



New Insights on the Role of Satellite Glial Cells

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Accepted: 30 September 2022 / Published online: 15 October 2022

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Abstract

Satellite glial cells (SGCs) that surround sensory neurons in the peripheral nervous system ganglia originate from neural crest cells. Although several studies have focused on SGCs, the origin and characteristics of SGCs are unknown, and their lineage remains unidentified. Traditionally, it has been considered that SGCs regulate the environment around neurons under pathological conditions, and perform functions of supporting, nourishing, and protecting neurons. However, recent studies demonstrated that SGCs may have the characteristics of stem cells. After nerve injury, SGCs up-regulate the expression of stem cell markers and can differentiate into functional sensory neurons. Moreover, SGCs express several markers of Schwann cell precursors and Schwann cells, such as CDH19, MPZ, PLP1, SOX10, ERBB3, and FABP7. Schwann cell precursors have also been proposed as a potential source of neurons in the peripheral nervous system. The similarity in function and markers suggests that SGCs may represent a subgroup of Schwann cell precursors. Herein, we discuss the roles and functions of SGCs, and the lineage relationship between SGCs and Schwann cell precursors. We also describe a new perspective on the roles and functions of SGCs.

Keywords Satellite glial cells · Dorsal root ganglia · Schwann cell precursors · Schwann cells · Stem cells

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Introduction

Dorsal root ganglia (DRG) sensory neurons can transmit information about the location, type, and intensity of noxious stimuli to the cerebral cortex via the spinal cord, and play an important role in the pain pathway [1–3]. Sensory neurons are surrounded by a layer of satellite glial cells (SGCs) that support, nourish, and protect these neurons [4]. It has been considered that under pathological conditions, SGCs regulate the environment around neurons through gap junctions or by releasing neuronal activity modulating factors, such as adenosine 5'-triphosphate (ATP), nitric oxide, and tumor necrosis factor- α (TNF- α) [3, 5–7]. Recent studies have demonstrated that following nerve injury, SGCs around the DRG sensory neurons upregulate nestin and sex-determining region Y-box 2 (Sox2) expression, and differentiate into neurons [3, 8]. Interestingly, several markers specific for Schwann cell (SC) precursors or SCs were also found to be expressed in SGCs [9, 10]. This review aims to provide an overview of changes that occur in SGCs following nerve injury and the lineage relationship among SGCs, SC precursors, and SCs. Specifically, our review will help researchers focusing on the roles and functions of SGCs.

Identification of SGCs

SGCs are located in the ganglia of the peripheral nervous system, such as DRG and trigeminal ganglion (TG), and wrap completely around the sensory neurons. Each SGC is separated from its parent neuron by a gap of approximately 20 nm [11, 12]. In general, several SGCs can form an SGC sheath enveloping each sensory neuron, which can slow down the diffusion of most substances, particularly large molecules [11]. Studies have shown that SGCs are connected to each other through gap junctions and express a variety of ion channels, such as inwardly rectifying K⁺ channels (Kir), voltage-dependent outward K⁺ channels, and small-conductance Ca²⁺-activated SK3 channels [13]. These properties of SGCs are thought to give these cells the ability to control over the neuronal environment.

Till date, SGCs have been identified mostly based on their location, morphology, and the expression of a combination of specific proteins, such as glutamine synthetase (GS), which is widely used to distinguish SGCs from other cell types in the DRG and TG both in vitro and in vivo [8, 11, 14–17]. Recently, using single-cell sequencing, Avraham et al. showed that GS mRNA is expressed in many cell types within the DRG [9]. However, GS protein is specifically expressed in SGCs [8, 9, 11, 18–22]. Moreover, several in vivo studies have also shown that only SGCs, but not SCs, express GS protein [11, 14, 18, 22, 23]. Accordingly, DRG and TG derived cells that express GS protein were identified as SGCs [20, 24–28].

