SSR Institute of International Journal of Life Sciences
ISSN (O): 2581-8740 | ISSN (P): 2581-8732
Ashwini *et al*., 2026
doi: 10.21276/SSR-IIJLS.2026.12.1.10

Original Article

open access

Clinical and Cytogenetic Trends of Down Syndrome: Evidence from Bagalkot District, India

Ashwini H[1], Sujayendra Kulkarni[2]*, Kavita MM[3], Sangamesh Kashinakunti[4], Bhuvaneshwari C Yelamali[4]

[1]Lecturer, Dept of Genetics, S Nijalingappa Medical College and HSK Hospital, Navanagar, Bagalkot, India

[2]Senior Lecturer, Professor, Dept of Genetics, S Nijalingappa Medical College and HSK Hospital, Navanagar, Bagalkot, India

[3]Professor, Dept of Biochemistry, S Nijalingappa Medical College and HSK Hospital, Navanagar, Bagalkot, India

[4]Professor, Dept of Pediatrics, S Nijalingappa Medical College and HSK Hospital, Navanagar, Bagalkot, India

***Address for Correspondence:** Dr Sujayendra Kulkarni, Senior Lecturer, Department of Genetics, S Nijalingappa Medical College and HSK Hospital, Navanagar, Bagalkot-587102, India
E-mail: sujayendra.kulkarni@gmail.com

Received: 02 Aug 2025/ Revised: 06 Oct 2025/ Accepted: 05 Dec 2025

ABSTRACT

Background: Down syndrome (DS), caused by trisomy of chromosome 21, is the most common chromosomal aneuploidy seen in live births and represents a significant public health concern. Cytogenetic evaluation is essential for accurate diagnosis, clinical management, and genetic counseling.

Methods: This retrospective study included 495 clinically suspected cases referred for cytogenetic analysis between 2020 and 2025. Peripheral blood samples were collected after informed consent was obtained. Conventional GTG-banded karyotyping was performed, and Fluorescence in Situ Hybridization (FISH) was used for confirmation. A minimum of 20 metaphases were analyzed for each case, with extended analysis in suspected mosaicism.

Results: Out of 495 suspected cases, 32 (6.46%) were confirmed as Down syndrome. Free trisomy 21 was the predominant cytogenetic abnormality, identified in 29 cases (90.6%), while mosaic trisomy 21 was observed in 3 cases (9.3%). The mean maternal age was 31.3 years in free trisomy cases and 26.2 years in mosaic cases, with 36% of mothers aged 35 or older. Cases were reported from both rural and urban areas, with a higher proportion from rural regions. No significant sex predilection was observed.

Conclusion: Free trisomy 21 is the most common cytogenetic pattern of Down syndrome in the Bagalkot district. Advanced maternal age remains an important risk factor. Early diagnosis using combined cytogenetic techniques and strengthened prenatal screening programs is essential for effective management and prevention.

Key-words: Cytogenetic pattern, Down syndrome (DS), Fluorescence in Situ Hybridization (FISH), Trisomy of Chromosome, Trisomy 21

INTRODUCTION

Down syndrome (DS), also known as trisomy 21, is the most common chromosomal aneuploidy observed in live births and remains a major cause of intellectual disability worldwide [1].

How to cite this article
Ashwini H, Kulkarni S, Kavita MM, Kashinakunti S, Yelamali BC. Clinical and Cytogenetic Trends of Down Syndrome: Evidence from Bagalkot District, India. SSR Inst Int J Life Sci., 2026; 12(1): 9034-9041.

Access this article online
https://iijls.com/

It results from an extra copy of chromosome 21, most commonly due to meiotic non-disjunction. The global incidence of Down syndrome is estimated to be approximately 1 in 700–1,000 live births, with variation influenced by maternal age and access to prenatal screening services [2].

Clinically, individuals with Down syndrome exhibit characteristic craniofacial features, hypotonia, developmental delay, and varying degrees of intellectual disability. In addition, affected individuals have an increased risk of congenital anomalies, particularly congenital heart defects, gastrointestinal and abdominal abnormalities such as duodenal atresia and Hirschsprung

doi: 10.21276/SSR-IIJLS.2026.12.1.10

disease, endocrine disorders, and hematological conditions [3]. Early recognition of these features is crucial for timely diagnosis and intervention.

