning via intermittent parental hypoxia confers stroke resilience in offspring. *Stroke*. ISSN: 0039-2499

<https://doi.org/10.1161/strokeaha.125.052885>

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Intergenerational Conditioning via Intermittent Parental Hypoxia Confers Stroke Resilience in Offspring

Ahmet B. Caglayan^{*1,2}, Mustafa C. Beker^{*2,3}, Favour Felix-Ilemhenbho^{*4}, Serdar Altunay^{2,5}, Hayriye E. Yelkenci², Aysun Caglayan², Enes Dogan^{2,6}, Nilay Ates⁷, Ok-Nam Bae⁸, David J. Burrows⁴, Ali Ali⁴, Milena De Felice^{9,10}, Ertugrul Kilic^{+2,3}, Arshad Majid^{+4,10}✉

Ahmet B. Caglayan, BSc, MSc, PhD: caglayan@umich.edu

Mustafa C. Beker, BSc, MSc, PhD: m.caglarbeker@gmail.com

Favour Felix-Ilemhenbho BSc, MSc, MRes, PhD: f.felix-ilemhenbho@sheffield.ac.uk

Serdar Altunay, BSc, MSc, PhD: saltunay@medipol.edu.tr

Hayriye E. Yelkenci, BSc, MSc, PhD: heyelkenci@medipol.edu.tr

Aysun Caglayan, BSc, MSc, PhD: aysuncag@umich.edu

Enes Dogan, BSc, MSc: doganenes60@gmail.com

Nilay Ates, BSc, PhD: nilay.ates@medeniyet.edu.tr

Ok-Nam Bae, BSc, MSc, PhD: onbae@hanyang.ac.kr

David J. Burrows, BSc, PhD: d.burrows@sheffield.ac.uk

Ali Ali, MBChB, MSc: ali.ali@sheffield.ac.uk

Milena De Felice, BSc, PhD: m.defelice@sheffield.ac.uk

Ertugrul Kilic, BSc, PhD: kilic44@yahoo.com

Arshad Majid, MBChB: arshad.majid@sheffield.ac.uk

¹Division of Hematology and Oncology, Department of Internal Medicine, University of Michigan, Ann Arbor, Michigan.

²Regenerative and Restorative Medical Research Center (REMER), Research Institute for Health Sciences and Technologies (SABITA), Istanbul Medipol University, Istanbul, Türkiye.

³Department of Physiology, Faculty of Medicine, Istanbul Medeniyet University, Istanbul, Türkiye.

⁴University of Sheffield, Sheffield Institute for Translational Neuroscience (SITraN), Sheffield, S10 2HQ, UK.

⁵Department of Physiology, Faculty of Medicine, Istanbul Medipol University, Istanbul, Türkiye.

⁶Department of Immunology, Faculty of Medicine, Istanbul Medeniyet University, Istanbul, Türkiye.

⁷Department of Medical Pharmacology, Faculty of Medicine, Istanbul Medeniyet University, Istanbul, Türkiye.

⁸College of Pharmacy Institute of Pharmaceutical Science and Technology, Hanyang University, Ansan, Republic of Korea.

⁹University of Sheffield, School of Clinical Dentistry, Sheffield, S10 2TA, UK.

¹⁰University of Sheffield, Neuroscience Institute, Sheffield, S10 2TN, UK.

*Authors contributed equally to the publication and share first-authorship.

+Authors contributed equally to the publication and share last-authorship.

✉ Corresponding author (arshad.majid@sheffield.ac.uk).

38 **Author contributions**

39 A.M. conceptualised the work. A.M.: designed the experiments; A.B.C, M.C.B., S.A., H.E.Y., A.C.,
40 carried out the animal work; F.F-I, A.B.C., M.C.B., O-N.B, D.J.B., A.A., M.D.F. and A.M analysed
41 the data from the animal work; F.F-I, M.C.B, and E.D. analysed the proteomics dataset. F.F-I, E.K.,
42 and A.M. wrote the original draft; M.D.F., D.J.B., A.A., O-N.B reviewed and edited the manuscript.
43 All authors have read and agreed to the published version of the manuscript.