The reason why SGCs express GS protein may be that they can convert glutamate into glutamine and participate in the rapid removal of glutamate from the perineuronal space by SGCs [13]. Studies have shown that SGCs express glutamate transporters, such as glutamate-aspartate transporter (GLAST) and glial glutamate transporter (GLT-1), which are responsible for the uptake of glutamate released by neurons into the synaptic cleft [11, 12, 29]. Under the action of GS, glutamate is converted into glutamine and released to the synaptic cleft. Then glutamine is returned to presynaptic terminals of neurons through glutamine transporters and converted back to glutamate to be reused [13]. Glutamate-glutamine cycle formed between neurons and SGCs can effectively prevent the cytotoxicity caused by a large accumulation of glutamate and realize the repeated recycling of glutamate.

S100 proteins are also expressed in SGCs; however, they are not considered as the ideal markers for SGCs because SCs also express these proteins [11]. Fatty acid binding protein 7 (Fabp7, also known as BLBP and BFABP) is expressed in astrocytes, radial glial cells and neuronal progenitors in the central nervous system [30]. It has been reported that Fabp7 can participate in neurogenesis as a

positive regulator of proliferation in neural stem progenitor cells and is important for dendritic growth and neuronal synapse formation as well as for astrocyte proliferation during reactive gliosis [31–33]. In the peripheral nervous system, Fabp7 is usually expressed in SC precursors and immature SCs [34–36] and participate in regulating Schwann cell-axon interactions [37]. However, recent in vivo studies have shown that in adult mice, Fabp7 is a specific marker for SGCs and does not label SCs surrounding axons in the DRG or in the sciatic nerve [9]. Thus, in adult mice, Fabp7 can be used to identify SGCs. Considering that SGCs might represent a subpopulation of SC precursors (For details, see 4. The close relationship between SGCs, SC precursors, and SCs) and that central nervous system injury most likely increases the immature state of cells in the adult, additional markers or morphology or location information are also needed to identify SGCs under pathological conditions.

Following nerve injury, glial fibrillary acidic protein (GFAP) protein expression is upregulated in SGCs, therefore, GFAP protein can also be used as a marker of SGCs under pathophysiological conditions [38–40]. In addition, Kir4.1, SK3, connexin 43, and endothelial PAS domain protein 1 (Epas1) can also be used as markers of SGCs [41].

Through Kir4.1 channel, SGCs can limit the extracellular levels of K⁺ in the sensory ganglia to maintain the neuronal resting membrane potential and neuronal excitability [42]. Studies has shown that injury suppresses Kir4.1 function in SGCs, which may contribute to pain [43]. Reduced Kir4.1 permeability likely depolarizes SGCs, inducing them to release excitatory mediators such as ATP that can activate the neurons. In the rat TG, specific silencing of Kir4.1 using RNA interference leads to spontaneous and evoked facial pain-like behavior in freely moving rats [44]. These findings suggested that a decrease in Kir4.1 expression after injury reduces K⁺ buffering capacity of SGCs, raises extracellular K⁺ concentration in the vicinity of neurons and thus results in depolarization and hyperexcitability of neuronal somata to give rise to chronic pain [13]. The results of immunohistochemistry showed that SGCs express Kir4.1, whereas the neurons, blood vessel endothelial cells and SCs do not [44]. Thus, Kir4.1 can be used for SGC recognition under physiological and pathophysiological conditions [44–48].

