

Summaries of Research Articles Published by Dr. George John and colleagues (2023–2026)

TRANSFORM **ONE**

Health | Sports | Wellness | Aesthetics & Women's Health | Research

1. John G, Semenova EA, Ahmetov II. How should we study the impact of professional sport on female longevity? Geroscience. 2026 Mar 7. doi: 10.1007/s11357-026-02191-1.

In this commentary, John et al. (2026), published in Geroscience, critically evaluate sex-specific associations between elite sport participation and longevity, focusing on female athletes. The authors discuss findings from a large observational dataset suggesting heterogeneous lifespan outcomes across sports, with potential benefits in some disciplines and apparent reductions in others. They argue that these associations are likely confounded by biological, hormonal, anthropometric, and socioeconomic factors rather than sport per se.

2. Rahimi MR, Faraji H, Sadeghi C, John G, Ahmetov II, Golpasandi H. Impact of Exercise Modalities on Pentraxin-3 (PTX3) Levels: A Systematic Review and Meta-Analysis. Muscles. 2025;5(1):1.

In this systematic review and meta-analysis published in Muscles, Rahimi et al. (2025) investigated the effects of different exercise modalities on circulating Pentraxin-3 (PTX3), an inflammatory biomarker. Nineteen studies (n = 3434 records screened) were included, showing that aerobic training increases PTX3, while resistance training decreases it, with HIIT showing no significant effect. The authors conclude that exercise modality differentially regulates PTX3, reflecting distinct immunometabolic adaptations.

3. Piri MM, Cerit M, Anılır M, Polat T, Karaduman AA, Szabo A, Antoun TGA, John G, Semenova EA, Larin AK, Kulemin NA, Generozov EV, Ahmetov II. Effects of Exercise Addiction and the COL1A1 Gene rs1800012 Polymorphism on Injury Susceptibility in Elite Female Volleyball Players. Genes. 2025;16(11):1300.

Piri et al. (2025), published in Genes, examined the role of exercise addiction and the COL1A1 rs1800012 polymorphism in injury susceptibility among elite female volleyball players. Using case-control data from Turkish and Russian athletes, they found that exercise addiction scores and the T allele were both associated with increased injury risk and prolonged recovery. The study concludes that behavioural and genetic factors jointly contribute to musculoskeletal injury risk in elite sport.

4. Cerit M, Tuncer SY, Piri MM, Anılır M, John G, Semenova EA, Larin AK, Generozov EV, Ahmetov II, Ulucan K, Szabo A. The ACTN3 R577X Nonsense Allele Is Underrepresented in Professional Volleyball Players and Associated with an Increased Risk of Muscle Injury in Female Players. Genes. 2025;16(9):1076.

In this genetic association study, Cerit et al. (2025) analysed the ACTN3 R577X polymorphism in relation to elite volleyball status and injury risk. Data from over 5000 individuals showed that the X allele is underrepresented in athletes and associated with higher injury risk in female players. The authors conclude that ACTN3-related muscle fibre composition may influence both athletic performance and injury susceptibility.

5. John G, Semenova EA, Mohamed DA, Georges Abi Antoun T, Yusupov RA, Ahmetov II. Air Pollution and Its Impact on Health and Performance in Football Players. Sports. 2025;13(6):170.

John et al. (2025), published in Sports, provide a narrative review on the impact of air pollution on football players' health and performance. The authors synthesise evidence showing that pollutants such as PM, NO₂, and O₃ impair respiratory function, increase oxidative stress, and reduce exercise capacity. They also propose mitigation strategies including training adjustments, nutritional interventions, and environmental monitoring.

6. Bulgay C, Zorba E, Kazan HH, Bayraktar I, Uca M, Ergün MA, John G, Yusupov RA, Sultanov RI, Semenova EA, Larin AK, Kulemin NA, Generozov EV, Ahmetov II. BDNF coexpresses with MTOR and is associated with muscle fiber size, lean mass and power-related traits. Eur J Appl Physiol. 2025;125(10):2781-2792.

Bulgay et al. (2025) investigated the relationship between BDNF and MTOR gene expression and muscle phenotypes. Using large-scale genomic and physiological datasets, they demonstrated that higher BDNF expression correlates with greater fast-twitch fibre size, lean mass, and power performance. The study concludes that BDNF may play a regulatory role in skeletal muscle hypertrophy and athletic power capacity.

