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Unveiling diversity of stem cells in dental pulp and apical papilla using mouse genetic models: A literature review

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Abstract

The dental pulp, a non-mineralized connective tissue uniquely encased within the cavity of the tooth, provides a niche for diverse arrays of dental mesenchymal stem cells. Stem cells in the dental pulp, including dental pulp stem cells (DPSCs), stem cells from human exfoliated deciduous teeth (SHEDs) and stem cells from apical papilla (SCAPs), have been isolated from human tissues with an emphasis on their potential application to regenerative therapies. Recent studies utilizing mouse genetic models shed light on the identities of these mesenchymal progenitor cells derived from neural crest cells (NCCs) in their native conditions, particularly regarding how they contribute to homeostasis and repair of the dental tissue. The current concept is that at least two distinct niches for stem cells exist in the dental pulp, e.g. the perivascular niche and the perineural niche. The precise identities of these stem cells and their niches are now beginning to be unraveled thanks to sophisticated mouse genetic models, which lead to better understanding on the fundamental properties of stem cells in the dental pulp and the apical papilla in humans. The new knowledge will be highly instrumental for developing more effective stem cell-based regenerative therapies to repair teeth in the future.

Keywords

Stem cell; dental pulp; mouse genetic models; dental pulp stem cells; dental mesenchymal stem cells; dental pulp stem cell niche

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Conflict of Interest

The authors declare no conflict of interest.

Ethical approval

This article does not contain any studies with animals performed by any of the authors.

Introduction

Tooth development is a unique process regulated by interactions between epithelial and mesenchymal tissues (Thesleff, 2003). Dental mesenchymal cells are derived from two different origins: the cranial neural crest cells (NCCs) and the non-neural crest mesoderm (Chai, et al., 2000). NCCs of the first branchial arch are the origin of the odontogenic ectomesenchyme that develop into the dental mesenchyme, which give rise to diverse arrays of dental pulp cells, dentin-forming odontoblasts, periodontal ligament cells, cementum-forming cementoblasts, osteoblasts and chondrocytes (Bronner-Fraser, 1993, Chai, Jiang, Ito, Bringas, Han, Rowitch, Soriano, McMahon and Sucov, 2000). Various signaling molecules such as TGF- β , BMP and Wnt are involved in regulating differentiation of NCCs (Chai, et al., 2003, Trainor, et al., 2002, Tucker, et al., 1999). At the cap stage, the dental papilla is formed as a result of invagination of dental lamina epithelial cells. At the subsequent bell stage, dental epithelial cells at the apical region of the tooth bud continue to invade further apically and interact with dental papilla mesenchymal cells inside the tooth bud; as a result, dental papilla mesenchymal cells subsequently develop into dental pulp cells and odontoblasts (Nanci, 2017).

The dental pulp, a non-mineralized connective tissue uniquely encased within the cavity of the tooth, is composed of heterogeneous cell populations, such as fibroblasts, vascular cells, neural cells and lymphocytes (Goldberg and Smith, 2004). These cells play an important role in tooth homeostasis and repair of damaged dentin. Since the discovery of dental pulp stem cells (DPSCs) (Gronthos, et al., 2002, Gronthos, et al., 2000), stem cells have been isolated from diverse dental tissues, such as exfoliated deciduous teeth (Miura, et al., 2003), apical papilla (Abe, et al., 2007, Sonoyama, et al., 2006), periodontal ligament (Seo, et al., 2004), gingiva (Zhang, et al., 2012) and dental follicle (Morsczeck, et al., 2005) (Figure 1, Table 1). DPSCs, stem cells from human exfoliated deciduous teeth (SHEDs) and stem cells from apical papilla (SCAPs) all possess a property as “mesenchymal stem cells (MSCs)”, therefore present great promise for regenerative therapies (Tatullo, et al., 2015, Yamada, et al., 2019). Fundamental aspects of stem cells in the dental pulp and the apical papilla are beginning to be unraveled. Despite the accumulating knowledge on the dental stem cells (Sharpe, 2016), it is imperative to understand how these stem cells regulate odontogenesis under both physiological and regenerative conditions, because the current regenerative therapies to repair dentin and tooth structures need to be improved for better clinical outcomes. The purpose of this review is to summarize the current understanding on stem cell populations in the dental pulp and the apical papilla, and the recent findings from *in vivo* mouse genetic models on how these stem cells contribute to tooth homeostasis and repair.

Search protocol

Outcome:

To identify stem cell populations that can differentiate into odontoblasts and produce dentin *in vivo*.

Population and intervention:

Our focus was on pre-clinical studies using mouse genetic models to define the lineage of stem cells in the dental pulp and the apical papilla. We included animal (mouse) studies using conditional knockout models based on the *cre-loxP* system, but excluded animal studies using conventional (global) knockout models.

Search strategy:

For searching *in vivo* stem cells in the dental pulp and the apical papilla, a literature search was conducted using PubMed, Web of Science and Google Scholar by the first author (M.N.). A search strategy for the database was performed to find studies that matched the following terms: (dental pulp stem cell OR dental pulp) AND (*cre* OR *creER*). The electronic search aimed to obtain all the studies that identified *in vivo* stem cells in the dental pulp and the apical papilla using mouse genetic models. Animal studies using the *cre-loxP* system was eligible for inclusion in this review, while animal studies using only conventional knockout mice were excluded. No restriction regarding the original language of the article or publication status were set. Databases were searched up to January 2020, with no limit on the year of publication. To complement the search, the reference list of the main articles related to this narrative review were also assessed. A total of 25 *in vivo* mouse genetic studies were included. Two authors (M.N. and W.O.) independently assessed the quality of the identified studies and resolving any disagreements through discussion.

In vitro* MSCs isolated from the dental pulp*Dental pulp stem cells (DPSCs)**

Smith et al. reported that the odontoblast layer can be stimulated to form reactionary dentin (otherwise known as tertiary dentin, which is formed in response to aggression) in response to enamel or dentin damage, suggesting that the dental pulp may contain MSCs that are responsible for tooth repair by producing newly formed dentin (Smith, et al., 1995, Smith and Lesot, 2001). MSCs have been isolated from dental mesenchymal tissues including the dental pulp (Sharpe, 2016). DPSCs, a postnatal stem cell population resident in the dental pulp, were initially isolated from extracted human third molars by Gronthos et al.; these cells possess high clonogenic abilities, rapid proliferative rates, and capabilities to produce mineralized tissues both *in vitro* and *in vivo* (Gronthos, Mankani, Brahim, Robey and Shi, 2000). Subsequent studies identified that DPSCs are capable of differentiating into adipocytes, osteoblasts, chondrocytes, melanocytes and endotheliocytes *in vitro* and after transplantation (d'Aquino, et al., 2007, Gronthos, Brahim, Li, Fisher, Cherman, Boyde, DenBesten, Robey and Shi, 2002, Hilkens, et al., 2013, Koyama, et al., 2009, Stevens, et al., 2008, Zhang, et al., 2008). Importantly, DPSCs present enhanced odontogenic capacity compared with bone marrow mesenchymal stem cells (BM-MSCs), indicating that DPSCs may represent a suitable source for repairing the dentin (Yu, et al., 2007).