SK3 immunoreactivity is described in peripheral neurons, which leads to the controversy of SK3 as a specific marker of SGC in peripheral ganglia [49, 50]. However, according to the results of some studies, SK3 is a specific immunomarker of SGCs in vivo [14, 51]. Like Kir4.1 protein, SK3 is involved in either directly or indirectly, in potassium ion (K⁺) buffering and can influence the level of neuronal excitability [51]. A recent study that induced trigeminal neuropathic pain in rats through a partial transection of the infraorbital nerve reported a decreased pain threshold, together with a lower expression of SK3 in the TG of the animals that underwent the infraorbital ligation when

compared to control group. In addition, administration of SK3 channel agonist (CyPPA) could significantly improve the pain threshold, and the pain threshold decreased after administration of SK3 channel antagonist (Apamin) [52, 53]. These findings suggest that SK3 play a pivotal role in neuropathic pain and may be one of the potential targets for the treatment of neuropathic pain. In all, SK3 can be used to mark SGCs under physiological and pathophysiological conditions [9, 14, 54].

Connexin 43, a gap junction protein expressed in SGCs has been shown to play an important role in several pain models [51, 55, 56]. Accumulating evidence demonstrates that after peripheral nerve injury, the expression of Connexin 43 increased in SGCs [55, 57, 58], and blockade of the gap junctions formed by Connexin 43 resulted in alleviated pain response of the mice [46, 59]. At present, Connexin 43 is commonly used to indicate activated SGCs after nerve injury.

Epas1, also referred to as hypoxia-inducible factor (HIF) 2α , plays an important role in tumours [60]. Recently, Epas1 was found to be expressed in SGCs by using single-cell RNA sequencing. validation by RNAscope confirmed unique expression of Epas1 in DRG SGCs, but not in sciatic nerve [41]. This result indicates that Epas1, as a new marker of SGCs, can be used to identify SGCs. In conclusion, with the increasing research on SGCs, the specific markers for SGCs recognition will be constantly discovered, and these specific markers enable us to better identify SGCs and investigate their functions.

Dynamics of Molecular Signaling in SGCs Following Peripheral Nerve Injury

Along with changes in neurons following injury to the proximal or distal part of the peripheral nerve, SGCs also undergo characteristic changes [12]. One noticeable change in SGCs following injury is an increase in GFAP expression. Under resting conditions, GFAP protein is expressed at low levels in SGCs, but the expression of this protein increases significantly following axonal damage or inflammation [38–40, 61]. It has been reported that GFAP protein expression in SGCs peaks between 3 and 6 h following carrageenin injection and returns to the basal level at 24 h, which coincides with the normalization of the mechanical nociceptive threshold [62]. GFAP can anchor the glutamate-aspartate transporter (Glast) to the plasma membrane of glial cells. Glast is responsible for the uptake of glutamate released by neurons into synaptic clefts so that glutamate can be converted into glutamine by the enzyme GS. Therefore, increased expression of GFAP in SGCs could be related to the rapid removal of the accumulated glutamate from the perineuronal space to prevent its cytotoxic effects [12, 13].

Using 5-bromo-2'-deoxyuridine (BrdU) labeling combined with immunohistochemistry for SGC-specific

proteins, researchers have demonstrated that SGCs proliferate following nerve injury [54]. In accordance with this, studies showed that following oxaliplatin injection, the number of activated SGCs in the DRG significantly increases [63], and in the monoarthritis or collagenase arthritis model, the arthritic rats exhibit SGC activation and proliferation [64, 65]. Studies also showed that activated SGCs express high levels of brain derived neurotrophic factor (BDNF), p75, and fibroblast growth factor 2 (FGF2) [4, 66]. It has been proposed that increased proliferation along with increased expression of growth factors in SGCs following injury contribute to recovery and regeneration.

