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Shc1 cooperates with Frs2 and Shp2 to recruit Grb2 in FGF-induced lens development

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eLife Assessment

This **fundamental** article significantly advances our understanding of FGF signalling, and in particular, highlights the complex modifications affecting this pathway. The evidence for the authors' claims is **convincing**, combining state-of-the-art conditional gene deletion in the mouse lens with histological and molecular approaches. This work should be of great interest to molecular and developmental biologists beyond the lens community. The manuscript itself deserves minor editorial improvements, in particular, the literature on FGFR and SHC should be expanded in the introduction and discussed in more detail in the discussion.

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Abstract

Fibroblast growth factor (FGF) signaling elicits multiple downstream pathways, most notably the Ras/MAPK cascade facilitated by the adaptor protein Grb2. However, the mechanism by which Grb2 is recruited to the FGF signaling complex remains unresolved. Here we showed that genetic ablation of FGF signaling prevented lens induction by disrupting transcriptional regulation and actin cytoskeletal arrangements, which could be reproduced by deleting the juxtamembrane region of the FGF receptor and rescued by Kras activation. Conversely, mutations affecting the Frs2-binding site on the FGF receptor or the deletion of Frs2 and Shp2 primarily impact later stages of lens vesicle development involving lens fiber cell differentiation. Our study further revealed that the loss of Grb2 abolished MAPK signaling, resulting in a profound arrest of lens development. However, disrupting the Grb2 binding site on Shp2 or abrogating Shp2 phosphatase activity only modestly influenced FGF signaling, whereas mutating the presumed Shp2 dephosphorylation site on Grb2 did not impede MAPK signaling in lens development, indicating that Shp2 is only partially responsible for Grb2 recruitment. In contrast, we observed that FGF signaling is required for the phosphorylation of the Grb2-binding sites on Shc1 and the deletion of Shc1 exacerbates the lens vesicle defect caused by Frs2 and Shp2 deletion. These results reveal that Shc1 collaborates with Frs2 and Shp2 to target Grb2 in FGF signaling.

Introduction

The lens is an exemplary model for studying signaling pathways (Cvekl and Zhang, 2017). In mice, the lens placode emerges as thickened epithelia within the lateral head ectoderm at E9.5 (**Fig. 1A**). It undergoes invagination to form the lens pit at E10.5, and upon separation from the surface ectoderm, progresses into the lens vesicle at E11.5. Following this, lens progenitor cells within the lens vesicle proliferate and migrate toward the equator of the lens, where they differentiate into lens fibers responsible for the lens's focusing power (Lovicu and McAvoy, 2005). Genetic modification of the FGF signaling cascade alters various lens developmental processes, including lens invagination (Carbe and Zhang, 2011; Pan et al., 2006), lens vesicle formation (Kuracha et al., 2011), the establishment of the transition zone (Li et al., 2019), lens epithelium proliferation and survival, as well as lens fiber differentiation and elongation (Lovicu and Overbeek, 1998; Qu et al., 2011b; Robinson et al., 1995; Zhao et al., 2008). Therefore, the lens provides valuable insights into the nuanced interplay of FGF signaling components during distinct stages of lens formation.

The current model of FGF signaling posits that its primary orchestration centers on the Frs2/Shp2/Grb2 complex (Beenken and Mohammadi, 2009; Brewer et al., 2016; Eswarakumar et al., 2005). According to this model, FGFR activation induces phosphorylation of the adaptor protein Frs2, creating a platform for recruiting Shp2 and Grb2. In conjunction with its constitutively bound partner Sos (a guanine nucleotide exchange factor), Grb2 subsequently initiates Ras/MAPK signaling (Hadari et al., 2001; Ong et al., 2000). Prior research in eye development supports this notion, revealing that Crk proteins augment Ras signaling by associating with the Frs2/Shp2/Grb2 complex (Collins et al., 2018; Li et al., 2014; Madakashira et al., 2012), while PI3K-AKT signaling is activated through direct Ras binding with the PI3K catalytic subunit p110 (Wang et al., 2021). However, unresolved questions persist regarding downstream mediators of FGF signaling. Earlier studies suggested that mice with Frs2 mutants lacking the Grb2 binding site can survive healthily, whereas those lacking the Shp2 binding site exhibit severe eye development defects and significantly reduced MAPK signaling (Gotoh et al., 2004). These results suggest the critical importance of Shp2 in Grb2-mediated Ras signaling, but the exact mechanism remains unclear. Additionally, Soriano and colleagues generated allelic series of *Fgfr1* and *Fgfr2* mutants disrupting the Frs2 binding sites and multiple tyrosine phosphorylation residues, both individually and in combination, yet their phenotypes proved less severe than those of the respective null mutants (Brewer et al., 2015; Clark and Soriano, 2024) These studies suggest that there may exist additional adaptor(s) other than Frs2 to mediate FGF signaling.

In this study, we demonstrated that genetic alterations to FGFR— whether by deleting all isoforms, the juxtamembrane region, or the specific Frs2 binding site—disrupt the successive phases of lens development, encompassing lens induction, vesicle formation, and fiber differentiation. Surprisingly, while we established that Grb2-Ras signaling serves as the primary conduit of FGF signaling, interfering with Grb2 dephosphorylation and binding by Shp2 or even abolishing Shp2 phosphatase activity did not eliminate either MAPK signaling or lens differentiation. Conversely, we observed that FGF-induced Shc phosphorylation hinges on the FGFR juxtamembrane domain rather than its Frs2 binding site. Although the deletion of Shc1 has only a modest impact on lens development and MAPK activity individually, its combination with Frs2 and Shp2 deletion results in a profound arrest of lens vesicle development. These results suggest that Shc functions independently of Frs2 and Shp2 to augment Grb2-Ras signaling within the FGF pathway.