7. John G, AlNadwi A, Georges Abi Antoun T, Ahmetov II. Injury Prevention Strategies in Female Football Players: Addressing Sex-Specific Risks. Sports. 2025;13(2):39.

In this narrative review, John et al. (2025) examined injury prevention strategies in female football players, with emphasis on sex-specific risk factors. The authors highlight higher ACL injury rates in women, linked to hormonal fluctuations, biomechanical differences, and neuromuscular control. They conclude that current prevention programmes are insufficiently tailored to female athletes and require sex-specific optimisation.

8. Çığırtaş R, Bulgay C, Kazan HH, Akman O, Sporiš G, John G, Yusupov RA, Sultanov RI, Zhelankin AV, Semenova EA, Larin AK, Kulemin NA, Generozov EV, Jurko D, Ahmetov II. The ARK2N (C18ORF25) Genetic Variant Is Associated with Muscle Fiber Size and Strength Athlete Status. Metabolites. 2024;14(12):684.

Çığırtaş et al. (2024) studied the ARK2N (C18ORF25) gene variant in relation to muscle fibre size and strength athlete status. Using multi-cohort genetic and transcriptomic analyses, they found that specific ARK2N variants are associated with greater fast-twitch fibre area and strength performance. The authors propose ARK2N as a candidate gene involved in muscle hypertrophy and power-oriented phenotypes.

9. Hall ECR, John G, Ahmetov II. Testing in Football: A Narrative Review. Sports. 2024;12(11):307.

Hall et al. (2024) conducted a narrative review of testing practices in football, covering physical, physiological, psychological, and genetic assessments. They report that testing strategies are widely used for talent identification, monitoring, and injury risk profiling, but vary significantly across clubs. The authors conclude that testing is constrained by resources and lacks standardisation across elite football systems.

10. Guilherme JPLF, Semenova EA, Kikuchi N, Homma H, Kozuma A, Saito M, Zempo H, Matsumoto S, Kobatake N, Nakazato K, Okamoto T, John G, Yusupov RA, Larin AK, Kulemin NA, Gazizov IM, Generozov EV, Ahmetov II. Identification of Genomic Predictors of Muscle Fiber Size. Cells. 2024;13(14):1212.

Guilherme et al. (2024) identified genetic variants associated with skeletal muscle fibre cross-sectional area. Using GWAS-linked SNP analysis and multi-cohort validation, they identified 57 variants associated with fast-twitch fibre size and athletic status. The study concludes that muscle fibre size is strongly polygenic and overlaps with strength and power performance traits.

11. Kazan HH, Kasakolu A, Koncagul S, Ergun MA, John G, Sultanov RI, Zhelankin AV, Semenova EA, Yusupov RA, Kulemin NA, Larin AK, Generozov EV, Bulgay C, Ahmetov II. Association analysis of indel variants and gene expression identifies MDM4 as a novel locus for skeletal muscle hypertrophy and power athlete status. Exp Physiol. 2025;110(11):1661-1671.

Kazan et al. (2025) investigated indel variants in MDM4 and their association with muscle hypertrophy and power athlete status. They found that specific MDM4 variants are associated with increased expression in fast-twitch muscle fibres and greater fat-free mass. The study concludes that MDM4 may regulate muscle fibre specification through pathways linked to p53 inhibition.

12. Rahimi MR, Semenova EA, John G, Fallah F, Larin AK, Generozov EV, Ahmetov II. Effect of ADORA2A Gene Polymorphism and Acute Caffeine Supplementation on Hormonal Response to Resistance Exercise: A Double-Blind, Crossover, Placebo-Controlled Study. *Nutrients*. 2024;16(12):1803.

Rahimi et al. (2024) conducted a double-blind crossover trial and genetic association study examining ADORA2A polymorphism and caffeine response. They found that TT genotype carriers exhibited stronger hormonal responses (testosterone and GH) to caffeine during resistance exercise. The authors conclude that ADORA2A variants modulate nutrigenetic responses to caffeine in exercise contexts.

13. Ahmetov II, John G, Semenova EA, Hall ECR. Genomic predictors of physical activity and athletic performance. Adv Genet. 2024;111:311-408.

Ahmetov et al. (2024) reviewed genomic predictors of physical activity and athletic performance. They summarise evidence for 149 variants associated with physical activity traits and over 250 variants linked to athlete status across endurance, strength, and power phenotypes. The review concludes that athletic performance is highly polygenic with complex gene–environment interactions.