The mitogen-activated protein kinase (MAPK) pathway plays an important role in the initiation and maintenance of nociceptive responses in glia and neurons of the sensory ganglion. MAPK pathway includes three major proteins: extracellular signal-regulated kinase 1/2 (ERK1/2), P38, and c-Jun N-terminal kinase (JNK) [42]. Accumulating evidence demonstrates that nerve or spinal cord injury leads to the profound activation of MAPK signaling in SGCs [67]. In CFA-treated TGs, the expression levels of p-ERK, p-P38, and p-JNK were readily observed in SGCs. Almost no p-MAPKs were expressed on SGCs in the vehicle group, but the expression levels of p-MAPKs were significantly increased in the CFA group. Similarly, upregulation of p-ERK has been reported in SGCs in animal models of local inflammation of the dura mater, temporomandibular joint inflammation, and migraine [68–70]. MAPKs phosphorylation is associated with SGCs activation and increased production of interleukin-1 β (IL-1 β) and TNF- α [16, 25]. It has been proposed that SGCs exhibit the features of inflammatory cells. Similar to macrophages, SGCs can be activated by monocyte chemoattractant protein-1 (MCP-1) through the CCR2 receptor to produce high levels of TNF- α and IL-1 β [12]. These inflammatory cytokines released from the activated SGCs can enhance the excitability of neurons in the trigeminal ganglion, which in turn may promote the development and maintenance of orofacial allodynia/hyperalgesia [71–73].

In addition to the above-mentioned changes, there is a large significant increase in the expression of gap junction, decrease in Kir expression, enhancement in ATP release, and increase in P2XR and P2YR expression in SGCs following nerve injury [13, 42]. These characteristic changes affect the ability of SGCs to regulate the environment around neurons and give rise to chronic pain conditions.

SGCs have the Characteristics of Stem Cells

Recent evidence has added a new aspect to the functions of SGCs by showing that these cells have differentiation potential. In DRG explant culture, it has been observed

that a subpopulation of cells expressing nestin and p75 protein migrate from these explants and have the ability to differentiate into glial cells, neurons, and smooth muscle cells *in vitro*. Further, BrdU pulse-chase analysis showed that these progenitors likely originate from SGCs [74]. *In vivo* studies also demonstrated that following peripheral nerve injury, the protein expression of nestin and Sox2 increases in SGCs [75–77], and proliferating SGCs can be transformed into doublecortin-positive cells in the DRGs [78]. Similarly, it has been observed that chronic pain induces proliferation and upregulation of progenitor markers in the Sox2- and platelet-derived growth factor receptor alpha (PDGFR α)-positive SGCs [8]. Moreover, data of BrdU-labeling and genetic fate mappings demonstrated a chronic pain-induced nociceptive neurogenesis in DRG from Sox2-positive SGCs [8]. In line with this, our previous study showed that DRG-derived SGCs highly express neural crest cell markers including nestin, Sox2, Sox10, and p75, and could differentiate into nociceptive sensory neurons in the presence of VPA, CHIR99021, RO4929097, and SU5402 [3]. Similar results were also found in TG derived SGCs (our unpublished results). These findings confirmed that SGCs indeed have differentiation potential.

Recently, using single-cell RNA sequencing and RNA scope, Segal et al. found that DRG-derived SGCs can be distinguished on the basis of high levels of *Epas1*, as this protein is not expressed in diverse SC types. Furthermore, *Epas1* has also been defined as a top marker of DRG glial precursors. In fact, several genes that are highly expressed in DRG-derived SGC clusters are also highly expressed in DRG glial precursors. These results suggest that DRG-derived SGCs retain the gene signature of DRG glial precursors [41].

As early as 2004, researchers proposed that SGCs have stem cell characteristics. The authors found a cell type of embryonic DRG of the PNS - the satellite cell - can develop into oligodendrocytes, SCs and astrocytes and proposed satellite cells of DRG are multi potential glial precursors [79]. Subsequently, evidence that SGCs express stem cell markers and can differentiate into neurons is also constantly being discovered. These evidences promote our further understanding of the roles and functions of SGCs, showing that SGCs not only have the functional properties of glia, but they could also play the role of stem cells under pathological conditions. However, we still know little about the mechanism of SGCs turning into neurons or even specific types of neurons. Strengthening research in this field will help us understand the mechanism of pathological pain and treat sensory neuron related diseases (Fig. 1).