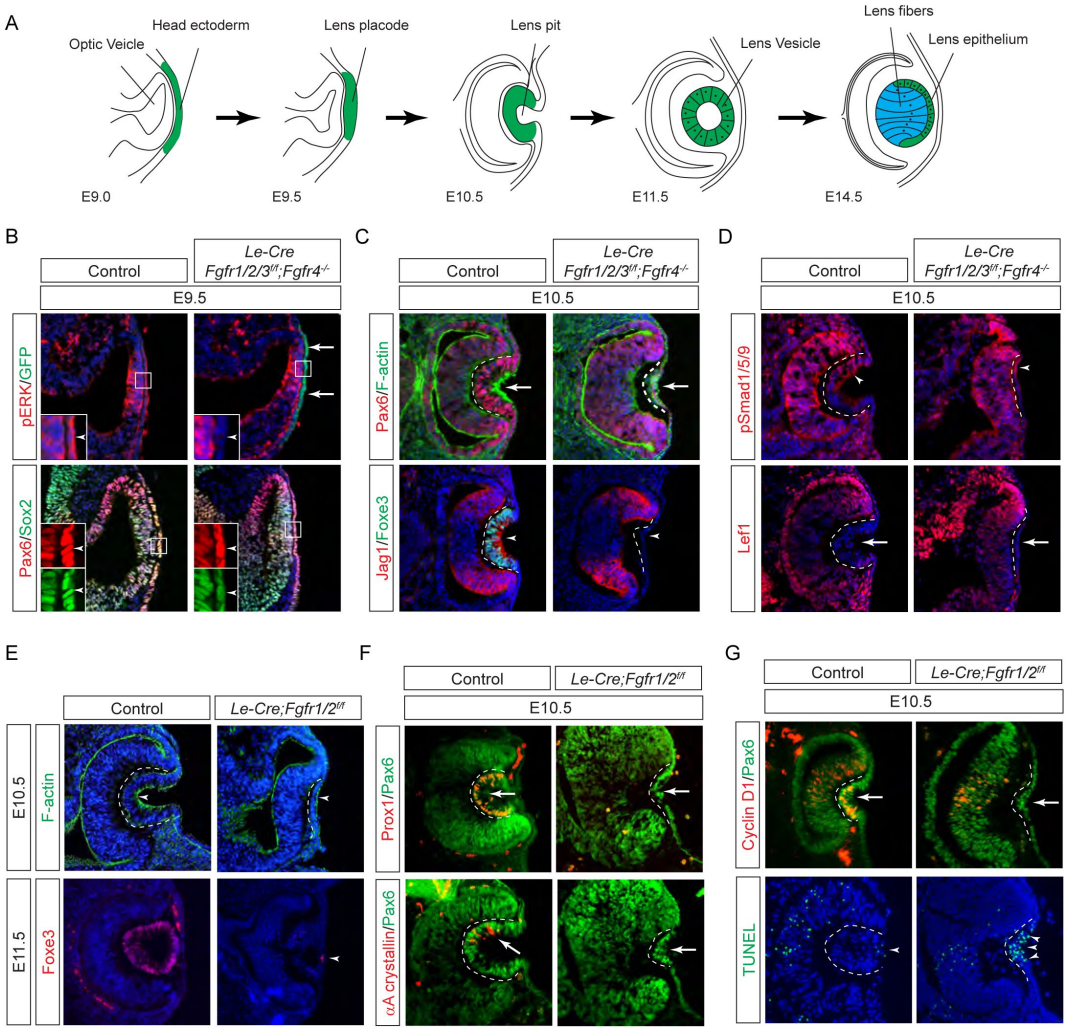


Figure 1.

FGF Signaling Regulates Lens Development in a Dose-Dependent Manner.

(A) Schematic diagram of murine lens development. The head ectoderm is induced by the underlying optic vesicle to become the lens placode, which subsequently folds inwards to become the lens pit. The closure of the lens vesicle sets the stage for the differentiation of the lens epithelium into the lens fibers. **(B)** Depletion of all four *Fgfr1/2/3/4*, driven by *Le-Cre* and traced with GFP, led to a thinner lens placode, evident from the absence of pERK signals and the failure to upregulate Sox2 like Pax6 (inserts, arrowheads). **(C)** *Fgfr1/2/3/4* mutants displayed disrupted apical constriction (F-actin accumulation, arrows) and lacked lens-specific expression of Foxe3 and Jag1 (arrowheads). Dotted lines outline the lens pit. **(D)** Despite *Fgfr1/2/3/4* mutations, BMP (pSmad1/5/9 staining, arrowheads) and Wnt signaling (Lef1 expression, arrows) remained unaffected. **(E)** The absence of *Fgfr1/2* alone did not impede the apical buildup of F-actin nor the expression of Foxe3, indicating partial retention of lens development processes. **(F)** Crucial lens markers, Prox1 and αA-crystallin, were absent in *Fgfr1/2* mutants, pointing to a significant developmental defect after the lens induction stage. **(G)** *Fgfr1/2* mutants exhibited loss of cell proliferation marker Cyclin D1 (arrows) and widespread apoptosis (TUNEL staining, arrowheads).