Moreover, the dental pulp may play an important role for defense against dentin-invading bacteria by inducing immune response (Farges, et al., 2015). Dental pulp cells express a diverse array of chemokines and cytokines (Farges, et al., 2009), particularly CXCL12 (chemokine C-X-C motif ligand 12), which is abundantly expressed by mesenchymal

stromal cells in the bone marrow stromal compartment (Matsushita, et al., 2020, Sugiyama, et al., 2006). Indeed, DPSCs ameliorate inflammation-related tissue injuries by suppressing T cell proliferation, therefore possessing immunomodulatory properties (Pierdomenico, et al., 2005, Tang and Ding, 2011, Zhao, et al., 2012). Therefore, DPSCs might also possess inherent capabilities to coordinate development and homeostasis of the dental pulp, in addition to their potential for regenerative medicine.

Stem cells from exfoliated deciduous teeth (SHEDs)

Deciduous teeth similarly possess a variety of immature cells within their dental pulp, thus considered as an ideal source of stem cells. SHEDs were first isolated by Miura et al. (Miura, Gronthos, Zhao, Lu, Fisher, Robey and Shi, 2003). These cells have a potential to differentiate into a variety of cell types including osteoblasts, adipocytes, chondrocytes, endothelial cells, neural cells and odontoblasts (Casagrande, et al., 2010, Cordeiro, et al., 2008, Miura, Gronthos, Zhao, Lu, Fisher, Robey and Shi, 2003, Sakai, et al., 2010, Wang, et al., 2012). After *in vivo* transplantation, SHEDs can undergo osteogenesis and dentinogenesis (Miura, Gronthos, Zhao, Lu, Fisher, Robey and Shi, 2003, Sakai, Zhang, Dong, Neiva, Machado, Shi, Santos and Nor, 2010, Shi, et al., 2005). SHEDs possess higher proliferation rates and osteo-inductive capacities after *in vivo* transplantation than those of DPSCs, suggesting that these cells demonstrate a great potential for mineralized tissue regeneration (Miura, Gronthos, Zhao, Lu, Fisher, Robey and Shi, 2003, Wang, Sha, Li, Yang, Ji, Wen, Liu, Chen, Ding and Xuan, 2012). In a recent human clinical trial, implantation of autologous SHEDs into necrotic immature permanent incisors of pediatric patients generated a functional dental pulp associated with blood vessels and sensory nerves (Xuan, et al., 2018). SHEDs have a unique advantage of being retrievable from exfoliated teeth, which otherwise had been considered as a disposable human tissue. SHEDs have been applied not only to pulp regeneration but also to extraoral application such as kidney (Hattori, et al., 2015), brain (Fujii, et al., 2015, Mita, et al., 2015), spinal cord (Nicola, et al., 2017, Taghipour, et al., 2012), liver (Yamaza, et al., 2015) and bone (Ma, et al., 2012, Novais, et al., 2019) in pre-clinical animal models (Shi, et al., 2020).

Stem cells from apical papilla (SCAPs)

The apical papilla, the apical portion of the dental papilla, is loosely attached to the apex of the developing tooth root in erupting permanent teeth. A cell-rich zone exists between the apical papilla and the dental pulp. The apical papilla has been considered to play an important role in tooth root formation as it contains an MSC-like cell population (Abe, Yamaguchi and Amagasa, 2007, Abe, et al., 2008, Huang, et al., 2008, Sonoyama, Liu, Fang, Yamaza, Seo, Zhang, Liu, Gronthos, Wang, Wang and Shi, 2006, Sonoyama, et al., 2008). SCAPs were initially isolated by Sonoyama et al. (Sonoyama, Liu, Fang, Yamaza, Seo, Zhang, Liu, Gronthos, Wang, Wang and Shi, 2006). These cells can differentiate into osteoblasts, odontoblasts and adipocytes *in vitro* with a higher proliferation rate than that of DPSCs, while expressing typical markers for stem cells (Sonoyama, Liu, Fang, Yamaza, Seo, Zhang, Liu, Gronthos, Wang, Wang and Shi, 2006). In addition, SCAPs have the ability to differentiate into other non-native cell types such as neural cells (Abe, Yamaguchi and Amagasa, 2007, Kim, et al., 2017, Sonoyama, Liu, Yamaza, Tuan, Wang, Shi and Huang, 2008), chondrocytes (Abe, Yamaguchi and Amagasa, 2007, Dong, et al., 2013, Patil, et al.,

2014) and hepatocytes (Kumar, et al., 2017, Patil, Kumar, Lee, Jeon, Jang, Lee, Park, Byun, Ahn, Kim and Rho, 2014) after transplantation. Interestingly, cultured SCAPs express several neural markers without neurogenic stimulation, such as Nestin, Musashi1 and TrkA (Abe, Yamaguchi and Amagasa, 2007). Additional neural markers are also expressed in SCAPs after neurogenic stimulation, such as glutamic acid decarboxylase (GAD), neuronal nuclear antigen (NeuN), neurofilament M (NFM), neuron-specific enolase (NSE), and glial markers 2', 3'-cyclic nucleotide 3'-phosphodiesterase (CNase) (Sonoyama, Liu, Yamaza, Tuan, Wang, Shi and Huang, 2008). Indeed, SCAPs and DPSCs participate in nerve regeneration upon transplantation (Kolar, et al., 2017). Compared with other dental MSCs such as DPSCs or periodontal ligament stem cells (PDLSCs), SCAPs has a higher ability for nerve regeneration in a rat sciatic nerve injury model (Kolar, Itte, Kingham, Novikov, Wiberg and Kelk, 2017). As SCAPs have the ability to differentiate into multilineage cells, they can be considered as a promising cell source for stem cell-based therapies (Kang, et al., 2019). In fact, SCAPs are applied clinically in the "cell-homing techniques" to support the root development of immature teeth that previously experienced pulp necrosis and periapical periodontitis (Palma, et al., 2019). Consistently, SCAPs demonstrate the capacity to promote mineralized tissue regeneration inside the root of previously necrotic teeth or in the periapical tissue after severe infection is resolved (Palma, et al., 2017).