44 **Author and department social media handle**

45 @fav.felix.ilem (Instagram) @FavFelixIlem (twitter)
46 @theuniversityofsheffield (Instagram) @sheffielduni (twitter)
47 @istmedeniyet (twitter)
48 @mcaglarbeker (twitter)

49 **Funding sources**

50 F.F-I was funded by the National Institute for Health and Care Research (NIHR) Sheffield
51 Biomedical Research Centre (NIHR203321). The views expressed are those of the author(s) and
52 not necessarily those of the NIHR.

53 **Brief summary**

54 Parental intermittent hypoxia induces intergenerational resilience to ischaemic stroke in mice,
55 reducing infarct size in offspring via sex- and lineage-specific molecular adaptations.

56 **Disclourses**

57 None

58 **Number of figures and tables**

59 3 Figures

60 **List of the supplemental materials**

61 Supplemental Tables S1-4
62 Supplemental Methods 1-6
63 Supplemental Discussion 1-2

64 **Abstract**

65 **Background:**

66 Intergenerational disease transmission, where parental exposures or experiences influence disease
67 susceptibility in offspring, may represent a crucial layer of stroke risk that extends beyond genetics
68 alone. Environmental conditioning, such as intermittent sub-lethal hypoxia, can induce adaptive
69 protective stress responses in the brain. However, whether such parental conditioning enhances
70 offspring resilience to cerebral ischaemia remains unclear. This study investigates whether
71 intermittent hypoxia in parents acts as an intergenerational conditioning stimulus, conferring
72 resilience to ischaemic stroke in offspring, and explores associated molecular mechanisms.

73 **Methods:**

74 Male and female Balb/C mice (F0; 8-10 weeks old) were exposed to intermittent hypoxia (8% O₂, 2
75 hours every other day, 16 cycles) prior to mating. To confirm parental neuroprotection, F0 mice
76 underwent transient middle cerebral artery occlusion (tMCAO). Offspring (F1) from hypoxia-exposed
77 F0 were divided into biparental, paternal-only, maternal-only hypoxia, and normoxic groups. Adult
78 F1 (8-10 weeks old) offspring also underwent tMCAO to model ischaemic stroke. Infarct volume and
79 brain swelling were assessed 48 hours post-ischaemia. A subgroup of F0 and F1 brains was
80 analysed by tandem mass tag proteomics to identify molecular pathways linked to neuroprotection.

81 **Results:**

82 Parental intermittent hypoxia significantly reduced infarct size and swelling in F0 mice. These
83 protective effects were inherited by F1 offspring, with biparental exposure producing the greatest
84 reduction in infarct volume, followed by maternal-only and paternal-only groups, and exhibiting sex-
85 specific differences. Proteomic profiling revealed distinct treatment and lineage clusters. Key
86 pathways implicated in offspring neuroprotection included metabolic regulation, immune signalling,
87 cytoskeletal organisation, and cell survival, notably involving PI3K-Akt and EGFR pathways.

88 **Conclusions:**

89 Intermittent hypoxia in parents acts as an intergenerational conditioning stimulus, conferring
90 offspring resilience to stroke. This neuroprotective phenotype is supported by coordinated molecular
91 adaptations in key pathways involved in survival and stress response. These findings highlight the
92 potential for parental environmental conditioning to shape stroke outcomes in offspring, opening
93 new avenues for therapeutic exploration.

94

95 **Non-standard Abbreviations and Acronyms**

Abbreviation	Definition
BALB/c	Inbred mouse strain originally derived from the Bagg albino lineage
DEP	Differentially expressed protein
F0	Parental generation
F1	First filial (offspring) generation
KEGG	Kyoto Encyclopedia of Genes and Genomes
LDF	Laser Doppler flowmetry
MCA	Middle cerebral artery
tMCAO	Transient middle cerebral artery occlusion
RIPC	Remote ischaemic preconditioning

96

1. Introduction

Ischaemic stroke is a leading cause of adult disability worldwide, and despite advances in acute management, outcomes remain highly variable. While genetic factors undoubtedly contribute to stroke susceptibility, a growing body of evidence suggests that intergenerational disease transmission, in which parental exposures or experiences influence offspring vulnerability, plays an important role in determining stroke risk and severity¹.