Results

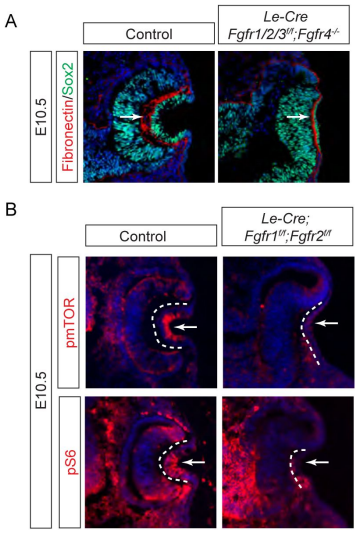
FGF signaling is required for lens induction

Previous studies have established the presence of all four FGF receptors in the surface ectoderm during lens induction (Garcia et al., 2011). However, despite the deletion of the primary FGFRs, *Fgfr1* and *Fgfr2*, only thinning of the lens placode occurred, with no discernible impact on lens determination transcription factors like Pax6, Sox2, and Foxe3. To explore whether the compensatory effects of remaining FGFRs obscure the role of FGF signaling in lens induction, we eliminated all four FGFRs using the *Le-Cre* deletor driven by the *Pax6* lens ectoderm (LE) enhancer (Ashery-Padan et al., 2000). The *Le-Cre* activity within the lens placode at E9.5, as indicated by the embedded GFP reporter (**Fig. 1B**, arrows), resulted in the complete loss of pERK in the ectoderm, confirming FGF signaling inactivation (**Fig. 1B**, inserts and arrowheads). Consequently, while the initial marker of lens induction, increased Pax6 expression as the surface ectoderm transitions into the lens placode, persisted in the mutant, Sox2 expression remained at basal levels. Furthermore, subsequent lens placode invagination, driven by apical constriction evidenced by polarized F-actin localization on the apical side by E10.5 (Chauhan et al., 2011), was disrupted (**Fig. 1C** arrows). This occurred despite the proper localization of Fibronectin at the basal side of the lens placode (**supplementary Fig. 1A**), suggesting that overall cell polarity remained unaffected. The *Le-Cre;Fgfr1$^{f/f}$;Fgfr2$^{f/f}$;Fgfr3$^{f/f}$;Fgfr4$^{-/-}$* mutant also failed to express lens-specific markers Foxe3 and Jag1, further underscoring impaired lens induction (**Fig. 1C**, arrowheads). Previous studies have highlighted FGF and BMP interaction during lens formation (Garcia *et al*., 2011), yet the dorsal-to-ventral gradient of BMP signaling, as indicated by pSmad staining, persisted in *Le-Cre;Fgfr1$^{f/f}$;Fgfr2$^{f/f}$;Fgfr3$^{f/f}$;Fgfr4$^{-/-}$* knockouts (**Fig. 1D**, arrowheads). Furthermore, Wnt signaling, a known negative regulator of lens induction (Smith et al., 2005), showed no signs of abnormal activity, as indicated by the absence of Lef1 expression (**Fig. 1D**, arrows). These results demonstrated that FGF signaling is required independently of Bmp and Wnt signaling for lens induction.

We next focused on the two primary FGFRs, Fgfr1 and 2, to scrutinize the latter phases of lens development. In contrast to mutants with deletion of all four FGFRs, we observed apical confinement of F-actin and expression of Foxe3 in the *Le-Cre;Fgfr1$^{f/f}$;Fgfr2$^{f/f}$* mutant lens cells (**Fig. 1E**, arrows). However, there was a conspicuous reduction in phosphorylation of mTOR and its downstream target S6 in the lens vesicle, suggesting that deletion of *Fgfr1/2* disrupted mTOR signaling (**Supplementary Fig. 1B**, arrowheads). Underscoring the lens differentiation defect, Prox1, a crucial transcription factor for lens fiber development, along with the lens-specific protein αA crystallin expression, was also lost in the *Le-Cre;Fgfr1$^{f/f}$;Fgfr2$^{f/f}$* mutant lens vesicle (**Fig. 1F**, arrows) (Garg et al., 2020; Ochi et al., 2003; Xie et al., 2016). Additionally, there was a notable decrease in Cyclin D1 expression and increasing TUNEL staining within the lens vesicle, indicating cell proliferation and apoptosis defects (**Fig. 1G**, arrows and arrowheads) (Garcia *et al*., 2011).

Ras mediates FGF signaling to suppress apoptosis in the development lens

FGF signaling is known to stimulate the Ras-MAPK signaling pathway. To explore the significance of Ras signaling, we employed a genetic rescue strategy utilizing an inducible *Kras* allele capable of expressing the constitutively active *Kras^{G12D}* upon Cre-mediated recombination (**Fig. 2A**) (Tuveson et al., 2004). When crossed with *Fgfr1/2* mutants, this allele effectively restored pERK expression and normalized lens vesicle invagination (**Fig. 2B**). By E13.5, the *Le-Cre;Fgfr1$^{f/f}$;Fgfr2$^{f/f}$;Kras^{G12D}* lens displayed robust phosphorylation of MEK, the upstream kinase of Erk, concomitant with the expression of lens fiber markers Prox1 and αA crystallin (**Fig. 2B** and



Supplementary Figure 1.

Lens development in Fgf receptor mutants.

(A) Depletion of all four *Fgfr1/2/3/4* did not disrupt the Fibronectin expression at the basal side of the lens placode (arrows).
(B) pmTOR and pS6 staining were lost in *Le-Cre;Fgfr1*$^{f/f}$*;Fgfr2*$^{f/LR}$lens.

C). Notably, the rescued lens reached about half the size of a control lens (**Fig. 2D**). These results suggest that Kras signaling acts as a primary conduit for FGF signaling during lens development.