14. Ström K, Oskolkov N, Karaderi T, Kalamajski S, Mir BA, ... Ahmetov II, Wang G, Pitsiladis Y, ... Lindgren CM, Franks PW, Hansson O. RAB3GAP2 is a regulator of skeletal muscle endothelial cell proliferation and associated with capillary-to-fiber ratio. Cell Rep. 2026;45(2):116961.

In this study, Ström et al. (2026), published in Cell Reports, investigated the genetic regulation of skeletal muscle capillarisation using a genome-wide association approach. They identified the RAB3GAP2 locus as a key determinant of capillary-to-fibre ratio, with low-expression alleles associated with increased capillary density and enrichment in endurance athletes. Functional analyses demonstrated that reduced RAB3GAP2 promotes endothelial proliferation and angiogenesis, suggesting a mechanistic link between genotype, microvascular adaptation, and endurance performance.

15. Kilaitė J, Pranckevičienė E, Ginevičienė V, Urnikytė A, Dadelienė R, Mastavičiūtė A, Jamontaitė IE, Alekna V, Ahmetov II. Causal relationships between sarcopenia, frailty, and health outcomes: A systematic review of Mendelian randomization studies. Exp Gerontol. 2025;212:112953.

In this systematic review, Kilaitė et al. (2025), published in Experimental Gerontology, synthesised Mendelian randomisation studies examining causal links between sarcopenia, frailty, and health outcomes. Analysis of over 160 MR studies revealed that muscle strength, lean mass, and gait speed exert protective causal effects across a wide range of diseases, while frailty increases risk across multiple systems. The authors conclude that sarcopenia-related traits are not only correlates but causal determinants of major health outcomes.

16. Ginevičienė V, Pranckevičienė E, Urnikytė A, Jurkūnaitė L, Gutauskaitė K, Dadelienė R, Kilaitė J, Jamontaitė IE, Mastavičiūtė A, Ahmetov II, Alekna V. A multi-omics investigation of sarcopenia and frailty: Integrating genomic, epigenomic and telomere length data. Exp Physiol. 2025 Sep 27. doi: 10.1113/EP092853.

Ginevičienė et al. (2025), published in Experimental Physiology, performed a multi-omics analysis integrating genomics, epigenomics, and telomere biology in elderly individuals. They identified novel genetic variants associated with handgrip strength, replicated known sarcopenia-related loci, and demonstrated widespread methylation changes linked to lean mass. The study concludes that sarcopenia and frailty are driven by complex interactions between genetic variation, epigenetic regulation, and biological ageing processes such as telomere shortening.

17. Kozuma A, Bulgay C, Zempo H, Saito M, Deguchi M, Homma H, Matsumoto S, Matsumoto R, Kasakolu A, Kazan HH, Bıyıklı T, Koncagül S, Baydaş G, Ergun MA, Szabo A, Semenova EA, Larin AK, Kulemin NA, Generozov EV, Okamoto T, Nakazato K, Ahmetov II, Kikuchi N. Genetic Factors of Elite Wrestling Status: A Multi-Ethnic Comparative Study. Genes. 2025;16(8):906.

In this genome-wide association study, Kozuma et al. (2025), published in Genes, investigated genetic determinants of elite wrestling status across Japanese, Turkish, and Russian cohorts. Cross-population meta-analysis identified ATP2A3 and UNC5C polymorphisms as consistently associated with elite status and linked to gene expression in skeletal muscle. The authors conclude that shared genetic factors underpin elite performance in wrestling across different ethnic backgrounds.

18. Sadaki S, Tsuji R, Hayashi T, Watanabe M, Iwai R, Wenchao G, Semenova EA, Sultanov RI, Zhelankin AV, Generozov EV, Ahmetov II, Sakakibara I, Ojima K, Sakurai H, Muratani M, Kudo T, Takahashi S, Fujita R. Large MAF transcription factors reawaken evolutionarily dormant fast-glycolytic type IIb myofibers in human skeletal muscle. *Skelet Muscle*. 2025;15(1):19.

In this mechanistic study, Sadaki et al. (2025), published in *Skeletal Muscle*, examined the role of large MAF transcription factors in regulating muscle fibre phenotype. They demonstrated that overexpression of MAF factors induces MYH4 expression and enhances glycolytic capacity in human muscle cells, effectively reactivating a fibre type previously considered absent in humans. The findings suggest a conserved regulatory pathway with potential implications for performance enhancement and prevention of muscle degeneration.