One potential mechanism by which parents might influence offspring stroke outcomes is via environmental conditioning². For instance, parental stress or toxin exposure has been linked to altered offspring neurodevelopment and increased susceptibility to neurological disorders via epigenetic modifications^{3,4}. Additionally, environmental conditioning such as exercise or caloric restriction in parents can improve offspring cognitive function and resilience to brain injury^{5,6}.

Intermittent sub-lethal hypoxia is a well-established preconditioning stimulus that can induce neuroprotective adaptations in the brain, largely through activation of stress response pathways, improved metabolic efficiency, and modulation of cell survival mechanisms^{2,7}.

Both remote ischemic preconditioning (RIPC) and intermittent hypoxia are established methods to induce a prolonged state of ischemic tolerance in preclinical models⁸. Delayed RIPC improves long-term sensorimotor deficits in neonatal rats up to five weeks after hypoxic-ischemic injury⁹. Interestingly, a key study in adult mice demonstrated that intermittent hypoxia conferred protection for up to eight weeks after the end of the conditioning regimen¹⁰. These results suggest a lasting change in neurovascular physiology, which could potentially serve as the basis for intergenerational transmission of resilience.

However, whether parental exposure to intermittent hypoxia can confer intergenerational resilience to ischaemic injury in offspring has not been fully explored. Here, we investigate whether parental intermittent hypoxia acts as an intergenerational conditioning stimulus to enhance offspring resilience to ischaemic stroke. Using a well-established BALB/c mouse model of transient middle cerebral artery occlusion (tMCAO)¹¹, we assess infarct volume and brain swelling in offspring from different parental hypoxia exposures.

To further enhance the clinical relevance of our findings, we included both male and female mice to investigate potential sex-specific responses, reflecting the known differences in stroke outcomes observed in human populations.

2. Materials and Methods

Availability of Data

The raw data from this study are available from the corresponding author upon reasonable request.

Animals and Experimental Procedures

All procedures were approved by the Ethics Committee of Istanbul Medipol University (2020/16) and conducted in accordance with the Declaration of Helsinki and relevant institutional guidelines. This study adhered to ARRIVE (Animal Research: Reporting of In Vivo Experiments) guidelines to ensure transparency, reproducibility, and ethical standards¹². All experimental procedures occurred in a controlled environment with standard housing conditions, including a 12:12-hour light-dark cycle, temperature control, and environmental enrichment.

BALB/c mice were selected for their extensive use and well-characterised profile in stroke, immune, and epigenetic studies¹³⁻¹⁸ (see Supplemental Method 1 for model rationale).

Experimental groups included F0 parental Balb/C mice exposed to intermittent hypoxia or normoxia, and their F1 offspring subdivided by parental exposure (biparental, maternal-only, paternal-only, and normoxic controls).

Details of the experimental design, sample size determination, randomisation procedures, and blinding strategy are provided in Supplemental Method 2.

Intermittent hypoxia was induced using a controlled 8% O₂ exposure paradigm¹⁹ (Figure 1A) adapted from established preconditioning protocols²⁰⁻²² (see Supplemental Method 3).

Transient Middle Cerebral Artery Occlusion (tMCAO)

tMCAO was performed using the standard intraluminal filament technique¹¹ under isoflurane anaesthesia (see Supplemental Method 4).

Laser Doppler flowmetry (LDF) recordings showed a consistent reduction in cerebral blood flow following MCA occlusion across all animals (Supplementary Table S1-3).

Infarct volume (mm³) and brain swelling (%) were quantified from cresyl violet–stained 2-mm coronal sections at 2 days post-ischæmia using established methods^{23,24} (see Supplemental Method 5). Oedema-corrected infarct volumes, expressed as a percentage of the ipsilateral hemisphere, are presented in Supplementary Table S4²⁵.

Proteomics

Damaged hemisphere samples were collected from the ipsilateral hemisphere at 55 days post-stroke, specifically encompassing both the infarct core and peri-infarct regions. Samples were obtained from F0 (12 weeks old) and F1 (8-10 weeks old) mice. Tissue was dissected, homogenised, and processed for protein extraction²⁶.

