CORRECTION   OPEN

Correction: Analyses of oligodontia phenotypes and genetic etiologies

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Following publication of this article,[1] it is noticed Table 2 in this article needs revision.

The correct Table 2 is provided in this Correction.

The original article has been updated.

REFERENCE

1. Zhou, M., Zhang, H. & Camhi, H. et al. Analyses of oligodontia phenotypes and genetic etiologies. *Int. J. Oral Sci.* **13**, 32 (2021).

Table 2. Frequencies of tooth absence (in percentage) among the study cases affected by *PAX9*, *MSX1*, *WNT10A*, *WNT10B*, *AXIN2*, *EDA*, *EDAR*, *EDARADD*, *LRP6*, *KREMEN1*, *SMOC2*, and *PITX2* gene mutations

Gene	Maxillary Teeth (% of Cases Missing)							Mandibular Teeth (% of Cases Missing)						
	Mo2	Mo1	PM2	PM1	Ca	LI	CI	Mo2	Mo1	PM2	PM1	Ca	LI	CI
AXIN2	50.0	33.3	83.3	56.3	31.3	62.5	8.3	37.5	37.5	83.3	35.4	18.8	47.9	66.7
PAX9	86.6	69.1	70.6	32.5	30.9	27.8	6.7	86.6	43.8	50.5	14.4	11.3	11.9	41.2
EDA	19.6	8.7	47.8	41.3	50.0	84.8	19.6	17.4	10.9	67.4	45.7	34.8	91.3	89.1
EDAR	23.3	20.0	53.3	50.0	50.0	66.7	6.7	20.0	13.3	63.3	33.3	23.3	66.7	36.7
WNT10A	40.7	26.0	82.4	64.2	40.2	64.7	6.4	44.6	24.5	77.9	50.0	33.3	42.2	53.4
WNT10B	25.0	25.0	50.0	50.0	58.3	83.3	50.0	25.0	33.3	66.7	8.3	50.0	91.7	66.7
LRP6	40.6	6.3	68.8	59.4	65.6	93.8	0.0	46.9	3.1	75.0	37.5	43.8	71.9	78.1
MSX1	30.7	14.0	84.2	75.4	13.2	39.5	15.8	46.5	33.3	88.6	29.8	14.0	21.1	50.9
EDARADD	0.0	0.0	80.0	40.0	30.0	40.0	0.0	50.0	0.0	100.0	50.0	0.0	0.0	0.0
KREMEN1	26.7	0.0	6.7	26.7	13.3	80.0	6.7	20.0	0.0	20.0	20.0	66.7	80.0	80.0
SMOC2	16.7	0.0	100.0	8.3	33.3	16.7	0.0	8.3	0.0	100.0	83.3	83.3	66.7	0.0
TSPEAR	62.5	50.0	25.0	50.0	50.0	100.0	0.0	25.0	12.5	25.0	25.0	50.0	75.0	100.0
SATB2	0.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	100.0	100.0	0.0
PITX2	68.2	36.4	59.1	54.5	86.4	81.8	90.9	22.7	0.0	59.1	54.5	68.2	77.3	81.8
BMP4	25.0	37.5	75.0	100.0	0.0	75.0	0.0	50.0	25.0	100.0	25.0	12.5	50.0	50.0
BMP2	16.7	16.7	100.0	33.3	0.0	100.0	0.0	33.3	66.7	50.0	0.0	0.0	16.7	100.0
OPN3	100.0	0.0	50.0	0.0	100.0	100.0	0.0	0.0	0.0	100.0	50.0	100.0	0.0	100.0
DSP	100.0	0.0	100.0	0.0	100.0	50.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0
IKBKG	50.0	0.0	100.0	50.0	0.0	50.0	0.0	50.0	50.0	100.0	100.0	0.0	0.0	0.0
GREMLIN2	100.0	0.0	100.0	100.0	100.0	100.0	0.0	100.0	0.0	100.0	0.0	100.0	100.0	50.0

Please note that the same type of tooth absent in the right and left arches were pooled together for the calculation. Numbers in gold color represent the highest frequency and numbers in blue color represent the lowest frequency of tooth type absence in each causative gene *Ca* canine; *CI* central incisor; *LI* lateral incisor; *Mo* molar; *PM* premolar.