19. Wang G, Fuku N, Miyamoto-Mikami E, Tanaka M, Miyachi M, Murakami H, Mitchell BD, Morrison E, Ahmetov II, Generozov EV, Filipenko ML, Gilep AA, Gineviciene V, Moran CN, Venckunas T, Cieszczyk P, Derave W, Papadimitriou I, Garton FC, Padmanabhan S, Pitsiladis YP. Multi-phase, multi-ethnic GWAS uncovers putative loci in predisposition to elite sprint and power performance, health and disease. Biol Sport. 2025; 42(3):141-159.

Wang et al. (2025), published in Biology of Sport, conducted a multi-phase, multi-ethnic GWAS to identify genetic determinants of sprint and power performance. They identified the GALNT13 locus as significantly associated with elite status and linked its expression to fast-twitch muscle fibre characteristics. The study also highlighted multiple genes related to neural, immune, and metabolic pathways, indicating a complex polygenic architecture underlying power performance.

20. Sellami M, Naja K, Almuraikhy S, Anwardeen N, Sultanov RI, Generozov EV, Ahmetov II, Elrayess MA. N-Lactoyl amino acids as metabolic biomarkers differentiating low and high exercise response. Biol Sport. 2025;42(2):331-344.

Sellami et al. (2025), published in *Biology of Sport*, investigated metabolomic signatures associated with variability in aerobic training response. They found that higher levels of N-lactoyl amino acids, particularly Lac-Phe, were associated with poorer improvements in exercise capacity. The authors propose these metabolites as biomarkers of low exercise responsiveness and potential indicators of muscle fibre composition and fatigue susceptibility.

21. Bulgay C, Kasakolu A, Bıyıklı T, Koncagul S, Kazan HH, Ahmetov II, Ergun MA, Griffiths MD, Szabo A. Genome-Wide Association Study of Exercise Addiction Among Elite Wrestlers. Brain Sci. 2025;15(2):102.

In this GWAS, Bulgay et al. (2025), published in Brain Sciences, explored the genetic basis of exercise addiction in elite wrestlers. They identified several SNPs associated with addiction risk, many of which are linked to psychiatric traits such as anxiety and depression. The study provides preliminary evidence that exercise addiction has a genetic component overlapping with broader neurobehavioural phenotypes.

22. Barbera MC, Guarrera L, Re Cecconi AD, Cassanmagnago GA, Vallergera A, Lunardi M, Checchi F, Di Rito L, Romeo M, Mapelli SN, Schoser B, Generozov EV; Molecular Genetics Group; Jansen R, de Geus EJC, Penninx B, van Dongen J, Craparotta I, Piccirillo R, Ahmetov II, Bolis M. Increased ectodysplasin-A2-receptor EDA2R is a ubiquitous hallmark of aging and mediates parainflammatory responses. Nat Commun. 2025;16(1):1898.

Barbera et al. (2025), published in Nature Communications, identified EDA2R as a robust, tissue-independent biomarker of ageing using integrative bioinformatics and experimental approaches. They showed that increased EDA2R signalling induces parainflammatory responses in muscle cells, recapitulating features of age-related sarcopenia. The authors propose EDA2R as a potential therapeutic target for mitigating ageing-associated functional decline.

23. Rahimi MR, Faraji H, Hajipoor SR, Ahmetov II. Effect of MCT1 A1470T Polymorphism on Lactate and Potassium Concentrations After Caffeine Ingestion During Acute Resistance Exercise. Nutrients. 2024;16(24):4396.

In this randomised crossover study, Rahimi et al. (2024), published in Nutrients, examined the interaction between MCT1 genotype and caffeine supplementation on metabolic responses to resistance exercise. They found that carriers of the A allele exhibited higher lactate accumulation and altered potassium responses compared to TT genotype individuals. The study concludes that MCT1 polymorphism modulates lactate transport and influences individual responses to caffeine during exercise.

24. Yang X, Li Y, Bao D, Yan B, Mei T, Liu X, Ciężczyk P, Ahmetov I, Mc Naughton L, He Z. Genomic predictors of fat mass response to the standardized exercise training. Int J Sports Med. 2025;46(2):127-136.