To ascertain whether cell death underpins the pronounced lens vesicle defect in *Le-Cre;Fgfr1*$^{f/f}$*;Fgfr2*$^{f/f}$ mutant, we targeted Bax and Bak, two core regulators of the intrinsic pathway of apoptosis, for deletion. This intervention notably reduced TUNEL signals within the lens placode (**Fig. 2E** and **F**) and resulted in a recovery of lens formation, as evidenced by the expression of Foxe3, Maf, and Jag1 (**Fig. 2G**), although the lens remained considerably smaller than the wild-type control (**Fig. 2H**). This underscores the critical role of FGF signaling in preventing excessive cell apoptosis during lens development.

The juxtamembrane domain and Frs2 binding site of FGFR regulate the consecutive steps of lens development

Previous studies have mapped the Frs2 binding site to the juxtamembrane domain of FGFR (Dhalluin et al., 2000; Ong *et al*., 2000). To probe the role of this region in lens development, we employed two distinct alleles: one entirely devoid of the juxtamembrane domain (amino acid 407-433 in Fgfr1, *Fgfr1*$^{\Delta Frs}$) (Hoch and Soriano, 2006), and another harboring mutations in two pivotal residues essential for Frs2 binding (L424A and R426A in Fgfr2, *Fgfr2*^{LR}) (**Fig. 3A**) (Eswarakumar et al., 2006). Intriguingly, while the *Fgfr1/2* compound mutant carrying *Fgfr1*$^{\Delta Frs}$ mirrored the null phenotype (**Fig. 3B**, arrowheads), the mutant featuring *Fgfr2*^{LR}exhibited sustained expression of pERK, Cyclin D1, and αA crystallin, with no discernible increase in cell death, as confirmed by cleaved caspase 3 staining (see **Fig. 3B** and **C**). This suggests that the juxtamembrane domain of FGFR likely serves additional functions beyond Frs2 binding in lens induction.

The absence of a lens induction phenotype in the *Le-Cre;Fgfr1*$^{f/f}$*;Fgfr2*$^{f/LR}$ mutant raised the question regarding the role of Frs2 in lens development. Upon examining the iSyTE lens gene expression database (Kakrana et al., 2018), we observed a rapid increase in *Fgfr3* expression in the murine lens from E11.5 onwards, surpassing the levels of both *Fgfr1* and *Fgfr2* by E12.5 (**Fig. 3D**). This led us to consider whether heightened *Fgfr3* expression could potentially mask the effects of *Fgfr2*^{LR}mutation during later stages of lens development. To explore this hypothesis, we further deleted *Fgfr3* in conjunction with the *Fgfr1* and *Fgfr2*^{LR} mutant, which indeed impeded the differentiation and elongation of posterior lens epithelial cells, as evidenced by the absence of αA crystallin, Jag1, and Maf at E11.5 (**Fig. 3E**). By E12.5, unlike the *Le-Cre;Fgfr1*$^{f/f}$*;Fgfr2*$^{f/LR}$ mutant, which retained pERK staining and generated lens fibers to populate the lens vesicle similar to controls, the *Le-Cre;Fgfr1*$^{f/f}$*;Fgfr2*$^{f/LR}$*;Fgfr3*$^{f/f}$triple mutant remained a hollow lens vesicle without any pERK expression (**Fig. 3F** and **G**). This observation bears a striking resemblance to the phenotype previously reported when all three FGFRs were deleted at this stage (Zhao *et al*., 2008). Thus, while the Frs2 binding site on FGFR is dispensable for lens induction and lens vesicle formation, it evidently emerges as crucial for the later stage of lens fiber differentiation.

Grb2 mediates FGF-MAPK signaling in lens cell differentiation

If Frs2 is responsible for lens fiber differentiation rather than lens induction, we anticipate that its downstream target, Grb2, would exhibit a similar phenotype. To test this hypothesis, we genetically deleted *Grb2* using the *Le-Cre* driver. Indeed, the *Le-cre;Grb2*$^{f/f}$mutant formed a lens vesicle at E12.5 but lacked pERK staining, correlating with decreased Cyclin D3 expression and increased TUNEL staining (**Fig. 4A**). Notably, the initial lens determination gene Foxe3 was unaffected, but differentiation marker Jag1 was absent while Maf and crystallin were reduced. This lens differentiation defect is evident as early as E11.5, characterized by a significant reduction in the expression of cell cycle regulators Cyclin D1 and p57, as well as the pro-differentiation transcription factor Prox1, suggesting dysregulation of the cell cycle and failure to initiate the lens fiber cell differentiation program (**Fig. 4B**). By E13.5, the lens vesicle remained hollow and