***In vivo* stem cell markers of the dental pulp**

Stem cell niches in the dental pulp

The dentin-pulp complex possesses the inherent capability for regeneration in order to protect itself against external insults such as caries and mechanical trauma (Smith, Cassidy, Perry, Begue-Kirn, Ruch and Lesot, 1995). The dental pulp contains niches for stem/progenitor cells, which provide precursor cells for odontoblasts and other types of mesenchymal cells (Sloan and Smith, 2007, Sloan and Waddington, 2009). Recently, two distinct niches for stem cells derived from NCCs have been identified in the dental pulp in mice; namely, the perivascular niche and the perineural niche (Feng, et al., 2011, Kaukua, et al., 2014, Vidovic, et al., 2017, Zhao, et al., 2014).

Cranial neural crest cells (NCCs)

The proto-oncogene *Wnt1* is expressed exclusively during early development of the central nervous system, and *Wnt1-cre* can mark a pre-migratory neural crest cell population. (Baggiolini, et al., 2015, Echelard, et al., 1994, Hari, et al., 2012, McMahon, et al., 1992, Wilkinson, et al., 1987). *Wnt1-cre* has been widely used to map the fate of NCCs during craniofacial development. Chai et al. reported that NCCs contribute to all dental mesenchymal tissue including the dental pulp using *Wnt1-cre*-based fate mapping experiments (Chai, Jiang, Ito, Bringas, Han, Rowitch, Soriano, McMahon and Sucov, 2000). *Wnt1-cre*-marked dental pulp cells exhibit multi-lineage differentiation into osteoblasts, adipocytes, neurons, and smooth muscles *in vitro* (Janebodin, et al., 2011). Upon *in vivo* subcutaneous transplantation with a hydroxyapatite/tricalcium phosphate carrier, *Wnt1-cre*-marked dental pulp cells differentiate into odontoblast-like cells and produce a dentin-like structure (Janebodin, Horst, Ieronimakis, Balasundaram, Reesukumal, Pratumvinit and Reyes, 2011). Moreover, implantation of *Wnt1-cre*-marked dental pulp cells contribute to

repair of critical-size calvarial bone defects (Collignon, et al., 2019). Transplanted *Wnt1-cre*-marked dental pulp cells are present up to 3 months after transplantation in the calvarial defect and they rapidly differentiate into chondrocyte-like cells (Collignon, Castillo-Dali, Gomez, Guilbert, Lesieur, Nicoletti, Acuna-Mendoza, Letourneur, Chaussain, Rochefort and Poliard, 2019). In fact, various signaling pathways in *Wnt1-cre*-marked dental pulp cells can modulate dentin formation. Oka et al. reported that dentin thickness and tooth size were reduced in *Wnt1-cre; Tgfb β 2^{fl/fl}* mutant mice associated with decreased *Colla1* and *Dspp* expression, suggesting that the TGF- β signaling pathway controls odontoblast maturation and dentin formation (Oka, et al., 2007). A transcriptional factor Kruppel-like factor 4 (KLF4) is expressed by the polarizing odontoblast layer, and dentin mineralization is impaired in *Wnt1-cre; KLF4^{fl/fl}* mutant mice (Tao, et al., 2019). KLF4 directly activates the TGF- β signaling pathway at the beginning of odontoblast differentiation associated with upregulation of dentin matrix protein (*Dmp1*) and Osterix (*Osx/Sp7*).

Protein 0 (P0) is expressed by migrating neural crest cells. As a result, *P0-cre* transgenic line represents a useful tool as a neural crest cell-specific *cre* driver (Komada, et al., 2012, Yamauchi, et al., 1999). *P0-cre* marks cells in the dental mesenchyme that contribute to development of the dentin-pulp complex. However, *P0-cre* also marks cells in the enamel organ (Wang, et al., 2011). Indeed, *P0-cre* marks cell populations that are different from *Wnt1-cre*-marked NCCs, especially in the midbrain and hindbrain region (Chen, et al., 2017); therefore, *P0-cre* and *Wnt1-cre* transgenic lines mark non-identical cell populations. Similarities and differences between *P0-cre* marked and *Wnt1-cre* marked NCCs remains to be studied.

Perivascular stem cell niche

Neural/glial antigen 2 (NG2) is a proteoglycan commonly used as a marker for pericytes that maintain hematopoietic stem cell quiescence in bone marrow (Chan-Ling and Hughes, 2005, Kunisaki, et al., 2013, Murfee, et al., 2005). Lineage-tracing experiments using *NG2-creER* mice revealed that pericytes can differentiate into odontoblasts during tooth root formation as well as in response to injuries in mouse incisors (Feng, Mantesso, De Bari, Nishiyama and Sharpe, 2011). Moreover, the tip of the mouse incisor pulp also contains a population of NG2⁺ pericytes that differentiate into odontoblast-like cells, suggesting that rapid and continuous mineralization occurs at the tip of the incisor to protect the dental pulp tissue from external stimuli (Pang, et al., 2016).

Glioma-associated oncogene homolog 1 (Gli1), a canonical transcriptional target of hedgehog (Hh) signaling, is expressed by both dental mesenchymal cells and epithelial cells in HERS (Feng, et al., 2017, Liu, et al., 2015). Gli1 marks perivascular MSC-like cells *in vivo*, and Gli1⁺ cells express typical MSC markers and possess an ability for trilineage differentiation *in vitro* (Kramann, et al., 2015). Gli1⁺ mesenchymal cells are slow-cycling and function as mesenchymal stem cells in developing mouse incisors (Zhao, Feng, Seidel, Shi, Klein, Sharpe and Chai, 2014). Gli1⁺ cells are located surrounding small arteries and mobilized in response to injuries. In addition, Gli1⁺ cells give rise to all NG2⁺ or CD146⁺ perivascular cells *in vivo*, indicating that NG2⁺ cells are a subset of MSC subpopulations derived from Gli1⁺ cells. Importantly, in contrast to incisors, adult mouse molars do not

contain Gli1⁺ cells surrounding the small arteries in the dental pulp, whereas NG2⁺ pericytes surround all vasculatures in the molars (Zhao, Feng, Seidel, Shi, Klein, Sharpe and Chai, 2014). These results indicate that Gli1⁺ cells may behave as transient root progenitor cells for the growth of the molar. Indeed, during tooth root development, several signaling pathways in Gli1⁺ cells affect tooth root formation. Constitutive activation of Hh signaling in Gli1⁺ root progenitor cells using *Gli1-creER; SmoM2* mice leads to shortened roots in molars; however, odontoblast marker gene *Dspp* expression is unaffected (Liu, Feng, Li, Zhao, Ho and Chai, 2015). Feng et al. reported that disruption of *Bmp* signaling in Gli1⁺ root progenitor cells (*Gli1-creER; Bmpr1a^{fl/fl}*) results in impaired root development associated with lack of *Dspp* expression in most of the apical region of molars (Feng, Jing, Li, Zhao, Punj, Zhang, Xu and Chai, 2017). Furthermore, overactivation of a transcriptional factor Klf4, which is a downstream target of BMP signaling, promotes odontogenic differentiation of MSCs, suggesting that BMP signaling specifically regulates Klf4 in odontogenesis.