From a cytogenetic perspective, free trisomy 21 accounts for most cases, while mosaicism and Robertsonian translocations constitute a smaller proportion [4]. Advanced maternal age is a well-established risk factor; however, Down syndrome can also occur in younger mothers, emphasizing the need for universal screening strategies rather than age-restricted approaches.

Cytogenetic techniques, such as conventional karyotyping, remain the gold standard for diagnosis, while Fluorescence in Situ Hybridisation (FISH) provides rapid and reliable confirmation, especially in neonatal and mosaic cases [5]. Studying regional cytogenetic trends is essential to strengthen genetic counselling services, improve prenatal screening programs, and guide preventive healthcare policies.

In the Indian context, especially in semi-urban and rural regions, limited awareness, late maternal age at conception, and restricted access to prenatal diagnostic facilities continue to influence the burden of Down syndrome. Region-specific cytogenetic data are therefore essential to understand local trends and risk factors. The present study was undertaken to evaluate the clinical and cytogenetic profile of Down syndrome cases referred to a tertiary care center in the Bagalkote district of Karnataka, with an emphasis on karyotypic patterns, maternal age distribution, and demographic characteristics, thereby contributing to improved diagnostic and preventive strategies.

MATERIALS AND METHODS

Study Design and Ethical Approval- The present study was a retrospective cytogenetic analysis conducted at the Cytogenetics Laboratory, S. Nijalingappa Medical College and HSK Hospital, Navanagar, Bagalkote, Karnataka. Ethical clearance was obtained from the Institutional Ethics Committee before commencement of the study.

Study Population- A total of 495 clinically suspected cases referred for cytogenetic evaluation during the period 2020–2025 were included. Of these, 32 cases were cytogenetically confirmed as Down syndrome and considered for analysis.

Sample Collection- Peripheral blood samples (4–5 ml) were collected in heparinized vacutainers from all cases following informed consent from parents or guardians.

Cytogenetic Analysis- Chromosome preparations were obtained from peripheral blood lymphocyte cultures. GTG banding was performed according to the method described by Seabright. A minimum of 20 metaphases were analyzed per case, with at least five well-spread metaphases photographed and karyotyped. In suspected mosaic cases, a minimum of 50 metaphases were evaluated.

Fluorescence In Situ Hybridization (FISH)- FISH analysis was performed on interphase nuclei using chromosome 21–specific probes for confirmation of trisomy 21. Analysis was carried out using an Olympus BX53 fluorescent microscope with ASI software (Japan).

Statistical Analysis- Clinical and cytogenetic data, including maternal age, sex distribution, karyotypic patterns, and rural or urban background, were compiled and analyzed using descriptive statistics. Results were expressed as frequencies, percentages, and mean values wherever applicable.

RESULTS

A total of 495 clinically suspected cases were referred to our diagnostic laboratory for cytogenetic analysis. Of which 32 cases were confirmed DS. The remaining 463 cases were found to be normal and did not show any chromosomal abnormalities. The mean maternal age for all DS cases was calculated, with a value of 31.3 years for free trisomy and 26.2 years for mosaic DS cases. The data analysis showed that maternal age was above 35 years in 36% cases. Among the 32 cases of DS, 29 showed free trisomy, of which 16 were from rural areas and 13 from urban areas. In the 3 cases of mosaic Down syndrome, 2 cases were reported from rural areas and 1 case from an urban area (Table 1) and (Fig. 1).

doi: 10.21276/SSR-IIJLS.2026.12.1.10

Table 1: Distribution of Down syndrome Karyotypes, FISH results, Maternal age, rural and urban backgrounds (n=32)

Karyotypes and FISH Results	Total cases	Mean Maternal Age	Rural (No of Cases)	Urban (No of Cases)
Free Trisomy 21 47, XY, +21 47, XX, +21	29(90.6%) 20(62.5%) 09(28.1%)	31.3	16	13
Mosaic 46, XY/47, XY, +21 46, XX/47, XX, +21	3(9.3%) 2(6.2%) 1(3.1%)	26.2	2	1
Total	32 (100%)			