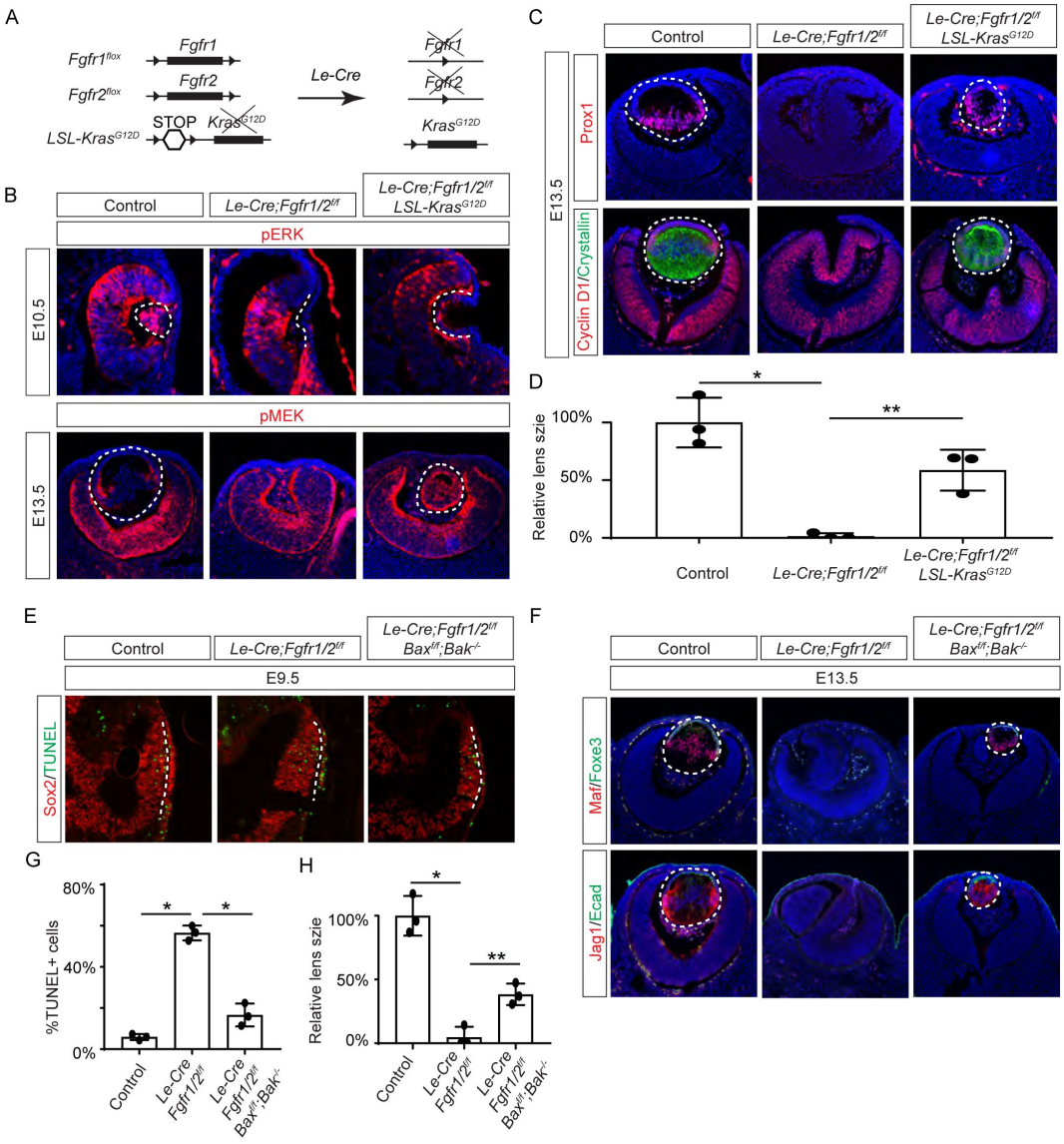


Figure 2.

Restoration of Lens Development in FGF Signaling Mutants via Kras Activation and Apoptosis Inhibition.

(A) The *Le-Cre* driver facilitated the excision of the floxed alleles of *Fgf1/2* along with the *LSL-STOP* cassette at the *Kras* locus, leading to the expression of the constitutively active $Kras^{G12D}$ allele within the *Fgf1/2* mutant background. **(B)** The activation of Kras signaling in the FGF signaling mutant lenses reinstated pERK activity at E10.5 and pMEK expression at E13.5, indicating restoration of MAPK signaling. **(C)** The lens-specific expression of Prox1 and αA-crystallin were also recovered, indicating successful lens development rescue. **(D)** Quantification of the lens size. One way ANOVA, n=3, *P<0.001, **P<0.02. **(E)** The deletion of pro-apoptotic genes *Bak* and *Bax* in *Fgf1/2* mutants suppressed apoptosis as shown by TUNEL staining. **(F)** Inhibiting apoptosis in *Fgfr1/2* mutants facilitated lens formation, as indicated by the expression of lens differentiation markers Prox1, Maf, and Jag1. **(G)** Quantification cell apoptosis. One-way ANOVA, n=3, *P<0.001. **(I)** Quantification of the lens size. One-way ANOVA, n=3, *P<0.0001, **P<0.05.