Alpha-smooth muscle actin (α SMA) is one of the markers for perivascular cells (Crisan, et al., 2009, Crisan, et al., 2011, Crisan, et al., 2008). Vidovic et al. reported that α SMA⁺ perivascular cells in the dental pulp differentiate into odontoblasts during tooth root formation (Vidovic, Banerjee, Fatahi, Matthews, Dymont, Kalajzic and Mina, 2017). After tooth root formation, α SMA⁺ perivascular cells lie dormant in the intact dental pulp. However, when the dental pulp is injured in an experimental pulp exposure model, α SMA⁺ perivascular cells rapidly proliferate and contribute to reparative dentinogenesis (Vidovic, Banerjee, Fatahi, Matthews, Dymont, Kalajzic and Mina, 2017). Furthermore, the delivery of exogenous fibroblast growth factor 2 (FGF2) leads to proliferation of α SMA⁺ dental pulp cells and accelerated differentiation into odontoblasts (Vidovic-Zdrilic, et al., 2018). Consistently, mild injuries leading to reactionary dentinogenesis activate α SMA⁺ perivascular cells to give rise to pulp cells as well as a few odontoblasts that are integrated into the pre-odontoblastic layer (Vidovic-Zdrilic, et al., 2019). These findings suggested that the perivascular niche harbors various MSC populations such as NG2⁺, Gli1⁺ and α SMA⁺ cells which contribute to homeostasis and injury repair in the dental pulp.

Perineural stem cell niche

Another subset of dental stem cells has been identified among peripheral nerve-associated glial cells (Kaukua, Shahidi, Konstantinidou, Dyachuk, Kaucka, Furlan, An, Wang, Hultman, Ahrlund-Richter, Blom, Brismar, Lopes, Pachnis, Suter, Clevers, Thesleff, Sharpe, Ernfors, Fried and Adameyko, 2014). Schwann cell precursors associated with innervating nerves are identified as a cellular origin of melanocytes in the skin, although Schwann cells and melanocytes were considered to be generated through entirely distinct pathways from NCCs (Adameyko and Lallemand, 2010, Adameyko, et al., 2009, Adameyko, et al., 2012). Lineage-tracing analyses of Schwann cell precursors using *PLP1-creER* and *Sox10-creER* demonstrates that neural crest-derived Schwann cells and Schwann cell precursors give rise to odontoblasts and dental pulp cells in mouse growing incisor (Kaukua, Shahidi, Konstantinidou, Dyachuk, Kaucka, Furlan, An, Wang, Hultman, Ahrlund-Richter, Blom, Brismar, Lopes, Pachnis, Suter, Clevers, Thesleff, Sharpe, Ernfors, Fried and Adameyko, 2014). Moreover, Schwann cell-derived odontoblasts contribute to reparative dentinogenesis

after mouse incisor injuries. Importantly, these Schwann cells do not express a pericyte marker, indicating that pericytes and Schwann cells represent two distinct subsets of dental pulp stem cell populations. These findings suggest that the dental pulp contains several distinct stem cell niches in the perivascular and neural-vascular bundle area.

Other progenitor cell populations of the dentin–pulp complex

Studies utilizing mouse genetics models have shed light on the mechanism of odontoblast differentiation. A transcriptional factor *Osx*, also known as *Sp7*, is broadly expressed in the dental mesenchyme by dental papilla cells, dental follicle cells, odontoblasts and alveolar bone osteoblasts during tooth development, and regulates cementogenesis (Cao, et al., 2012, Chen, et al., 2009). *Osx* plays a critical role in proliferation and differentiation of both ameloblasts and odontoblasts (Bae, et al., 2018). Major signaling pathways play important regulatory roles in *Osx*⁺ root progenitor cells and dentinogenesis. Rakian et al. reported that conditional deletion of *Bmp2* in *Osx*⁺ cells by *Osx-cre; Bmp2^{fl/fl}* results in loss of tooth root formation with reduction of odontoblast marker genes such as *Dmp1*, *Colla1* and *Sp7* (Rakian, et al., 2013). In addition, Wang et al. reported that conditional deletion of *Tgfrb2* in *Osx*⁺ cells (*Osx-cre; Tgfrb2^{fl/fl}*) results in failure of tooth root formation and tooth eruption associated with reduction in dentin matrix density in molars (Wang, et al., 2013). Li et al. reported that conditional deletion of intraflagellar transport 140 (IFT140), which is specialized for retrograde transportation in the cilia, in *Osx*⁺ cells (*Osx-cre; IFT140^{fl/fl}*) reduces dentin thickness and delays dentin formation (Li, et al., 2018). Moreover, mTOR signaling plays an important role in odontoblast differentiation in dental pulp cells (GEORGE and Eapen, 2015, Kim, et al., 2011), as conditional deletion of Raptor/mTORC1 in *Osx*⁺ cells (*Osx-cre; Raptor^{fl/fl}*) causes dentinogenesis imperfecta associated with a smaller tooth volume (Xie, et al., 2019).

We previously reported that conditional deletion of parathyroid hormone (PTH) / parathyroid hormone-related protein (PTHrP) receptor (PPR) signaling in *Osx*⁺ cells (*Osx-cre; PPR^{fl/fl}*) disrupts tooth root formation and causes severe failure of tooth eruption (Ono, et al., 2016). As PTHrP is a locally acting autocrine/paracrine ligand that is mainly expressed by the dental follicle, *Osx*⁺ root progenitor cells may functionally overlap with dental follicle cells during tooth root formation (Nagata, et al., 2019, Ono, Sakagami, Nishimori, Ono and Kronenberg, 2016, Takahashi, et al., 2019). Moreover, *Osx-creER*⁺ dental root progenitor cells differentiate into all relevant cell types contributing to formation of the tooth root and periodontal tissues, such as odontoblasts, cementoblasts, alveolar bone osteoblasts and periodontal ligament (PDL) cells; these progenitor cells continue to provide these cells even after root formation is complete, suggesting that *Osx*⁺ cells also play important roles in tooth root maintenance (Takahashi, et al., 2017).