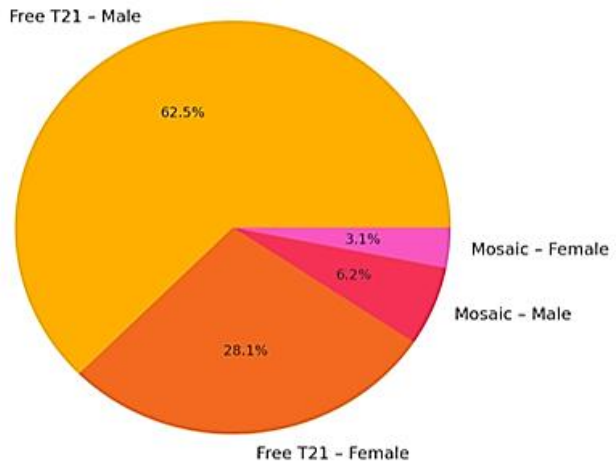

Fig. 1: Distribution of Down syndrome Karyotypes (n=32)

Representative GTG-banded karyotype of a male child with Down syndrome showing free trisomy 21 (47, XY, +21). The karyogram demonstrates an additional chromosome 21, characteristic of Down syndrome, and confirms the diagnosis at the cytogenetic level. Conventional karyotyping remains the gold standard for identifying numerical chromosomal abnormalities and is essential for accurate diagnosis, prognosis, and genetic counseling (Fig. 2).

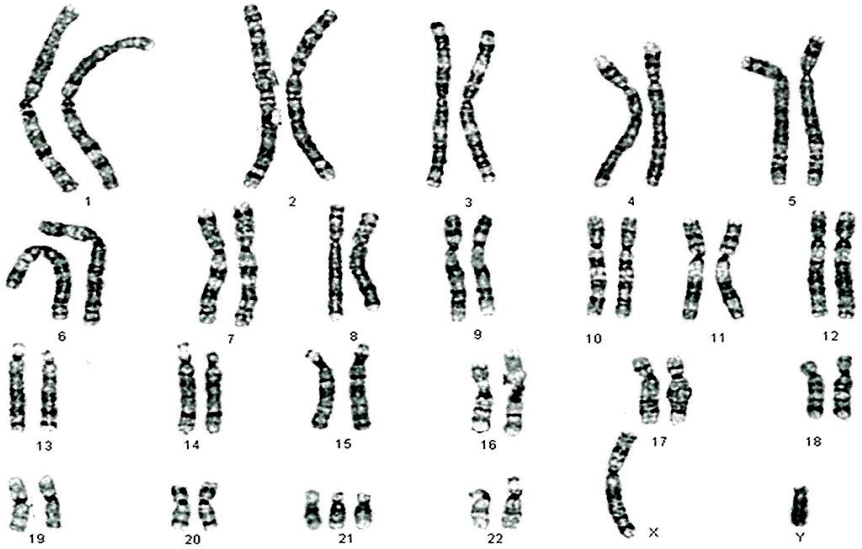

Fig. 2: Trisomy 21 Karyogram (Male) (XY)

doi: 10.21276/SSR-IIJLS.2026.12.1.10

Representative GTG-banded karyotype of a female child with Down syndrome showing free trisomy 21 (47,XX,+21). The karyogram clearly demonstrates an additional chromosome 21, confirming the cytogenetic diagnosis of Down syndrome. Such chromosomal analysis remains the gold standard for accurate postnatal diagnosis and aids in appropriate clinical management and genetic counselling (Fig. 3).