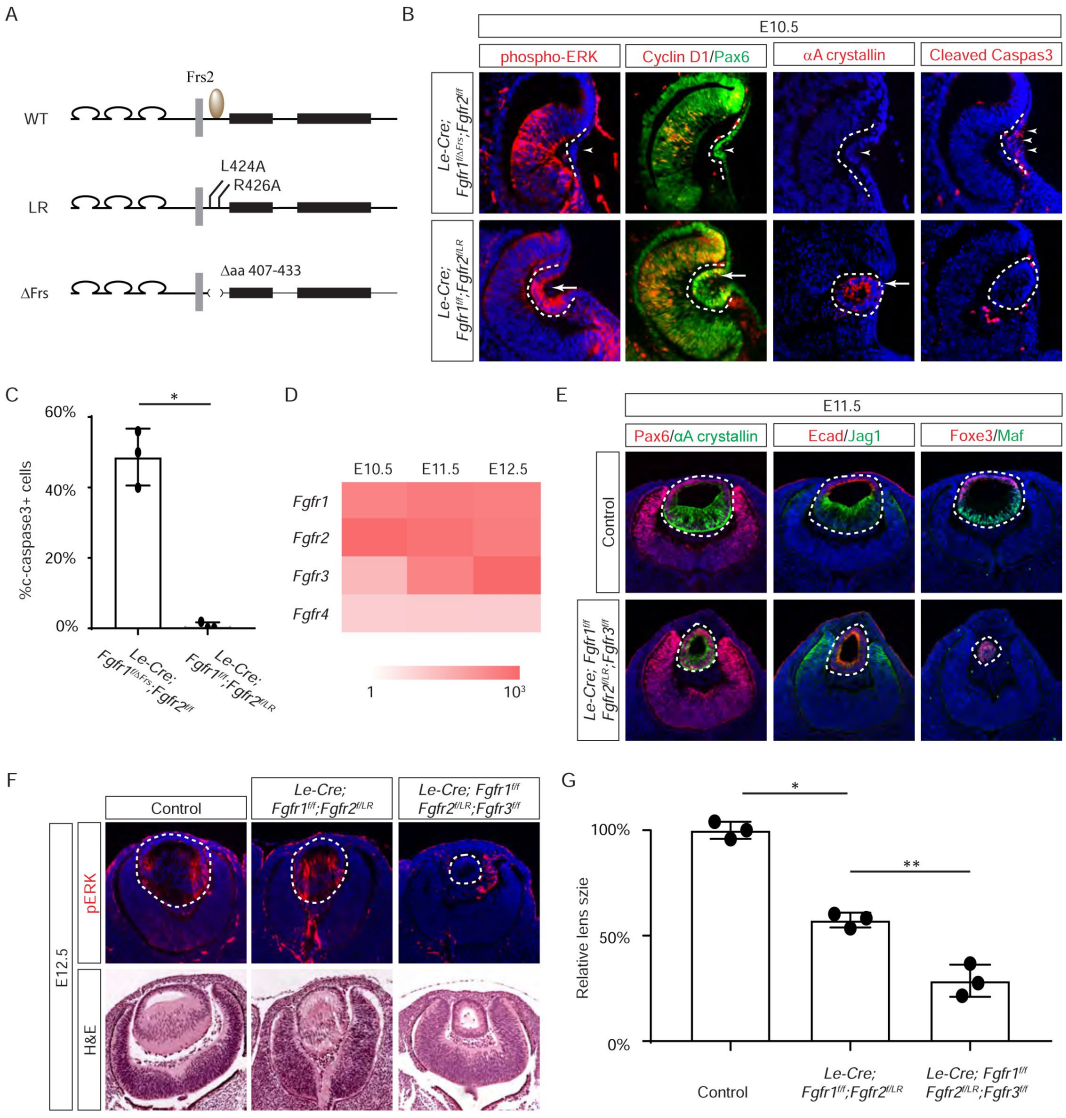


Figure 3.

The Frs2 binding site on FGFR is only required for lens vesicle differentiation.

(A) Overview of *Fgfr* mutant alleles. *Fgfr1*$^{\Delta Frs}$ lacks the Frs2 binding domain (amino acid 407-433), and *Fgfr2*^{LR} has point mutations disrupting Frs2 binding (L424A and L426A). **(B)** In *Fgf1/2* compound mutants, loss of pERK, CyclinD1, αA-crystallin and increased cleaved caspase3 were observed with the *Fgfr1*$^{\Delta Frs}$ allele but not the *Fgfr2*^{LR} allele. **(C)** Quantification of cleaved caspase3 staining. Student's t-test, n=3, *P<0.001. **(D)** Heatmap depicts *Fgfr* expression levels during lens development. **(E)** *Fgfr2*^{LR} mutants in the *Fgfr1/2/3* genetic background showed impaired lens vesicle differentiation, with posterior lens epithelial cells failing to elongate and activate lens fiber cell markers Jag1 and Maf. **(F)** *Fgfr1/2/3* triple mutants with *Fgfr2*^{LR} lost pERK staining and displayed a shallow lens vesicle at E12.5. **(G)** Quantification of the lens size. One-way ANOVA n=3, *P<0.001, **P<0.05.

smaller compared to the control (**Fig. 4B** and **C**). The deletion of Grb2 affects lens differentiation without hindering the formation of the lens vesicle, mirroring the effect of Frs2 binding site mutation, thus supporting the notion that Grb2 is the primary downstream effector of Frs2 in promoting lens fiber differentiation.

The Grb-Shp2 binding plays a modest role in FGF signaling

While both Frs2 and Shp2 possess phosphotyrosine residues that can engage with Grb2 (**Fig. 5A**), it's noteworthy that only mutations in the Shp2 binding sites, rather than those in the Grb2 binding sites on Frs2, led to severe eye development defects (Gotoh *et al*., 2004). This intriguing observation spurred us to investigate the potential role of Shp2 as an adaptor in facilitating the interaction between Frs2 and Grb2. To this end, we engineered a mouse model with mutations in the Grb2 binding sites of Shp2 (Sun et al., 2013) by substituting the C-terminal tyrosine residues 542 and 580 with phenylalanine ($Shp2^{YF}$) (**Fig. 5B**), which was confirmed by southern blot analysis using both 5' and 3' probes and Sanger sequencing (**Fig. 5C**). However, homozygous mice carrying the $Shp2^{YF}$ mutation died around E12.5 with visibly paler and smaller bodies (**Fig. 5D** and **E**). Histological analysis of mutants revealed a significantly thinner labyrinth zone in placentas, crucial for oxygen and nutrient supplies (**Fig. 5E**, dotted lines). To test whether this placental defect is responsible for the embryonic lethality, we combined the $Shp2^{YF}$ mutation with the *Shp2* conditional allele using *Sox2Cre*, which is specifically active in the epiblast-derived embryonic tissues but not in the trophoblast-derived placenta (**Fig. 5F**)(Hayashi and McMahon, 2002). *Sox2Cre*;$Shp2^{f/YF}$ embryos indeed survived past embryonic day 15.5 without evident morphological abnormalities, yet they succumbed shortly after birth for reasons yet unknown (**Fig. 5G**).