Transcription factor paired-related homeobox gene 1 (*Prrx1*) regulates early mesenchymal cell fates in myogenesis, osteoblastogenesis, chondrogenesis and tooth morphogenesis; as a result, *Prrx1-cre* is widely used to mark MSCs (Elefteriou and Yang, 2011, Hu, et al., 1998, Lu, et al., 1999, Lu, et al., 2011, Martin, et al., 1995, Mitchell, et al., 2006, Peterson, et al., 2005, ten Berge, et al., 1998). In tooth development, *Prrx1* is exclusively expressed by mesenchymal cells. *Prrx1^{-/-} Prrx2^{-/-}* embryos that do not survive postnatally exhibit molar

malformation with cuspal changes and ectopic epithelial projection, suggesting that *Prrx1* plays a role in molar tooth morphogenesis (Mitchell, Hicklin, Doughty, Hicklin, Dickert Jr, Tolbert, Peterkova and Kern, 2006). Wang et al. reported that *Prrx1*⁺ mesenchymal cells and their descendants were located in the dental pulp, particularly in the pulp horn using *Prrx1-cre; R26R^{mTmG}* mice, whereas overexpression of Sirtuin 1 (Sirt1) in *Prrx1*⁺ cells (*Prrx1-cre; Sirt1^{TG}*) increases tooth size (Wang, et al., 2018). Furthermore, overexpression of Sirt1 in *Prrx1*⁺ cells rescues the reduced cell proliferation and differentiation as well as the increased cell apoptosis induced by deficiency of B-lymphoma Mo-MLV insertion region 1 (*Bmi1*). Consistently, overexpression of Sirt1 in *Prrx1*⁺ cells increases alveolar bone mass associated with enhanced MSC proliferation and osteogenic differentiation (Wang, et al., 2019).

CD90/Thy1 is one of the putative cell surface markers of MSCs that is widely used to isolate MSCs *in vitro* (Dominici, et al., 2006, Lin, et al., 2013). An et al. reported that a sub-population of MSCs characterized by expression of CD90/Thy1 is located in the dental pulp between the labial and lingual cervical loop of mouse incisors and contributes to formation of the dental pulp and the dentin (An, et al., 2018b). Interestingly, CD90/Thy1⁺ cell populations are quiescent and barely detectable in adulthood when homeostasis is established; however, these cells reappear under regenerative conditions and provide a source of cells for tissue repair. During tissue regeneration stimulated by clipping of the mouse incisor, a population of *Celsr*⁺ quiescent cells in the dental pulp become mitotic and replenish the CD90/Thy1⁺ MSCs. These results support the evidence that MSCs in the dental pulp can be re-activated during injury repair.

Wnt/ β -catenin signaling plays an essential role in osteogenic differentiation of MSCs (Glass II, et al., 2005, Logan and Nusse, 2004, Matsushita, Nagata, Kozloff, Welch, Mizuhashi, Tokavanich, Hallett, Link, Nagasawa and Ono, 2020) as well as in tooth root formation (Lohi, et al., 2010). *Axin2*, also known as axis inhibition protein 2, is one of the major Wnt target genes (Jho, et al., 2002, Lustig, et al., 2002). An et al. reported that *Axin2*⁺ cells were located in the odontoblast layer and the dental pulp in the proximal region of the mouse incisor (An, et al., 2018a). Lineage-tracing analysis of *Axin2*⁺ cells with *Axin2-creER; R26R^{mTmG}* mice revealed that *Axin2*⁺ cells and their descendants demonstrate a transiently increased contribution to dental pulp cells and odontoblast by 2 weeks after pulse, indicating that *Axin2*⁺ cells mark transit-amplifying cells (TACs) that temporally give rise to dental pulp cells. Moreover, polycomb repressive complex 1 (PRC1), a mitotic spindle-associated cyclin-dependent kinases (CDKs) essential for cell cleavage, is crucial for coordinating TACs phenotype by regulating Wnt/ β -catenin signaling activities, suggesting that the Wnt/ β -catenin activity downstream of PRC1 is required for stem cell maintenance. Similarly, *Axin2*⁺ dental pulp cells in molars differentiate into new odontoblast-like cells that secrete the reparative dentin via Wnt/ β -catenin signaling in response to injuries (Babb, et al., 2017). Disruption of Wntless (Wls) in osteocalcin-expressing odontoblasts (*Osteocalcin-cre; Wls^{co/co}*) leads to reduction of dentin thickness and shorter roots with decreased Wnt10a and *Axin2* expression in odontoblasts (Bae, et al., 2015). These results suggest that Wnt-responsible gene *Axin2* is crucial for odontoblast maturation and dentin formation.

Platelet-derived growth factor (PDGF) is one of the most abundant growth factors in platelets and promote tissue regeneration after injury (Andrew, et al., 1995, Antoniades, et

al., 1979, Pierce, et al., 1988). PDGF-BB and its receptor PDGF receptor beta (PDGFR β) pathway has been demonstrated to play an important role for odontoblast differentiation in dental pulp cells (Yokose, et al., 2004). PDGF signaling is also critical for differentiation of bone marrow (BM) MSCs into multilineage cells such as osteoblasts, adipocytes and chondrocytes (Ng, et al., 2008). Walker et al. reported that PDGFR β^+ cells mark most of MSCs in the cervical loop (CL-MSCs) and mesenchymal TACs (MTACs) in the mouse incisor and differentiate into odontoblasts using *Pdgfrb-creER* mice (Walker, et al., 2019). When incisors are fully erupted and functioning, PDGFR β^+ cells remain as CL-MSCs and MTACs in the cervical loop, indicating that PDGFR β^+ mesenchymal cells represent distinct MSC populations from those maintained in the neuro-vascular niches (Kaukua, Shahidi, Konstantinidou, Dyachuk, Kaucka, Furlan, An, Wang, Hultman, Ahrlund-Richter, Blom, Brismar, Lopes, Pachnis, Suter, Clevers, Thesleff, Sharpe, Ernfors, Fried and Adameyko, 2014, Zhao, Feng, Seidel, Shi, Klein, Sharpe and Chai, 2014). Cai et al. reported that isolated PDGFR β^+ /c-kit $^+$ dental pulp cells possess stem cell properties with high proliferative and osteogenic differentiating abilities *in vitro*. Moreover, in an emptied rat incisor root canal therapy model, transplanted PDGFR β^+ /c-kit $^+$ dental pulp cells produce globular dentin-like structures and pulp-like tissue, suggesting that a subset of PDGFR β^+ /c-kit $^+$ dental pulp cells are capable of regenerating dentin/pulp (Cai, et al., 2016).