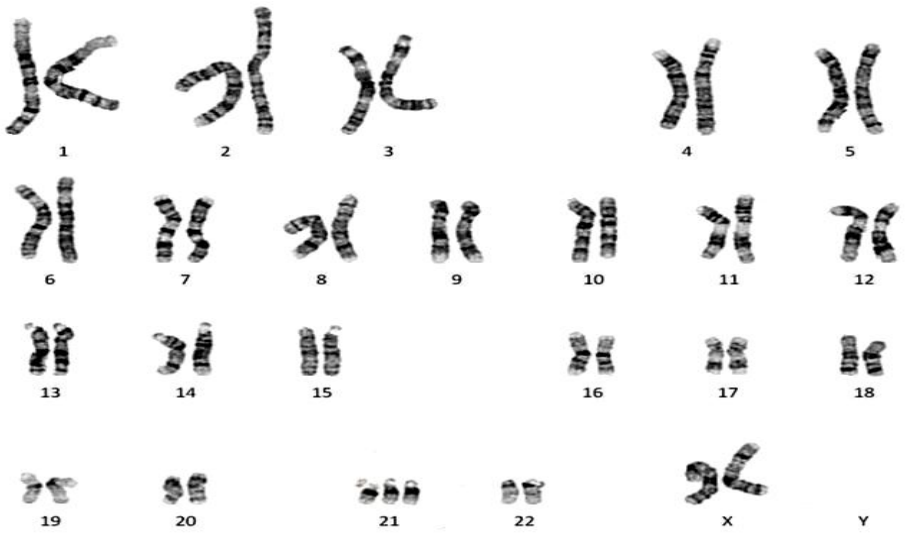

Fig. 3: Trisomy 21 Karyogram (Female) (XX)

Fig. 4 (A) GTG-banded karyotype of a female child showing free trisomy 21 (47, XX,+21), confirming the presence of an extra chromosome 21. Fig. 4 (B) Normal female karyotype (46, XX) shown for comparison. The figure highlights the chromosomal difference between trisomy 21 and a normal diploid complement, emphasizing the role of conventional karyotyping in definitive diagnosis of Down syndrome.

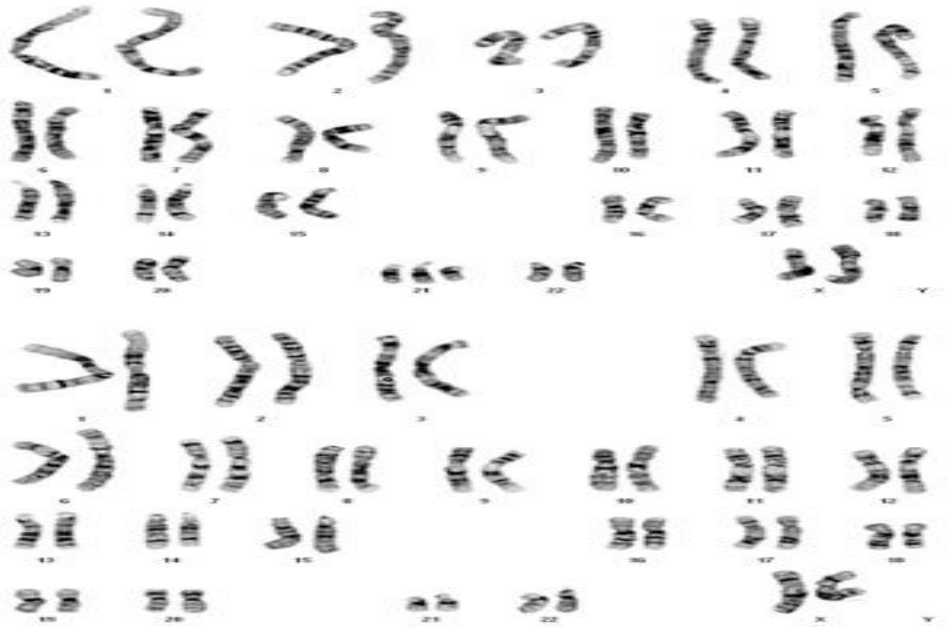

Fig. 4: (A) karyotype of 47, XX, +21 and (B) a karyotype of 46, XX

Fluorescence In Situ Hybridization (FISH) analysis for chromosome 21. Fig. 5 shows trisomy 21 with three distinct fluorescent signals in interphase nuclei, confirming the presence of an extra copy of chromosome 21. Fig. 6 demonstrates a mosaic pattern, with nuclei showing both trisomic (three signals) and diploid (two signals) cell populations. These findings highlight the utility of FISH for rapid confirmation of trisomy 21 and detection of mosaic Down syndrome.

doi: 10.21276/SSR-IIJLS.2026.12.1.10

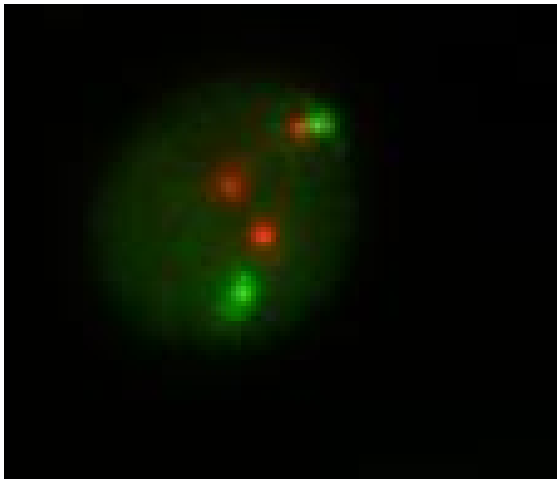

Fig. 5: Trisomy 21 by Fluorescence in Situ Hybridization (FISH).