The survival of *Sox2Cre*;$Shp2^{f/YF}$ mutant beyond embryonic development permitted the isolation of mouse embryonic fibroblast (MEF) cells for biochemical analysis. As anticipated, the phosphorylation of Shp2 (pShp2^{Y542}) induced by FGF was abolished in *Sox2Cre*;$Shp2^{f/YF}$MEF cells, yet the activation of pERK was only partially impaired (**Fig. 5H**). This contrasts with the more pronounced reduction in PDGF-induced ERK phosphorylation, underscoring a distinct requirement for Shp2-Grb2 binding across related receptor tyrosine kinase (RTK) pathways (Araki et al., 2003). In line with the subtle impact on FGF signaling, neither the pattern of pERK staining nor the size of the lens showed discernible alterations in *Sox2Cre*;$Shp2^{f/YF}$ mutants (**Fig. 5I**, arrowheads). We further investigated lacrimal gland development due to its remarkable sensitivity to FGF signaling intensity, where even a heterozygous *Fgf10* mutation has been shown to stunt gland growth (Garg and Zhang, 2017; Qu et al., 2011a). Notably, we observed a slight reduction in pERK staining in the lacrimal gland primordia at E14.5 and fewer lacrimal gland buds at birth (**Fig. 5I**, arrows). These nuanced ocular phenotypes, alongside the overall normal morphology of *Sox2Cre*;$Shp2^{f/YF}$ mutant embryos, collectively suggest that Shp2-Grb2 binding exerts a modest influence on FGF signaling.

Inactivation of Shp2 phosphatase activity failed to abrogate FGF-induced MAPK signaling

The results presented above indicate that the direct binding of Grb2 to the Shp2 C-terminus is not essential for FGF signaling. This led us to explore an alternative hypothesis that Shp2 might function by removing inhibitory tyrosine phosphorylation on Grb2, thereby promoting its interaction with Sos and subsequent Ras-MAPK activation (Ahmed et al., 2013; Vemulapalli et al., 2021). Based on the PhosphoSitePlus database, we identified Y209 as the most frequently phosphorylated tyrosine residue in Grb2 (**Fig. 6A**). Notably, previous studies have demonstrated that Shp2 dephosphorylates this specific site upon stimulation by various receptor tyrosine kinases (RTKs) (Ahmed *et al*., 2013; Haines et al., 2009; Li et al., 2001; Riera et al., 2010). To assess the functional significance of Y209 phosphorylation, we generated a mutant *Grb2* allele where Y209 was replaced with phenylalanine ($Grb2^{YF}$) using the ES cell-based gene targeting

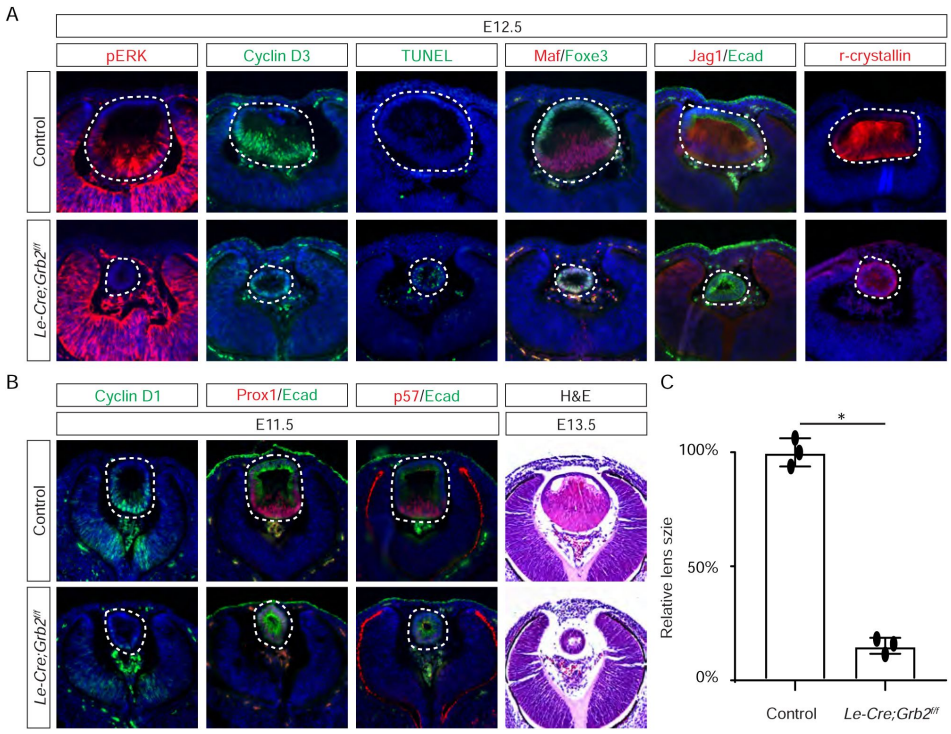


Figure 4.

Grb2 is essential for lens vesicle survival, proliferation, and differentiation.

(A) The targeted removal of Grb2 in the lens led to a loss of pERK signaling, reduced CyclinD3 expression, increased apoptosis (TUNEL staining), and disrupted expression of critical lens development genes Maf, Foxe3, Jag1 and γ-crystallin expression at E12.5. **(B)** Grb2 mutants Grb2 mutants displayed absent CyclinD1, Prox1, and p57 expression at E11.5 and remained an undifferentiated hollow vesicle at E13.5, failing to undergo normal lens fiber elongation. **(C)** Quantification of the lens size. Student's t-test, n=3, *P<0.0001.