In this genome-wide association study, Yang et al. (2025), published in International Journal of Sports Medicine, investigated genetic determinants of inter-individual variability in fat mass response to a 12-week exercise intervention. They identified ten SNPs associated with fat loss response, with a polygenic predictor score explaining 40.3% of the variance and demonstrating the strongest contribution. The authors conclude that genetic profiling may enable prediction of exercise-induced fat loss efficiency and highlight key biological pathways such as insulin signalling and adipocyte differentiation.

25. Parfenteva OI, Kulemin NA, Bondareva EA, Ahmetov II. Prevalence and Predictors of Normal-Weight Obesity among Women. Nutrients. 2024;16(16):2579.

Parfenteva et al. (2024), published in Nutrients, examined the prevalence and determinants of normal-weight obesity (NWO) in women using detailed body composition assessment. They demonstrated that BMI substantially underestimates obesity prevalence, with nearly 30% of high body fat individuals misclassified, and identified subcutaneous fat thickness as a reliable diagnostic marker. The study concludes that lifestyle factors, particularly diet and physical activity, play a key role in NWO and should be targeted in prevention strategies.

26. Kazan HH, Bulgay C, Zorba E, Dalip M, Ceylan HI, Semenova EA, Larin AK, Kulemin NA, Generozov EV, Ahmetov II, Cerit M. Exploring the relationship between caffeine metabolism-related CYP1A2 rs762551 polymorphism and team sport athlete status and training adaptations. Mol Biol Rep. 2024;51(1):841.

In this genetic association study, Kazan et al. (2024), published in Molecular Biology Reports, investigated the CYP1A2 rs762551 polymorphism in relation to team sport athlete status and training adaptations. They found that the CC genotype was underrepresented in elite athletes, while the CA genotype was associated with superior improvements in aerobic performance following training. The authors conclude that caffeine metabolism-related genetic variation may influence both athlete selection and responsiveness to training.

27. Baumert P, Mäntyselkä S, Schönfelder M, Heiber M, Jacobs MJ, Swaminathan A, Minderis P, Dirmontas M, Kleigrew K, Meng C, Gigl M, Ahmetov II, Venckunas T, Degens H, Ratkevicius A, Hulmi JJ, Wackerhage H. Skeletal muscle hypertrophy rewires glucose metabolism: An experimental investigation and systematic review. J Cachexia Sarcopenia Muscle. 2024;15(3):989-1002.

Baumert et al. (2024), published in Journal of Cachexia, Sarcopenia and Muscle, investigated metabolic adaptations during skeletal muscle hypertrophy using experimental and systematic approaches. They demonstrated that hypertrophy induces metabolic rewiring, redirecting glycolytic intermediates into anabolic pathways such as serine synthesis, which is essential for protein synthesis. The study concludes that muscle growth involves coordinated metabolic reprogramming with implications for interventions targeting muscle wasting.

28. Bojarczuk A, Egorova ES, Dzitkowska-Zabielska M, Ahmetov II. Genetics of Exercise and Diet-Induced Fat Loss Efficiency: A Systematic Review. J Sports Sci Med. 2024;23(1):236-257.

In this systematic review, Bojarczuk et al. (2024), published in Journal of Sports Science and Medicine, evaluated genetic factors influencing variability in fat loss response to exercise and diet. They identified 54 genetic markers associated with weight loss efficiency, primarily derived from candidate gene studies. The authors conclude that genetic variability contributes significantly to differential fat loss responses and supports the development of personalised interventions.

29. Ginevičienė V, Pranckevičienė E, Kilaitė J, Mastavičiūtė A, Dadelienė R, Jamontaitė IE, Letukienė A, Ahmetov II, Alekna V. Bibliometric and scientometric analysis on biomarkers and molecular mechanisms for physical frailty and sarcopenia. Front Med. 2024;11:1326764.

Ginevičienė et al. (2024), published in Frontiers in Medicine, conducted a bibliometric and scientometric analysis of research on biomarkers and molecular mechanisms of frailty and sarcopenia. They identified key research trends, highlighting inflammation, myokines, and genetic and proteomic markers as central themes in the field. The study concludes that research activity is increasing and moving towards integrative biomarker approaches to better characterise these complex conditions.

30. Bondareva EA, Parfenteva OI, Troshina EA, Ershova EV, Mazurina NV, Komshilova KA, Kulemin NA, Ahmetov II. Agreement between bioimpedance analysis and ultrasound scanning in body composition assessment. Am J Hum Biol. 2024;36(4):e24001.