The cases include neonates and infants, with ages ranging from 1 day to a few months at the time of testing. This highlights the emphasis on early genetic testing soon after birth or during pregnancy (in cases where advanced maternal age is noted). Both male and female neonates are represented. The dataset suggests no gender-based bias, consistent with global trends in Down syndrome incidence (Fig. 6).

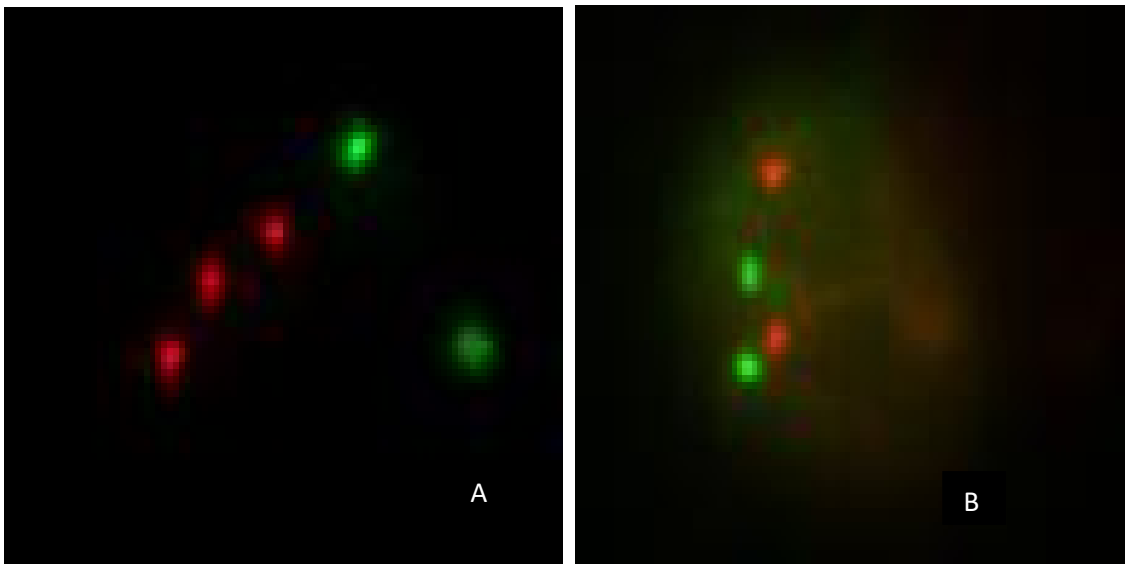

Fig. 6: (A) FISH of Trisomy 21 and (B) Diploid for 21 (Mosaic Pattern)

Sex-wise distribution of Down syndrome cases. The pie chart illustrates the proportion of male (n=22) and female (n=10) cases among the confirmed Down syndrome patients, showing a higher prevalence in males, with no significant gender bias (Fig. 7a).

Distribution of mosaic Down syndrome cases based on area of residence. Fig. 7b shows that most mosaic cases were reported from rural areas (n=2) compared to urban areas (n=1), indicating a higher rural representation.

Distribution of free trisomy 21 cases according to rural and urban residence. Among the confirmed free trisomy 21 cases, a higher proportion was observed in rural areas (n = 16) compared to urban areas (n = 13), highlighting regional differences in case distribution (Fig. 8).