The Close Relationship Between SGCs, SC Precursors, and SCs

Besides SGCs, SCs are also a much-touted cell type with stem cell properties in the peripheral nervous system.

Increasing evidence suggests that SC precursors and even adult SCs can give rise to several cell types including those of parasympathetic ganglia during neurodevelopment as well as after injury, highlighting the broad developmental potential of these cells [80–86]. Studies showed that SC precursors, unlike SCs, die when separated from axons *in vitro*. It is traditionally believed that SC precursors, which are a transient population and dependent on axonal contact for survival, are specified during embryonic day 14 (E14) and E15 (mouse E12 and 13), and differentiate into immature SCs during E15–17 and mature SCs during perinatal stages [87–91]. At present, there is little evidence regarding the persistence of SC precursors after E17/18 in rats [92].

Studies suggest a close relationship between SGCs, SC precursors, and SCs. CDH19, MPZ, PLP1, SOX10, ErbB3, and FABP7 are specific markers for SC precursors and have been used to identify these cells [80, 88, 89, 92–95]. Based on the PLP1 or SOX10 promoter, many researchers have investigated the progeny of SC precursors in transgenic mice [80, 83, 96–100]. However, recent studies showed that these genes are also expressed in SGCs (Table 1) [8, 9, 101, 102]. *Egr2* (also known as *Krox20*) is expressed in boundary cap cells, immature SCs, and myelinating SCs, and is not expressed in SGCs *in vivo* [10, 103, 104]. Interestingly, *Egr2* is expressed in cultured SGCs [10, 102]. George et al. [18] showed that SGCs are transcriptionally, morphologically, and functionally identical to SCs. Considering that SGCs are multipotent, these studies suggest that SGCs might represent a subpopulation of SC precursors; however, a recent single-cell RNA-sequencing study indicated that SGCs are molecularly distinct from SCs [9]. Studies also suggest that SGCs adopt the morphology of SCs when cultured for extended period of time [18, 28] and SCs exhibit, to some extent, plasticity upon nerve injury [84, 92] raising an interesting possibility concerning the lineage of SGCs with respect to SC precursors or SCs.

The Origin of SGCs

It is well known that SGCs, sensory neurons, and SCs originate from neural crest cells (NCCs), a transient population in the embryo that can give rise to multiple cell types, including most neuronal and all glial components of the peripheral nervous system (Fig. 1) [104, 105]. During sensory neuron development, multiple signaling pathways such as Wnt, FGF, and Notch, induce the expression of sensory neuron-specific transcription factors including *Ngn1*, *Ngn2*, *Brn3a*, *Isl1*, *Runx1*, *Shox2* and *Runx3* in NCCs leading to their differentiation into nociceptive sensory neurons, mechanical sensory neurons, and proprioceptive neurons [3, 106, 107]. Moreover, during SCs development, NCCs differentiate into SC precursors and immature SCs before finally differentiating into myelinating and non-myelinating SCs [34, 89, 108].