Proteomic profiling was performed by LC-MS/MS, and pathway enrichment analysis was conducted using established bioinformatics tools (see Supplemental Method 6).

Statistical analysis

Data were analysed using t-tests or one-way ANOVA with Dunnett's multiple comparisons test, as appropriate, in GraphPad Prism (v10.4.2) and R. Results are reported as mean ± SEM, with $p < 0.05$ considered statistically significant. All reported results met parametric assumptions.

3. Results

Hypoxic preconditioning in F0 mice reduces ischaemic brain injury

To determine the effect of intermittent hypoxia on stroke outcomes, we compared infarct volumes and brain swelling in F0 mice subjected to tMCAO. As previously demonstrated by us and others, intermittent hypoxia significantly reduced infarct volume (25.01% reduction; $p = 0.0032$) and brain swelling (24.86% reduction; $p = 0.0099$) compared to normoxic controls (Figure 1B).

Breeding from hypoxia-exposed parents produced four F1 groups: paternal-only, maternal-only, biparental hypoxia, and normoxic controls. Following tMCAO in adult F1 offspring, all hypoxic groups exhibited reduced infarct volume and brain swelling, with sex-specific differences (Figure 1C-D).

175 In males (Figure 1C), infarct volume was significantly reduced in the paternal (37.5% reduction; $p =$
176 0.0030), maternal (45% reduction; $p = 0.0005$), and biparental (42.5% reduction; $p = 0.0007$) groups
177 compared to normoxic controls. However, only the maternal (56.52% reduction; $p < 0.0001$) and
178 biparental (34.78% reduction; $p = 0.0125$) groups showed significantly reduced brain swelling;
179 paternal hypoxia showed a non-significant trend (26.10% reduction; $p = 0.0929$).

180 In females (Figure 1D), infarct volume was significantly reduced in the maternal (26.92% reduction;
181 $p = 0.0272$) and biparental (40.38% reduction; $p = 0.0007$) groups, with a non-significant trend in
182 the paternal group (19.23% reduction; $p = 0.1883$). Brain swelling showed a similar pattern, with
183 significant reductions in the maternal (53.33% reduction; $p = 0.0008$) and biparental (40.0%
184 reduction; $p = 0.0185$) groups, but no reduction in the paternal group compared to normoxic controls.

185 **Proteomic insights into intergenerational neuroprotection**

186 Building on the observed neuroprotection in both F0 and F1 mice, we performed proteomic analysis
187 to explore underlying molecular mechanisms. For F0 mice, we analysed both male and female
188 brains. F1 analyses focused on females, as the maternal and biparental hypoxia groups consistently
189 exhibited the most robust reductions in infarct volume and brain swelling. This approach aimed to
190 enhance the signal-to-noise ratio and increase the likelihood of identifying molecular signatures
191 associated with intergenerational neuroprotection.

192 Unsupervised hierarchical clustering of the proteomic data revealed clear segregation by treatment
193 and lineage (Figure 2A). F0 and F1 normoxic female samples clustered together, indicating
194 consistency across generations in the absence of hypoxic preconditioning. In contrast, F1 hypoxic
195 groups (maternal, paternal, and biparental) formed a distinct cluster, suggesting coordinated protein
196 expression changes linked to ancestral hypoxia exposure. Interestingly, F0 hypoxic and normoxic
197 males clustered together, indicating limited proteomic alterations, while F0 hypoxic females diverged
198 from normoxic controls, highlighting a sex-specific response to intermittent hypoxia.

199 **Differential proteomic responses in F0 hypoxic mice**

200 Consistent with the hierarchical clustering, differential expression analysis revealed that hypoxia
201 exposure altered the expression of 31 proteins in F0 males and 477 proteins in F0 females
202 compared to their respective normoxic controls ($p < 0.05$; Figure 2B-E). Seventeen proteins were
203 commonly differentially expressed in both sexes, suggesting a shared molecular response (Figure
204 2B). Among these, *Gnai3* was upregulated and *Marcks11* was downregulated in both hypoxic males
205 and females. Notably, *Gnai3* has been implicated in cerebral ischaemic injury and identified as a
206 target of Astragaloside IV in a rat stroke model ²⁷, highlighting its potential relevance to
207 neuroprotection. *Marcks11* has been identified as a differentially expressed gene in the mouse
208 corpus callosum of ageing mice ²⁸, suggesting a potential role in age-related neurological disorders.