Challenges and future directions

We now have better understanding of stem cells in the dental pulp and the apical papilla and their characteristics both *in vitro* and *in vivo*. Particularly, use of cell type-specific *cre-LoxP* transgenic systems has facilitated in-depth characterization of mesenchymal progenitor cells in the dental pulp (Figure 2, Table 2). The majority of dental pulp cells are derived from NCCs. Various markers for NCCs and their descendants have been utilized to identify stem cells in the dental pulp *in vivo*. However, the limitation of these approaches is that these stem cell populations tend to be overestimated due to rather broad expression patterns of these utilized markers. To identify the regulatory mechanism of these stem cells, it is important to identify specific markers for a *bona fide* mesenchymal progenitor cell population in the dental pulp. Additionally, a majority of lineage-tracing experiments of dental pulp cells have been performed exclusively in the mouse incisor model, which is characterized by a life-long continuous growth. The relevance of these studies to more static molars, as well as human incisors and molars, remains largely unknown. Further characterization of mesenchymal progenitor cells in the dental pulp and the apical papilla of molars are required to define the function of these tooth-derived stem cells in an environment similar to the human dental pulp.

Stem cells are important factors of tissue engineering, and the combinational use of various MSCs, signaling molecules and nanostructures has been developed in the dental field in recent decades (Chieruzzi, et al., 2016). However, the functional and complete regeneration of the dental tissue, i.e. the dentin-pulp complex and periodontal apparatus, is still difficult in a clinical setting. Identifying the dental stem cell population *in vivo* will facilitate our understanding on the regulatory mechanism of tissue repair, which may lead to the predictable regeneration of the functional dental tissue in the future.

Conclusion

In the last decade, *in vitro* studies have identified stem cells in the dental pulp and the apical papilla as a promising MSC source for regenerative medicine. Thanks to lineage-tracing analyses of dental pulp cells using mouse genetics model, diversity of stem cell populations in the dental pulp and the apical papilla *in vivo* is beginning to be unraveled. For much better understanding of the fundamental biological property of these important stem cells, we need to develop more specific genetic tools that allow functional analysis of specific groups of dental mesenchymal progenitor cells in the dental pulp. These technological advances will shed light the regulatory mechanism of repairing teeth and could be applied for effective stem cell-based regenerative therapies in the future.

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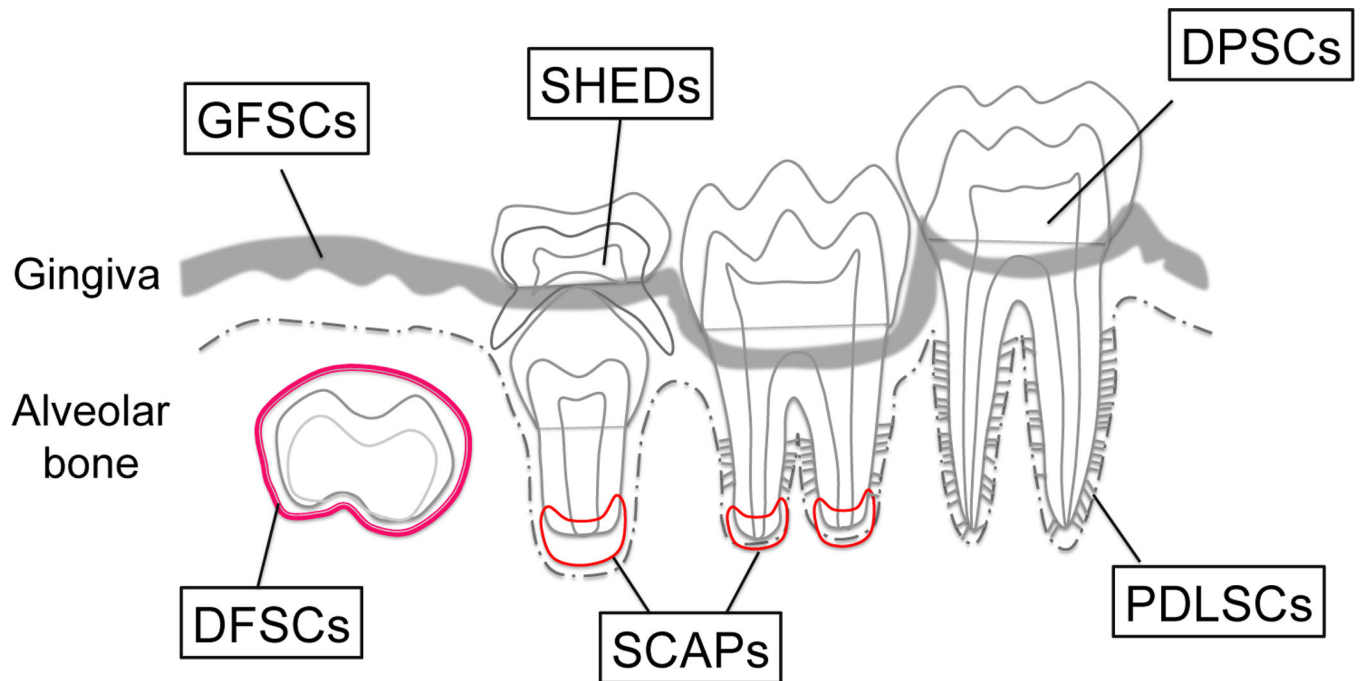


Figure 1. Isolated tooth-derived stem cells (TDSCs)

Schematic diagram of TDSCs populations. From tooth pulp, dental pulp stem cells (DPSCs), stem cells from human exfoliated deciduous teeth (SHEDs) and cells from apical papilla (SCAPs) can be isolated. From supporting tissue, periodontal ligament stem cells (PDLSCs), gingival fibroblastic stem cells (GFSCs) and dental follicle stem cells (DFSCs) can be isolated.

