

1 **Elucidating the Genomic Basis of Rare Paediatric Neurological Diseases in Central Asia**
2 **and Transcaucasia**

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65 Significant advancements in genomic medicine since the Human Genome Project have
66 provided molecular diagnoses to many families with rare diseases, including rare paediatric
67 neurological diseases (RPND). These advancements have paved the way for personalized
68 medicine, significantly increasing our understanding of human physiology and biochemical
69 pathways. They have also opened new avenues for innovative and more effective treatments,
70 benefiting not only those with rare diseases but also individuals with more common conditions.

71 However, despite these advancements and the decreasing cost of high-throughput sequencing,
72 many regions worldwide remain underrepresented in human genetic research. Even in
73 developed countries with access to state-of-the-art medical facilities, many families remain
74 without a definitive diagnosis. A significant challenge in diagnosing neurogenetic disorders is
75 the difficulty in interpreting sequence variants and the high prevalence of variants of uncertain
76 significance, largely due to the incomplete catalogue of human variants across populations.
77 This issue is further exacerbated by the scarcity of patients with genetically confirmed rare
78 diseases, driven by limited access to next-generation sequencing and comprehensive genetic
79 testing for the majority of patients globally.

80 Central Asia and Transcaucasia (CAT) is one such underrepresented region. This area is
81 populated by genetically unique ethnic groups residing in the middle of Eurasia^{1,2}. The modern
82 geopolitical boundaries of CAT encompass Kazakhstan, Kyrgyzstan, Uzbekistan, Tajikistan,
83 and Turkmenistan in Central Asia, as well as Armenia, Azerbaijan, and Georgia in
84 Transcaucasia (Fig. 1). It is important to note that the factual geographic distribution of many
85 ethnic Central Asians and their ancestral homelands extends beyond the currently defined
86 boundaries of CAT³. The region's geographic location at the crossroads between Europe and
87 East Asia, along with its history of numerous wars, invasions, diverse geography and climate,
88 mass migrations, famines, nomadic lifestyles, and trade through the Silk Road, have all
89 significantly shaped the genetic landscape of these populations. Furthermore, the complex
90 interplay of ancient and historical civilizations, such as the Persians, Scythians, Turks, Arabs,
91 Mongols, and Russians, has contributed to the region's genetic diversity³. Additionally, the
92 Soviet Union's massive deportations during the 20th century forcibly relocated various ethnic
93 groups to and within the CAT region, further influencing the genetic composition of its
94 populations. These eight post-Soviet Union countries, with an overall regional population of
95 about 93 million, range from upper-middle to low-middle-income economies. Consanguinity
96 is prevalent in several of these countries, exacerbating the burden of rare recessive diseases.
97 Despite this, very little is known about the genetic causes of RPND in CAT.

98 To address this gap, University College London Queen Square Institute of Neurology (UCL
99 IoN) partnered with several institutions from CAT in 2018, forming the Central Asian and
100 Transcaucasian Rare Paediatric Neurological Diseases (CAT-RPND) consortium
101 (<https://www.cat-genomics.com/>). This initiative aims to elucidate the genetic background of
102 RPND in CAT through a large-scale international collaboration. Our focus on RPND was
103 strategic, as nearly half of all rare diseases affect the nervous system and predominantly
104 children, with 90% of rare childhood diseases having significant neurological implications⁴.

105 Over the past four years, we recruited over 2,200 families affected by RPND from 17 centres
106 across CAT (Fig. 1), after obtaining ethical approval and appropriate permissions from local
107 institutional review boards. Our research primarily utilized proband- and trio-exome
108 sequencing at UCL IoN, providing molecular diagnoses for many families, including the
109 discovery of actionable genes that have notably improved patient care and management.
110 Moreover, molecular diagnosis has given families essential information for decision-making.

111 In addition to identifying causative variants in established disease-causing genes, our project
112 has characterized several novel gene-disease associations in the CAT region. Notable findings
113 include new recessive conditions associated with variants in *ACBD6*⁵, *SLC38A3*⁶, and
114 *SPATA5L1*⁷. Our work in CAT contributed to the phenotype expansion of the following disease
115 genes: *BRAT1*⁸, *NFUI*⁹, *ZNF142*¹⁰, *SLC18A2*¹¹, *PIGH*¹², *ITPA*¹³, *CA8*¹⁴, and *EMC10*¹⁵.
116 Numerous studies involving other novel disease-associated genes identified in CAT are
117 currently in progress.

118 The consortium is compiling a report on the exome sequencing outcomes for the 2,200 families
119 with RPND from CAT. For families with negative exome sequencing results, further
120 investigations will include genome sequencing, RNA sequencing, and long-read sequencing.
121 This effort has also led to the establishment of a sequence variant database for the CAT region,
122 now part of the Queen Square Genomics Database. This database highlights overlapping
123 variants with neighbouring populations, as well as unique and distinct variants specific to each
124 country in the region. This further underscores the importance of obtaining genetic data from
125 all populations globally.

126 Beyond scientific discovery, the consortium has facilitated academic exchanges, empowering
127 researchers and clinicians from CAT with advanced skills in clinical phenotyping and genetic
128 analysis of rare neurological diseases. Our network has demonstrated an efficient and scalable

129 model for resource and skill sharing, promoting open science to establish genomics research in
130 genetically underrepresented regions. The project has also established trial-ready cohorts and
131 natural history study cohorts for several RPNDs in the CAT region.

132 The consortium aims to raise awareness of RPND in the CAT region both within the region
133 and among international researchers, industries, and pharmaceutical companies. Identifying
134 CAT-specific genetic variants that give rise to RPND is critical for developing newborn and
135 carrier screening and prevention programs. Emphasizing the need for sustainable
136 infrastructure, we advocate for creating national biobanks, databases, and registries for rare
137 diseases within the CAT region.

138 We believe this initiative will enrich the global genomics landscape and highlight the critical
139 importance of international collaboration in addressing rare diseases and genetic studies in
140 underrepresented regions.

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152 **Competing interests**

153 The authors have no competing interests.

154 **Author contributions**

155 R.K. and R.M. wrote the paper. N.Z., U.G., M.G., Z.T., T.G., K.S., S.G., M.I., M.K., B.S.,

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159 **Figure legend**

160 **Fig. 1. The map of Central Asia and Transcaucasia and Diagnostic Outcomes of Exome**

161 **Sequencing.** A. Pins on the map mark the locations of centres participating in the Central

162 Asian and Transcaucasian Rare Paediatric Neurological Disease Genetics Consortium. The

163 centers are as follows: Kazakhstan: South Kazakhstan Medical Academy, Astana Medical

164 University, Shashkin Clinic, Neurolab Clinic. Tajikistan: Avicenna Tajik State Medical

165 University. Armenia: National Institute of Health, Arabkir Medical Complex, Yerevan State

166 Medical University. Azerbaijan: MediClub Baku Center, Hb Guven Clinic Baku, Republican

167 Pediatric Center, Children Neurology Hospital, Azerbaijan Medical University. Georgia:

168 MediClub Georgia Medical Center, Tbilisi State Medical University, Central Children's

169 Hospital Tbilisi, Givi Zhvania Pediatric Academic Clinic. **B.** Diagnostic Outcomes of Exome

170 Sequencing (ES).

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