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Genotypic and Phenotypic Spectrum of Children with Genetic West Syndrome From India – A Multicentre study Balamurugan Nagarajan¹, Vykuntaraju K Gowda², Sangeetha Yoganathan³, Indar Kumar Sherawat⁴, Kavita Srivastava⁵, Nitish Vora⁶, Rahul Badheka ⁶, Sumita Danda³, Umesh Kalane⁵, Anupriya Kaur¹, Priyanka Madaan¹, Sanjiv Mehta⁶, Sandeep Negi¹, Prateek Kumar Panda⁴, Surekha Rajadhyaksha⁵, Arushi Gahlot Saini¹, Lokesh Saini¹, Siddharth Shah⁶, Varunvenkat M Srinivasan², Renu Suthar¹, Maya Thomas³, Sameer Vyas¹, Naveen Sankhyan¹, **Jitendra Kumar Sahu¹** 1- PGIMER, Chandigarh, 2- IGICH, Bengaluru, 3- CMC, Vellore, 4- AIIMS, Rishikesh, 5- BVDUMC, Pune, 6- RICN, Ahmedabad, India

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INTRODUCTION	MATERIAL
 Etiology of IESS (West syndrome) is diverse Genetic Metabolic Structural Approximately in 30 % of West syndrome (WS), no etiology is identified Genetic cause accounts approximately for 40 % of unexplained IESS Paucity of literature globally on genetic IESS and even scarce from the Indian subcontinent Michaud II. et al from Canada: 	 Inclusion Criteria Children (under follow-up of IESS (confirmed after Januar sequencing or sanger sequent microarray and others) Exclusion Criteria Children with known structure type 1, Tuberous Sclerosis Cand structural neurometabolic
Need for large multicentric international cohorts to find possible crucial information which could have potential therapeutic and prognostic implication	Genetically confirmed WS - panel, CMA, etc., (Newly d (Only Pathogenic and likely
<u>OBJECTIVES</u>	
To describe the genotypic and phenotypic profile of children with West syndrome (WS) of genetic etiology.	DetailedIn-personassessment in the centreof follow up
MATERIALS AND METHODS	Collection and entry of data
Study Design: Ambispective-observational, multicentric study	excel; Collation of data from a DISCUS
 Place of Study: Pediatric Neurology Unit, PGIMER, Chandigarh in collaboration with five pediatric centres across India over 15 months Study Period: January 2021 to March 2022 	

S AND METHODS



Down syndrome, ALDH7A1, SCN2A, CDKL5, ALG13 are the common causes of genetic WS Central hypotonia, developmental delay prior to the onset of spasms, autistic features, and facial dysmorphism were notable findings observed.



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<u>RESULTS</u> (Total 124 genetically confirmed cases)