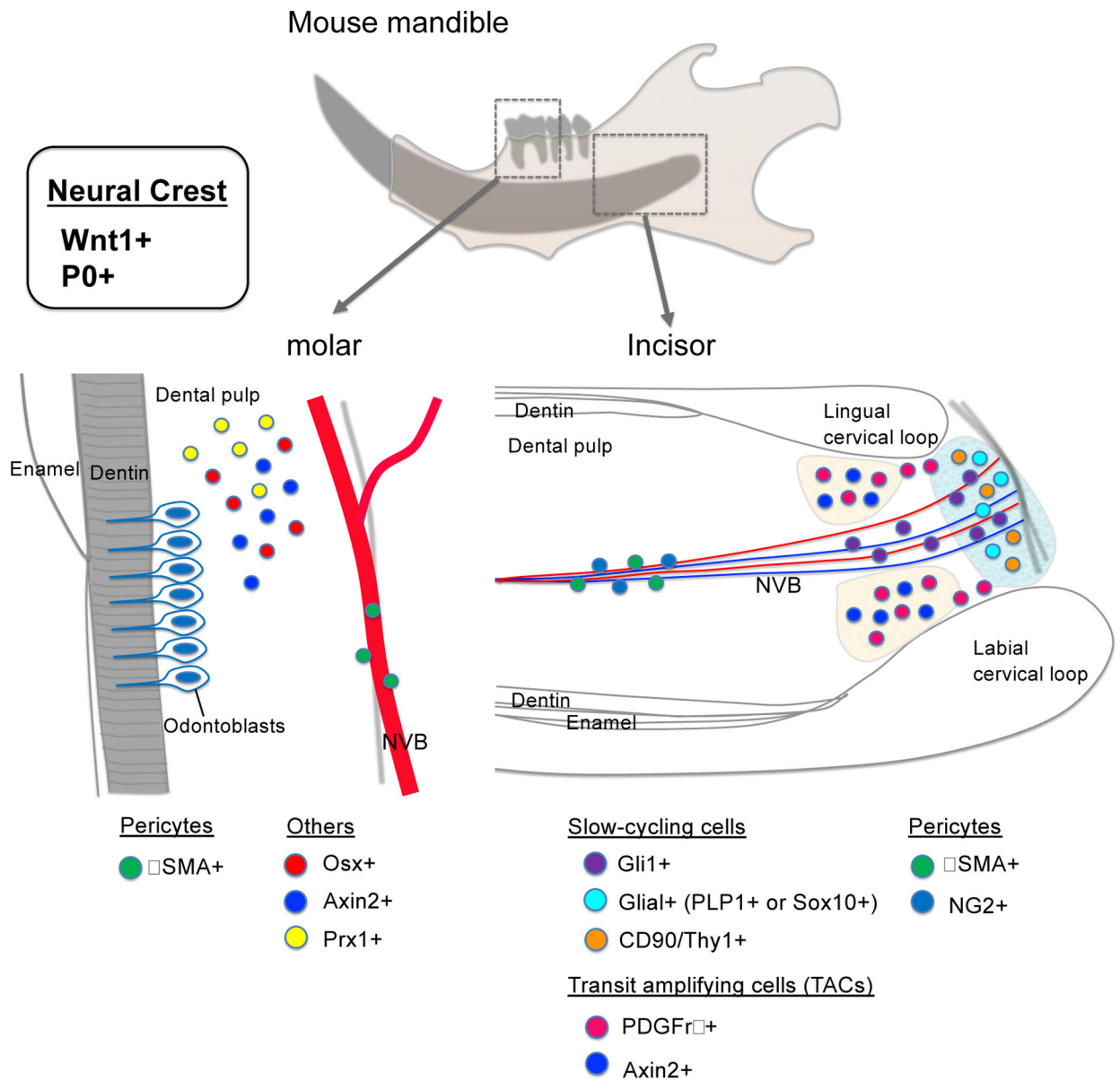


Figure 2. Stem cell populations in the dental pulp

Schematic diagrams of stem cell populations both in mice. During tooth development, dental pulp cells are derived from NCCs such as Wnt1⁺ or P0⁺. In the molar, Osx⁺, Axin2⁺ and Prx1⁺ mesenchymal progenitor cells and αSMA⁺ pericytes differentiate into odontoblasts. In the incisor, Gli1⁺, PLP1⁺ or Sox10⁺ glial, and CD90/Thy1⁺ slow cycling cells, PDGFRβ⁺ and Axin2⁺ TACs, αSMA⁺ and NG2⁺ pericytes differentiate into odontoblasts and contribute to dentin formation. NVB: Neurovascular bundle

Table 1.

Isolated tooth-derived stem cells

Cells	Location	Ref.
<i>In dental pulp</i>		
DPSCs	Dental pulp in permanent teeth	Gronthos, et al, 2000
SHEDs	Immature dental pulp in deciduous teeth	Miura, et al., 2003
SCAPs	Apical papilla of growing tooth roots	Sonoyama, et al., 2006
<i>Others</i>		
PDLSCs	Periodontal ligament	Seo, et al., 2004
DFSCs	Dental follicle	Morszeck et al., 2005
GFSCs	Gingiva	Zhang, et al., 2012

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Table 2.

