

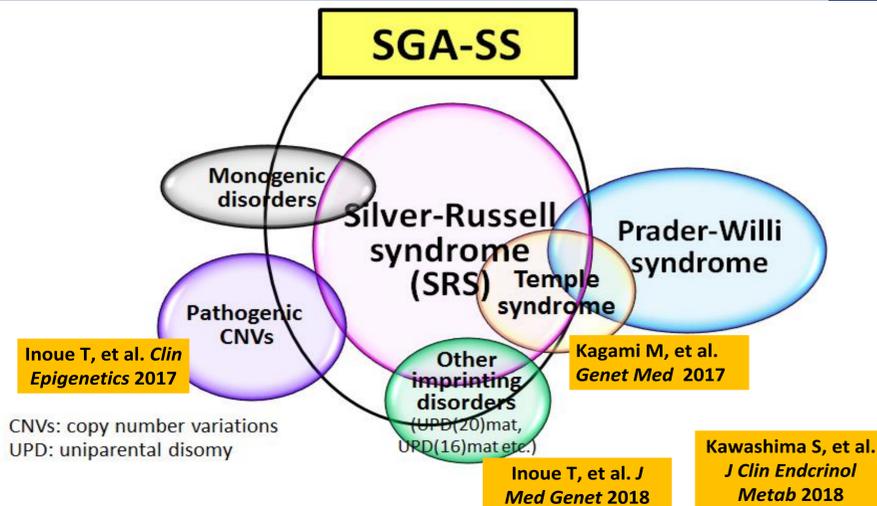


Imprinting defects and copy number variations in short children born small for gestational age

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Introduction

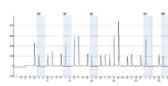


- SGA-short stature (SGA-SS) is a heterogeneous condition.
- Some imprinting disorders, monogenic disorders, and pathogenic copy number variations lead to SGA-SS.
- Silver-Russell syndrome (SRS) is a typical imprinting disorder having SGA-SS.

Methods

SGA-SS cases

Methylation analysis using pyrosequencing



- *H19*-DMR (ch11)
- *PEG1*, *PEG10*-DMR (ch7)
- *PLAGL1*-DMR (ch6)
- *KvDMR* (ch11)
- *IG*-DMR (ch14)
- *MEG3*-DMR (ch14)
- *SNRPN*-DMR (ch15)
- *A/B*-DMR (ch20)
- *ZNF597*-DMR (chr16)

Hypomethylation of the *H19*-DMR

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H19-DMR Hypomethylation

Hypomethylation of the *PEG1*- and *PEG10*-DMR

↓

Microsatellite analysis for chromosome 7

↓

UPD(7)mat

Abnormal methylation levels of the DMR(s) other than *H19*-, *PEG1*-, and *PEG10*-DMR

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- MS-MLPA
- aCGH analysis
- FISH

↓

Imprinting disorders other than SRS

- Temple syndrome
- Prader-Willi syndrome
- UPD(20)mat etc.

Normal methylation status in 10 DMRs

↓

- Catalog aCGH analysis (8X60k)

↓

Genetic disorders

- Williams syndrome
- 4p- syndrome etc.

Aim

To clarify the contribution of imprinting defects and pathogenic copy number variations to SGA-SS.

Subject

Subjects:

346 patients clinically diagnosed with SRS or SGA-SS by presenting doctors

Inclusion criteria

SGA : Birth weight and height < 10 percentile

Short stature:

- Age ≥ 2years
- Height < -2.0 SDS before initiation of GH treatment

The cases clinically or genetically diagnosed as known syndromes were not included (ex. Prader-Willi syndrome, Turner syndrome).

Netchine-Harison clinical scoring system (NH-CSS)

1. SGA (birth weight and/or birth length ≤ -2 SD)
2. Postnatal growth failure (height ≤ -2 SD)
3. Relative macrocephaly at birth
4. Protruding forehead
5. Body asymmetry
6. Feeding difficulties and/or low BMI (≤ -2 SD)

SRS: ≥4 of 6 items

- NH-CSS ≥ 4 : SRS compatible group (n=163)
- NH-CSS = 3 + α (triangular face and/or fifth finger clinodactyly): SRS-like group (n=52)
- NH-CSS ≤ 3 : non-SRS group (n=131)

Results

Genetic causes	SRS-compatible n=163	SRS-like n=52	non-SRS n=131
Genetic causes of SRS	47 (29%)	11 (21%)	5 (4%)
• Hypomethylation of the <i>H19</i> -DMR	40	8	3
• UPD(7)mat	7	3	2
Imprinting disorders other than SRS	20 (12%)	4 (8%)	7 (5%)
• Temple syndrome	8	1	2
• Prader-Willi syndrome	2	0	1
• UPD(20)mat	3	1	1
• UPD(16)mat	2	0	0
• UPD(6)mat	1	1	1
• Parthenogenesis	1	0	0
• UPD(11)mat mosaic	1	0	0
• Trisomy 14/UPD(14)mat mosaic	0	0	1
• 11p15 maternal duplication	2	1	0
• 20q13 maternal duplication	0	0	1
Pathogenic CNVs	5 (3%)	7 (14%)	7 (5%)
Unknown	91 (56%)	30 (58%)	112 (85%)

Details of pathogenic CNVs	SRS- Compatible		
	SRS-compatible	SRS-like	non-SRS
4p deletion (Wolf-Hirschhorn syndrome)	1	1	
1q24q25 deletion	1		
Mosaic trisomy 18	1		
17p12 duplication	1		
Xq26.2 duplication	1		
12q14 deletion (including <i>HMGA2</i>)		2	
7q11.23 deletion (Williams syndrome)		2	
19q13.11-12 deletion		1	
2p21.1 duplication		1	
1q21.2 deletion			1
22q11.2 deletion (22q11.2 deletion syndrome)			1
1p32.2 duplication/3p12.1 duplication/Xp22.3 3 duplication			1
8p23.2 duplication/19p13.12 deletion			1
5q35.2 duplication (including <i>NSD1</i>)			2
Xp deletion (Turner syndrome)			1

Discussion

- In this study, we clarified the involvement of the imprinting disorders and pathogenic copy number variations for SRS and SGA-SS.
- Imprinting disorders other than SRS with hypomethylation of the *H19*-DMR and UPD(7)mat were detected over 10% of SRS-compatible group.
- For the patients with negative SRS genetic test results, genetic testing of TS14 should be considered.
- Our results highlight the clinical importance of imprinting defects and pathogenic CNVs as genetic causes of SGA-SS.

Conclusion

A part of SRS and SGA-SS is caused by imprinting defects other than *H19*-hypo and UPD(7)mat and pathogenic CNVs.