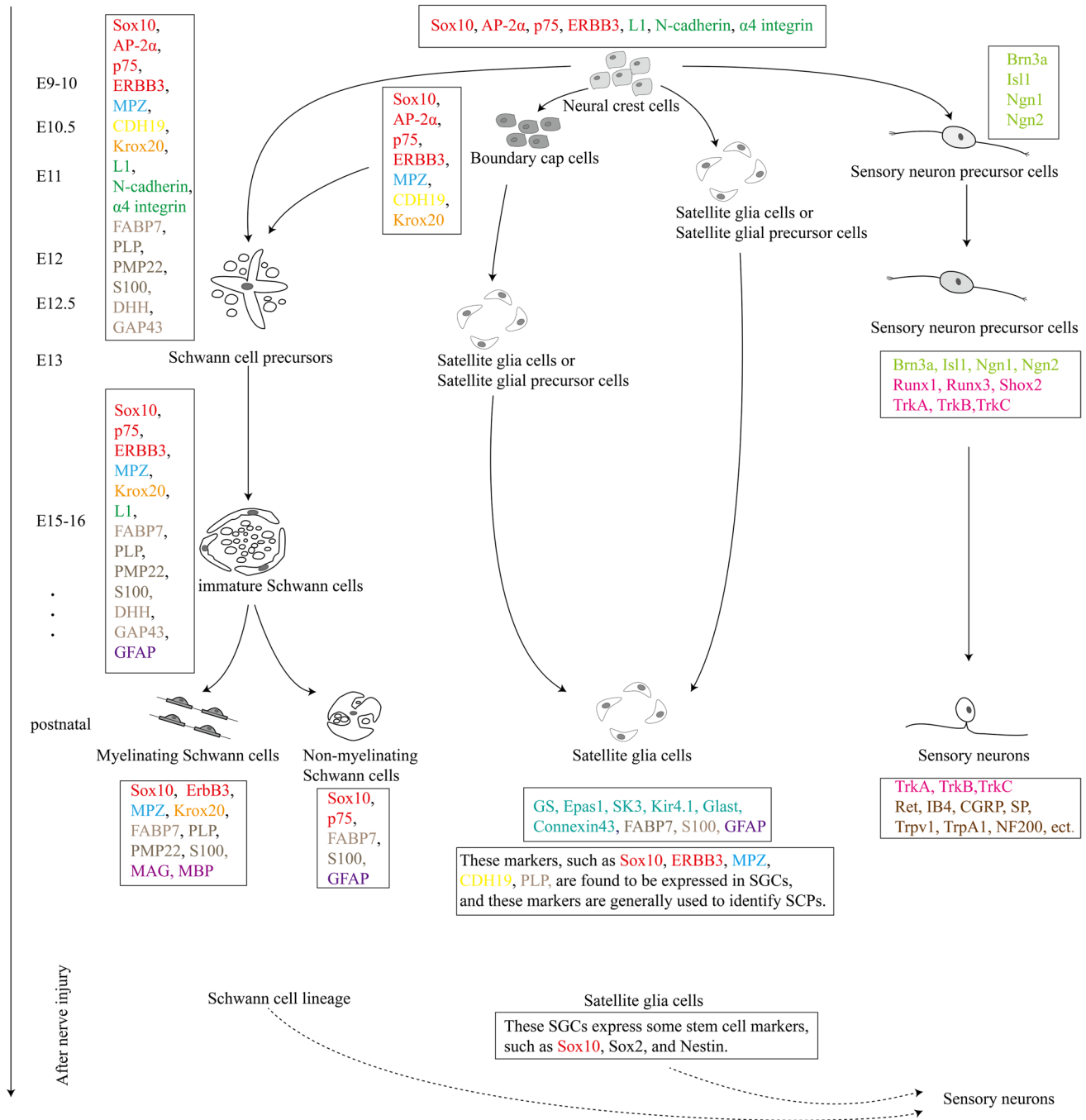


Fig. 1 The development of satellite glial cells, Schwann cells and sensory neurons and molecular expression at the main development stages. Font colors are used for easier identification of markers that

are expressed in several lineages. The embryonic stage (E) corresponds to mouse development time

However, unlike the detailed understanding of the development of sensory neurons and SCs, little is known about the development of SGCs.

Studies suggest there are two waves of peripheral gliogenesis during embryonic development. For SGCs development, the first wave is at E11 in mice. At this time, a fraction of SGCs is specified directly from the migratory NCCs [102,

109]. Another source of SGCs is the boundary cap cells, which are also derived from NCCs. Boundary cap cells are found at E10.5 at the dorsal sensory entry point and the ventral motor exit point, and give rise to the remaining fraction of SGCs at E12.5 [102, 104].