Bondareva et al. (2024), published in American Journal of Human Biology, assessed the agreement between bioelectrical impedance analysis and ultrasound in measuring body composition in women. While both methods showed similar results at the group level, individual-level agreement was limited, particularly for body fat percentage and fat-free mass. The authors conclude that method-specific prediction equations are necessary to improve comparability between techniques.

31. Bezuglov E, Ahmetov II, Lazarev A, Mskhalaya G, Talibov O, Ustinov V, Shoshorina M, Bogachko E, Azimi V, Morgans R, Hackney AC. The relationship of testosterone levels with sprint performance in young professional track and field athletes. *Physiol Behav.* 2023;271:114344.

Bezuglov et al. (2023), published in *Physiology & Behavior*, examined the association between testosterone levels and sprint performance in young athletes. They found that higher testosterone levels were associated with faster sprint times in males but showed no significant associations in females. The study concludes that testosterone contributes to performance variability in male sprint athletes, potentially mediated by maturation and body composition.

32. Demirci B, Bulgay C, Ceylan Hİ, Öztürk ME, Öztürk D, Kazan HH, Ergun MA, Cerit M, Semenova EA, Larin AK, Generozov EV, Ahmetov II, Cepicka L. Association of ACTN3 R577X Polymorphism with Elite Basketball Player Status and Training Responses. Genes. 2023;14(6):1190.

Demirci et al. (2023), published in Genes, investigated the ACTN3 R577X polymorphism in elite basketball players and its influence on training adaptations. They found that the XX genotype was underrepresented in athletes, while RR genotype carriers showed significant improvements in performance tests. The authors conclude that the ACTN3 R allele is advantageous for basketball performance and training responsiveness.

33. Rahimi MR, Semenova EA, Larin AK, Kulemin NA, Generozov EV, Łubkowska B, Ahmetov II, Golpasandi H. The ADORA2A TT Genotype Is Associated with Anti-Inflammatory Effects of Caffeine in Response to Resistance Exercise and Habitual Coffee Intake. *Nutrients*. 2023;15(7):1634.

Rahimi et al. (2023), published in *Nutrients*, investigated the role of ADORA2A polymorphism in modulating inflammatory responses to caffeine and exercise. They showed that TT genotype carriers exhibited reduced exercise-induced inflammation and higher habitual coffee intake compared to C allele carriers. The study concludes that ADORA2A genotype influences both physiological and behavioural responses to caffeine.

34. Zhelankin AV, Iulmetova LN, Ahmetov II, Generozov EV, Sharova EI. Diversity and Differential Expression of MicroRNAs in the Human Skeletal Muscle with Distinct Fiber Type Composition. Life. 2023;13(3):659.

Zhelankin et al. (2023), published in Life, investigated microRNA expression profiles in skeletal muscle with differing fibre type composition. They identified distinct miRNA signatures associated with fast- and slow-twitch fibres, including regulatory interactions with key muscle-related genes. The study concludes that miRNAs play an important role in determining muscle fibre phenotype and functional specialisation.

35. Bulgay C, Kasakolu A, Kazan HH, Mijaica R, Zorba E, Akman O, Bayraktar I, Ekmekci R, Koncagul S, Ulucan K, Semenova EA, Larin AK, Kulemin NA, Generozov EV, Balint L, Badicu G, Ahmetov II, Ergun MA. Exome-Wide Association Study of Competitive Performance in Elite Athletes. Genes. 2023;14(3):660.

Bulgay et al. (2023), published in Genes, conducted a whole-exome sequencing study to identify genetic variants associated with elite athletic performance. They identified several replicated variants, including SIRT1, TRPM2, and AGRN, linked to endurance capacity, VO_2 max, and muscle fibre characteristics. The authors conclude that exome-wide approaches can uncover novel genetic markers contributing to sport-specific performance phenotypes.

The background is a solid dark blue. Overlaid on this are several thin, light blue lines that form a series of overlapping, flowing waves. These waves originate from the left and right edges and move towards the center, creating a sense of motion and depth. The waves are composed of many closely spaced lines, giving them a ribbon-like or smoke-like appearance. In the center of the image, the text 'TRANSFORM ONE' is displayed in a clean, white, sans-serif font. The word 'TRANSFORM' is in all caps and a regular weight, while 'ONE' is also in all caps but in a significantly bolder weight, making it the focal point of the text.

TRANSFORM **ONE**

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