209 KEGG (Kyoto Encyclopedia of Genes and Genomes) pathway enrichment analysis of differentially
210 expressed proteins (DEPs) in F0 females revealed significant enrichment in pathways related to
211 protein digestion and absorption, thyroid hormone synthesis, mineral absorption, endocrine
212 signalling, and cytoskeletal regulation (Figure 2F). Although these pathways are not directly linked
213 to ischaemic injury, they may reflect broader systemic or metabolic adaptations to intermittent
214 hypoxia. We focused on F0 females because they showed the most distinct clustering from normoxic
215 controls and the highest number of DEPs, suggesting a more pronounced proteomic response to
216 hypoxic preconditioning.

217 **Differential proteomic responses in F1 hypoxic mice**

Differential expression analysis revealed that parental hypoxia exposure altered the expression of 44 proteins in the paternal group, 33 proteins in the maternal group, and 58 proteins in the biparental group compared to F1 normoxic controls (Figure 3A-E). Six proteins were commonly downregulated across all three groups, suggesting a shared molecular response (Figure 2E). These included *Akr1a1*, *Atp12a*, *Csde1*, *Gnaz*, *Impa1*, and *Srgap3*.

Given its robust and consistent phenotypic protection across infarct volume and brain swelling, we focused pathway enrichment analysis on the F1 biparental group. This group also exhibited the highest number of differentially expressed proteins, increasing the power to detect enriched biological pathways.

KEGG pathway enrichment analysis in the F1 biparental group revealed significant involvement of pathways related to HPV infection, focal adhesion, insulin resistance, apoptosis, Hippo signalling, PI3K-Akt signalling, T cell receptor signalling, and EGFR signalling. Collectively, these pathways point towards alterations in cell survival, immune modulation, and intracellular signalling cascades that may underlie the observed intergenerational neuroprotection.

4. Discussion

Taken together, these results demonstrate that intermittent hypoxia reduces infarct volume and brain swelling in F0 mice and that this protective effect is transmitted to F1 offspring. Both maternal and paternal hypoxia exposure contributed to reduced injury, with biparental hypoxia showing the greatest protection.

The observed sex-specific differences suggest distinct mechanisms of inherited resilience. These findings support the idea that intermittent hypoxia induces heritable changes that improve stroke outcomes in offspring, potentially via epigenetic mechanisms and highlighting novel avenues for stroke prevention.

Our proteomic data reveal intra-group consistency that aligns with the observed phenotypes. Normoxic F0 and F1 females clustered together, while hypoxia-exposed F1 groups (maternal, paternal, biparental) formed a distinct cluster, indicating a heritable proteomic shift. F0 females exhibited the most pronounced proteomic changes, consistent with their distinct clustering and higher number of differentially expressed proteins (DEPs), justifying their selection for pathway analysis. In F1 offspring, the biparental group demonstrated the most robust phenotypic protection and the highest number of DEPs, supporting its selection for pathway enrichment analysis. Interestingly, F0 males showed limited proteomic changes despite their protective phenotype, suggesting divergent or subtler molecular mechanisms.

Several of our findings align with existing literature, including the differential expression of *Gnai3* and *Marcks11*, which are implicated in brain injury and ageing, respectively. Key pathways enriched in the biparental group, such as PI3K-Akt²⁹ and EGFR signalling³⁰, are established mediators in ischaemic stroke.

The divergent protein expression patterns between male and female F0 mice suggest sex-dependent molecular adaptations to hypoxic preconditioning³¹⁻³⁴, potentially influenced by hormonal or transcriptional factors³⁵⁻³⁷ (see Supplemental Discussion 1 for detailed interpretation).

These results from Balb/C mice may extend to other mammals, including humans, due to conserved stroke-related pathways. Including both sexes improves clinical relevance by reflecting human sex

259 differences in stroke outcomes. However, further studies are needed to confirm translation to
260 humans and other models.

261 Findings are limited by a single mouse strain, preclinical stroke and hypoxia models^{38,39}, female-
262 only proteomic analysis in F1, and absence of causal validation and behavioural outcomes⁴⁰⁻⁴³
263 (Supplemental Discussion 2).