Evidence suggests that histone deacetylases1 and 2 (HDAC1/2) are essential for differentiation of NCCs to

Table 1 Comparison of satellite glial cells and Schwann cell precursors

Cell type	Satellite glial cells	Schwann cell precursors
Common identification markers	GS [8, 11, 21, 22, 48]; FABP7 [9]; Epas1[41]; SK3 [14, 51]; S100 [46, 47, 110]; GFAP [46, 70, 111]; Kir4.1[44–48]; Glast [112, 113]; Connexin 43 [19]. According to the literature, the specific markers for SGCs are GS, Epas1, SK3, Kir4.1, and Connexin 43. Markers specific for SC precursors, such as CDH19, MPZ (mRNA), PLP1 (mRNA), SOX10, ERBB3 and FABP7, are also expressed in SGCs [8, 9, 18, 101, 102].	SOX10; CDH19; ERBB3; MPZ; PLP1; FABP7; DHH; GAP43; PMP22; AP-2 α ; L1; Krox20; Ncad; α 4 integrin [34, 88, 89, 102].
Origin	Neural crest cells (at E11) [109, 114] Boundary cap cells (at E11.25) [104]	Neural crest cells (at E11) [109, 114] Boundary cap cells (at E12.5) [104]
progeny	1. Satellite glial cells 2. Neurons [3, 8, 74]	1. Schwann cell lineage 2. Parasympathetic neurons [80, 115] 3. Some mesenchymal stem cell [116]

SGC lineage. In mice, NCC-specific deletion of *HDAC1/2* leads to a strong reduction in Sox10 and Pax3 expression in NCCs along with the loss of SGCs and SC precursors in the DRG and peripheral nerves [109]. In NCCs, HDAC1/2 bind to the Pax3 promoter and induce the expression of this transcription factor, which was required to maintain high Sox10 levels and trigger the expression of Fabp7. In addition, HDAC1/2 also activate P0 transcription by binding to the P0 promoter. Therefore, HDAC1/2 direct the specification of NCCs to SC precursors and SGCs by controlling the expression of Pax3 and the concerted action of Pax3 and Sox10 on their target genes [102, 109].

The time of development of SGCs is slightly later than that of sensory neurons, but similar to that of SC precursors. Although several studies have described the process and mechanism of neural crest specification into peripheral glia, the focus of description has always been SC lineage, and very few studies have paid close attention to the development of SGCs. Considering the increasing evidence that SGCs have stem cell characteristics and are similar to SC precursors, it is necessary to investigate the SGC lineage in the future (Table 1).

Conclusion

SGCs are the most important type of glial cells in the sensory ganglion. Following nerve injury, SGCs undergo a series of changes, leading to their proliferation, high expression of neurotrophins and cytokines, and activation of MAPK kinases. Activated SGCs regulate the environment around neurons, and participate in the repair process. It has been suggested that SGCs may have the ability to replenish damaged neurons, which expands the role of these cells. With the application of single-cell sequencing technology to SGCs, researchers have explored the characteristics of SGCs and the differences between SGCs and SCs. These studies have undoubtedly advanced our understanding of SGCs.

However, based on present literature, it is still impossible to distinguish SGCs from SC precursors. Although several studies have focused on SGCs, the origin and nature of these cells remain unclear, and their lineage remains uncharacterized. Further investigation is required to establish a criteria for distinguishing SGCs from SC precursors and SCs, and to determine the lineage of SGCs.

Acknowledgements We thank Jigang Pan and Lu Wang for their help in writing this paper.

Author Contributions All authors contributed to the study conception and design. The first draft of the manuscript was written by Junhou Lu, Dongyan Wang, and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

Funding This work was supported by the Young Scientific Talents Growth Project of Guizhou Provincial Education Department (KY [2022]228), Doctoral Foundation of Guizhou Medical University [2021]020, and the Science and Technology Fund Project of Guizhou Health Commission (gzwkj2022-511, gzwkj2022-257).

Data Availability Not applicable.

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Competing Interests The authors declare that they have no competing interests.

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