Transgenic mice line used for stem cell population in the dental pulp

Gene	Marked cell population	Cre transgenic line	Gene manipulation	Findings	Ref.
<i>Wnt1</i>	All neural crest cell lineage	<i>Wnt1-cre</i>	-	Clonal <i>Wnt1-cre</i> cells differentiate into neural crest cell lineage <i>in vitro</i> culture	Janebodin et al. 2011
		<i>Wnt1-cre</i>	-	Implanted <i>Wnt1-cre</i> cells promote bone healing in critical-size calvaria bone defect	Collignon et al. 2019
		<i>Wnt1-cre</i>	<i>Wnt1-cre; Tgfr b2fl/fl</i>	Dentin thickness and tooth size are decreased with reduction of <i>Coll1a1</i> and <i>Dspp</i> expression	Oka et al. 2007
		<i>Wnt1-cre</i>	<i>Wnt1-cre; KLF 4fl/fl</i>	Dentin mineralization is impaired and root pulp/root canal are enlarged	Tao et al. 2019
<i>Gli1</i>	Perivascular cells in the incisor	<i>Gli1-creER</i>	-	Differentiate to all mesenchymal cells in the dental pulp and located at reparative dentin after tooth injury	Zhao et al. 2014
	All root progenitor cells in the molar	<i>Gli1-creER</i>	<i>Gli1-creER;Bmpr1afl/fl</i>	Failure of tooth root formation with lack of <i>Dspp</i> expression in the periapical region	Feng et al. 2017
		<i>Gli1-creER</i>	<i>Gli1-creER;SmoM2</i>	Shorter root with reduction of Ki67 ⁺ proliferative cells	Liu et al. 2015
<i>NG2</i>	Pericytes	<i>NG2-creER</i>	-	Differentiate into <i>Dspp</i> ⁺ odontoblasts after mandible damage	Feng et al. 2011
		<i>NG2-creER</i>	-	Differentiate into <i>Dspp</i> ⁺ odontoblasts at the tip of incisors	Pang et al. 2016
<i>αSMA</i>	Pericytes	<i>αSMA-creER</i>	-	Differentiate into Col2.3-GFP ⁺ cells composed <i>Dspp</i> ⁺ odontoblasts and <i>Bsp</i> ⁺ osteoblasts in reparative dentin after pulp exposure	Vidovic et al. 2017
		<i>αSMA-creER</i>	-	FGF2 promotes αSMA ⁺ cells to differentiate into Col2.3-GFP ⁺ odontoblasts in reparative dentin after pulp exposure	Vidovic et al. 2018
		<i>αSMA-creER</i>	-	Proliferate in dental pulp and differentiate into some odontoblasts after mild dentin injury	Vidovic et al. 2019
<i>PLP</i>	Schwann cell precursor cells	<i>PLP-creER</i>	-	Differentiate into pulp cells and odontoblasts during tooth development and regeneration after tooth damage	Kaukua et al. 2014
<i>Sox10</i>		<i>Sox10-creER</i>	-		
<i>Osx</i>	Mesenchymal root progenitor cells in the molar	<i>Osx-cre</i>	<i>Osx-cre;Bmp2fl/fl</i>	Failure of tooth root formation with reduction of <i>Dmpl</i> , <i>Coll1a1</i> and <i>Osx</i> expression	Rakian et al. 2013
		<i>Osx-cre</i>	<i>Osx-cre; Tgfrbf1/fl</i>	Failure of tooth root formation and delayed tooth eruption with reduction of <i>Dspp</i> and <i>Bglap</i> expression	Wang et al. 2013
		<i>Osx-cre</i>	<i>Osx-cre;IFT140fl/fl</i>	Lead to shorter root and thin dentin with loss of primary cilia and impair reparative dentin formation in a tooth drilling model	Li et al. 2018
		<i>Osx-cre</i>	<i>Osx-cre;Partorfl/fl</i>	Lead to small tooth volume and reduce of proliferation, differentiation of odontoblasts and <i>Dspp</i> expression	Xie et al. 2019

Gene	Marked cell population	Cre transgenic line	Gene manipulation	Findings	Ref.
		<i>Osx-cre</i>	<i>Osx-cre;PPRfl/fl</i>	Disrupt tooth root formation and failure of tooth eruption with reduction of EdU ⁺ proliferative cells	Ono et al. 2016
		<i>Osx-creER</i>		Differentiate into odontoblasts, cementoblasts, PDL cells and alveolar cryptal bone osteoblasts	Takahashi et al. 2017
<i>Prrx1</i>	Mesenchymal cells in the region of pulp horns	<i>Prrx1-cre</i>	<i>Prrx1-cre;Sirt1TG</i>	Increase tooth size with upregulation of <i>Dspp</i> , <i>Dmpl</i> and <i>Ocn</i> expression	Wang et al. 2018
<i>CD90/Thy1</i>	Slow cycling cells in the incisor	<i>CD90/Thy1-cre</i>	-	CD90/Thy1 ⁺ cells are quiescent in adulthood but proliferate rapidly and differentiate into pulp cells and odontoblasts after clipping of the incisor	An et al. 2018a
<i>Axin2</i>	TACs in the incisor	<i>Axin2-creER</i>	<i>Axin2-creER;Wlsfl/fl</i>	Axin2 ⁺ cells located in the proximal region of the incisor, transiently proliferate and differentiate into dental pulp cells and odontoblasts by 2 weeks	An et al. 2018b
	Odontoblasts at the periphery of the pulp	<i>Axin2-creER</i>	<i>Axin2-creER;Wlsfl/fl</i>	Proliferate rapidly and differentiate into <i>Dspp</i> ⁺ odontoblasts in reparative dentin after pulp exposure	Babb et al. 2017
<i>PDGFRβ</i>	TACs in the incisor	<i>Pdgfrb-creER</i>	-	PDGFRβ ⁺ cells mark most of CL-MSCs and MTACs in the incisor and differentiate into odontoblasts	Walker et al. 2019

Table 3.

Abbreviations of gene or cytokine

Abbreviation	Definition
α SMA	Alpha-smooth muscle actin
Axin2	Axis inhibition protein 2
BMP	Bone morphogenetic protein
Bmp2	Bone morphogenetic protein 2
Bmpr1	Bone morphogenetic protein receptor type 1
CD90/Thy1	Cluster of differentiation 90
CDKs	Cyclin-dependent kinases
CNPase	Glial markers 2', 3'-cyclic nucleotide 3'-phosphodiesterase
Colla1	Collagen, type I, alpha 1
CXCL12	Chemokine C-X-C motif ligand 12
Dmp1	Dentin matrix acidic phosphoprotein 1
Dspp	Dentin sialophosphoprotein
FGF2	Fibroblast growth factor 2
GAD	Glutamic acid decarboxylase
Gli1	Glioma-associated oncogene homolog 1
Hh	Hedgehog
IFT140	Intraflagellar Transport 140
KFL4	Kruppel-like factor 4
NeuN	Neuronal nuclear antigen
NFM	Neurofilament M
NG2	Neural/glial antigen 2
NSE	Neuron-specific enolase
Ocn/Bglap	Osteocalcin
Osx/Sp7	Osterix
P0	Protein 0
Pdgfr β	Platelet derived growth factor receptor beta
PLP1	Proteolipid protein 1
PPR	Parathyroid hormone / Parathyroid hormone-related protein receptor
PRC1	Polycomb repressive complex 1
Prrx1	Paired related homeobox 1
Prrx2	Paired related homeobox 2
PTHrP	Parathyroid hormone-related protein
Raptor/mTORC1	Regulatory-associated protein of mTOR /Mammalian target of rapamycin complex 1
Sirt1	Sirtuin 1
Sox10	SRY-box transcription factor 10
TGF β	Transforming growth factor beta
TrkA	Tropomyosin receptor kinase A

Abbreviation	Definition
Wls	Wntless
Wnt1	Wnt family member 1

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