264 **5. Concluding remarks**

265 This study demonstrates that intermittent hypoxic preconditioning confers a significant reduction in
266 ischaemic brain injury in both treated F0 mice and their untreated F1 offspring. The intergenerational
267 nature of this effect was most pronounced in biparental exposure, with sex-specific differences
268 observed in both the extent of protection and the associated proteomic responses. Proteomic
269 profiling revealed distinct patterns in protein expression patterns linked to ancestral hypoxia, with
270 F0 females and F1 biparental groups showing the most prominent signatures. Pathway enrichment
271 analyses identified processes related to metabolism, immune modulation, and intracellular signalling
272 that may underlie the observed effects.

273 These findings suggest that parental environmental exposures can prime offspring for improved
274 stroke outcomes through sex- and lineage-dependent proteomic adaptations. This work adds to the
275 emerging evidence supporting the intergenerational impact of preconditioning⁴⁴⁻⁴⁶ and highlights
276 potential proteins and molecular pathways for future therapeutic exploration in stroke and other
277 neurovascular diseases.

Figures

Figure 1. Parental intermittent hypoxia reduces infarct volume and brain swelling following ischaemic stroke in F0 and F1 mice. **A)** Schematic of the in vivo mouse model. F0 mice were exposed to intermittent hypoxia prior to tMCAO. A subset was bred to generate F1 offspring, which also underwent tMCAO to assess intergenerational effects. Image created with BioRender. **B) Top** = Representative coronal brain sections stained with cresyl violet showing infarcted regions in normoxic and hypoxia-exposed F0 mice (scale bar = 2.5 mm). **Bottom** = Quantification of infarct volume and brain swelling in F0 mice (N=20-21; equal male and female distribution). Data are shown as mean \pm SEM. Statistical analysis: unpaired *t*-test. **C) Top** = Representative cresyl violet-stained brain sections from F1 male offspring of normoxic and hypoxia-exposed breeders (scale bar = 2.5 mm). **Bottom** = Quantification of infarct volume and brain swelling in F1 male offspring (N=11-12). Analyses are one-way ANOVA with Dunnett's multiple comparisons test. **D) Top** = Representative cresyl violet-stained brain sections from F1 female offspring (scale bar = 2.5 mm). **Bottom** = Quantification of infarct volume and brain swelling in F1 female offspring (N=14-15).

Figure 2. Proteomic analysis of hypoxia-induced changes in F0 mice brain cortex. **A)** Heatmap displaying scaled average protein expression across sample groups (N=6-8). Each row represents a protein, and each column represents a sample group. Expression values were averaged per group and scaled by protein (row-wise z-score). **B)** Venn diagram illustrating the number of differentially expressed (DE) proteins common to F0 male and female hypoxic mice compared to normoxic controls. **C-D)** Volcano plot showing DE proteins in hypoxic vs normoxic F0 male (**C**) and female (**D**) mice. Differential expression was defined by p-value < 0.05. **E)** Scatter plot showing the 17 DE proteins shared between hypoxic F0 male and female mice. **F)** KEGG pathway enrichment analysis showing the top 10 significantly enriched pathways for proteins differentially expressed in hypoxic vs normoxic F0 female mice.

Figure 3. Proteomic analysis of hypoxia-induced changes in F1 mice brain cortex **A-C)** Volcano plot showing differentially expressed (DE) proteins in paternal-hypoxic vs normoxic F1 female mice (**A**), maternal-hypoxic vs normoxic F1 female mice (**B**), and biparental-hypoxic vs normoxic F1 female mice (**C**). Differential expression was defined by p-value < 0.05. **D)** Venn diagram displaying commonly DE proteins shared among paternal-, maternal-, and biparental-hypoxic F1 mice compared to normoxic controls. **E)** Bar plot illustrating the six DE proteins that are consistently altered across paternal-, maternal-, and biparental-hypoxic F1 groups relative to normoxic controls. **F)** KEGG pathway enrichment analysis showing the top 10 significantly enriched pathways for proteins differentially expressed in biparental-hypoxic vs normoxic F1 female mice.

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