doi: 10.21276/SSR-IIJLS.2026.12.1.10

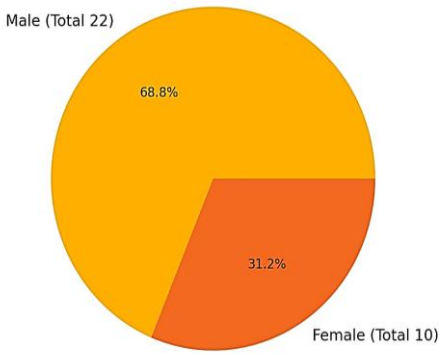

Fig. 7a: Sex-wise distribution of Down syndrome cases

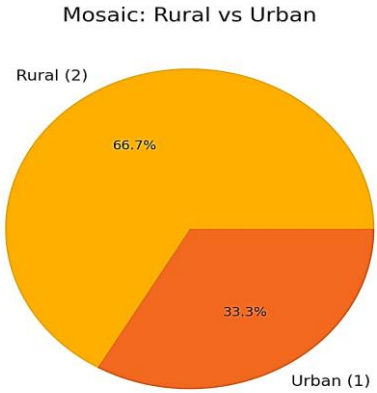

Fig. 7b: Distribution of mosaic Down syndrome cases

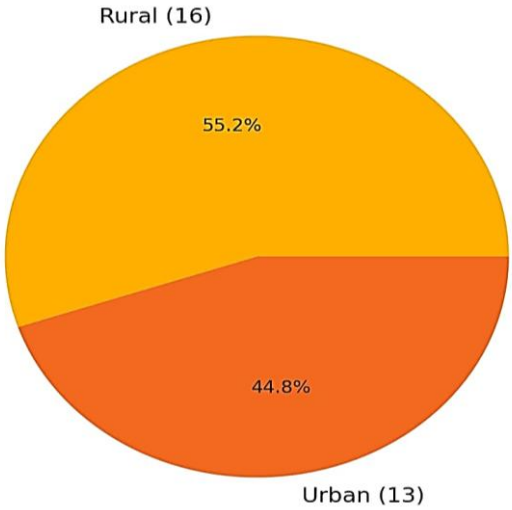

Fig. 8: Free trisomy 21: Urban/Rural, Mosaic: Rural/Urban

DISCUSSION

Down syndrome (DS) is the most frequent chromosomal disorder encountered in clinical genetics, predominantly caused by free trisomy 21 [6]. In the present study, out of 495 suspected cases, 32 were cytogenetically confirmed as Down syndrome. Free trisomy 21 was the most common cytogenetic abnormality (90.6%), whereas mosaic trisomy 21 was observed in 9.3% of cases. This distribution aligns with previously reported data, which show that free trisomy 21 accounts for over 90% of Down syndrome cases worldwide [7,8]. Mosaicism, although less frequent, highlights the importance of thorough cytogenetic examination, particularly in cases with atypical clinical features.

Advanced maternal age is a well-established risk factor for trisomy 21. In the current cohort, the mean maternal age was 31.3 years for free trisomy cases and 26.2 years for mosaic cases, with 36% of mothers aged 35 or older. These findings corroborate prior studies that emphasise that increasing maternal age significantly increases the risk of nondisjunction events [9,10]. However, the occurrence of Down syndrome among younger mothers in this dataset underscores the necessity for universal prenatal screening rather than age-restricted approaches [11].

Geographically, a higher proportion of cases were reported from rural areas, particularly for mosaic and free trisomy 21 cases. This may reflect limited awareness, lower access to prenatal diagnostic facilities, and the potential influence of consanguinity in rural populations. Similar regional trends have been observed in other studies from India and neighboring countries [12,13]. Early detection and referral by pediatric and obstetric departments, as evident in this dataset, are crucial for timely intervention, genetic counseling, and

doi: 10.21276/SSR-IIJLS.2026.12.1.10

management of associated congenital anomalies, including cardiac and gastrointestinal defects.

The combined use of GTG-banded karyotyping and Fluorescence in Situ Hybridization (FISH) enhanced diagnostic accuracy, particularly in detecting mosaic patterns. FISH serves as a rapid confirmatory tool that complements conventional cytogenetics, which is critical in neonatal settings [14]. Understanding regional cytogenetic trends is instrumental for strengthening prenatal screening programs, improving community awareness, and supporting informed decision-making through preventive genetics initiatives [15].

CONCLUSIONS

In conclusion, this study reinforces the predominance of free trisomy 21 in Down syndrome, confirms the significance of advanced maternal age as a risk factor, and emphasizes the utility of combined cytogenetic techniques for early and accurate diagnosis. Regional epidemiological data, such as presented here, provide valuable insights for healthcare planning, genetic counseling, and the implementation of effective preventive strategies.

CONTRIBUTION OF AUTHORS

Research concept - Ashwini H, Sujayendra Kulkarni
Research design - Sujayendra Kulkarni, Kavita MM
Supervision - Kavita MM, Sangamesh Kashinakunti, Bhuvaneshwari C Yelamali
Materials - Ashwini H, Sujayendra Kulkarni
Data collection - Ashwini H, Sujayendra Kulkarni
Data analysis and interpretation - Sujayendra Kulkarni, Kavita MM, Sangamesh Kashinakunti
Literature search - Ashwini H, Bhuvaneshwari C Yelamali
Writing article - Ashwini H, Sujayendra Kulkarni
Critical review - Kavita MM, Sangamesh Kashinakunti, Bhuvaneshwari C Yelamali
Article editing - Sujayendra Kulkarni, Kavita MM
Final approval - Sujayendra Kulkarni, Sangamesh Kashinakunti, Bhuvaneshwari C Yelamali

REFERENCES

[1] Malini SS, Ramchandra NB. Influence of advanced age of maternal grandmother on Down syndrome. BMC Med Genet., 2006; 7: 4.
[2] Coppedè F, Bosco P, Lorenzoni V, Denaro M, Anello G, et al. The MTRR c.66A>G polymorphism and maternal risk of birth of a child with Down syndrome in Caucasian women: a case control study and a meta-analysis. Mol Biol Rep., 2014; 41(9): 5571–83.
[3] Shalaby HMA. A study of new potential risk factors for Down syndrome in Upper Egypt. Egypt J Med Hum Genet., 2011; 12: 15–19.
[4] Seabright M. A rapid banding technique for human chromosomes. Lancet, 1991; 2: 971–72. oi: 10.1016/s0140-6736(71)90287-x.
[5] Fisch H, Hyun G, Golden R, Hensle TW, Olsson CA, Liberson GL. The influence of paternal age on Down syndrome. J Urol., 2003; 169: 2275–78.
[6] Cytogenetic Study of Down Syndrome in Algeria: Report and Review-Scientific Figure on ResearchGate. Available from: https://www.researchgate.net/figure/Karyotype-analysis-of-22-Down-syndrome-cases-Karyotype-n-Percentage_tbl2_301796258 [Accessed 26 Nov 2025].
[7] Sherman SL, Freeman SB, Allen EG, Lamb NE. Risk factors for non-disjunction of trisomy 21. Cytogenet Genome Res., 2005; 111(3–4): 273–80. doi: 10.1159/000086900.
[8] Azman BZ, Ankathil R, Siti Mariam I, Suhaida MA, Norhashimah M, et al. Cytogenetic and clinical profile of Down Syndrome in Northeast Malaysia. Singapore Med J., 2007; 48: 550–54.
[9] Jaouad IC, Cherkaoui DS, Sbiti A, Natiq A, Elkerch F, Sefiani A. Cytogenetic and epidemiological profiles of Down syndrome in Moroccan population: A report of 852 cases. Singapore Med J., 2010; 51: 133–36.
[10] Sheth F, Rao S, Desai M, Vin J, Sheth J. Cytogenetic analysis of Down syndrome in Gujarat. Indian Pediatr., 2007; 44: 774–77.
[11] Chandra N, Cyril C, Lakshminarayana P, Nallasivam P, Ramesh A, et al. Cytogenetic evaluation of Down Syndrome: A review of 1020 referral cases. Int J Hum Genet., 2010; 10: 87–93.
[12] Kaur A, Singh J. Chromosomal abnormalities: Genetic disease burden in India. Int J Hum Genet., 2010; 10(1–3): 1–14.
[13] Global Down Syndrome Foundation. Down Syndrome Facts and Statistics. Available from: https://www.globaldownsyndrome.org/contact-global/ [Accessed 26 Nov 2025].

doi: 10.21276/SSR-IIJLS.2026.12.1.10

[14]Shalaby HMA. A study of new potential risk factors for Down syndrome in Upper Egypt. Egypt J Med Hum Genet., 2011; 12: 15–19.

[15]Malini SS, Ramchandra NB. Influence of advanced age of maternal grandmother on Down syndrome. BMC Med Genet., 2006; 7: 4.