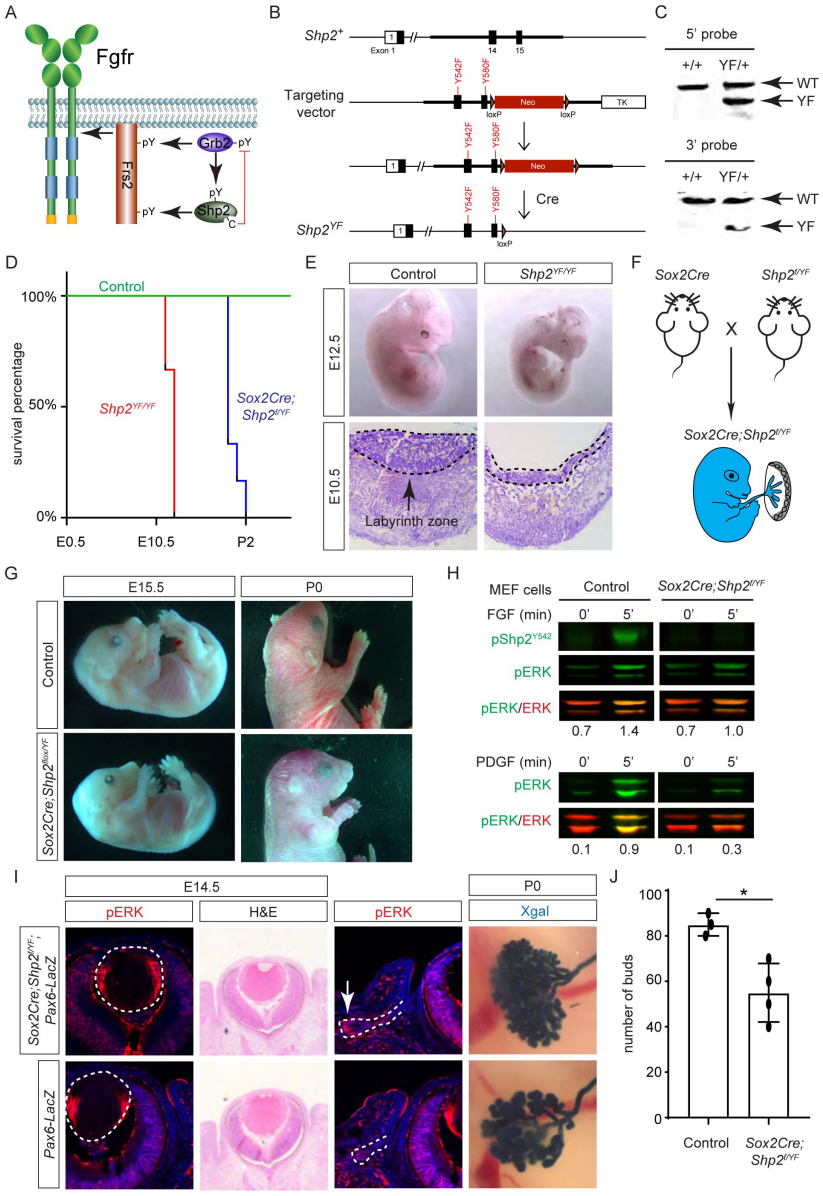


Figure 5.

Shp2 C-terminal tyrosine phosphorylation is required for embryonic survival but dispensable for lens development.

(A) Schematic of the core FGF signaling pathway. FGFR activation leads to phosphorylation of the adaptor Frs2 on N- and C-terminal tyrosines, recruiting Grb2 and Shp2 respectively. Shp2 can also bind Grb2 via its own C-terminal phosphotyrosines, and dephosphorylates Grb2 via its catalytic cysteine residue. **(B)** Generation of the *Shp2*^{YF} allele by homologous recombination to introduce *loxP*-flanked Neo and point mutations (Y542F and Y580F) disrupting the Shp2 C-terminal phosphotyrosine sites. The Neo cassette was subsequently excised by Cre-mediated recombination. **(C)** Validation of the *Shp2*^{YF} allele targeting was confirmed through Southern blot analysis with both 5′ and 3′ probes. **(D)** Kaplan-Meier survival curves demonstrate early lethality of *Shp2*^{YF} embryos (E12.5) and perinatal lethality of *Sox2Cre;Shp2*$^{f/YF}$mutants. n=5 for *Shp2*$^{YF/YF}$and n=6 for *Sox2Cre;Shp2*$^{f/YF}$ mutants. **(E)** *Shp2*$^{YF/YF}$ embryos displayed reduced body size at E12.5 and thinner labyrinth zones in their placenta E10.5. **(F)** *Sox2Cre*-mediated targeting restricts Shp2 deficiency to the embryonic proper, circumventing placental abnormalities. **(G)** *Sox2Cre;Shp2*$^{f/YF}$ mutants appeared grossly normal at E15.5 but failed to survive after birth. **(H)** While Y542 phosphorylation in Shp2 was lost as expected, *Sox2Cre;Shp2*$^{f/YF}$MEFs exhibited a more pronounced reduction in pERK response to PDGF stimulation compared to FGF stimulation. **(I)** *Sox2Cre;Shp2*$^{f/YF}$mutant lens displayed normal pERK staining and morphology, but reduced pERK in lacrimal glands at E14.5 and decreased bud numbers at P0. **(J)** Quantification of the number of lacrimal gland buds. Student's t-test, n=3, *P<0.02.

technique (**Fig. 6B** and **C**). Surprisingly, our findings revealed that *Grb2*$^{YF/YF}$ homozygous mutants exhibited normal viability and fertility without any obvious phenotype. Additionally, the intensity of pERK staining in mutant lenses remained unchanged in mutant lenses compared to controls, and markers of the cell cycle (Ki67 and p57) as well as differentiation (Jag1, Foxe3, and Maf) were unaffected. These results suggest that despite being a frequent target for phosphorylation, Y209 on Grb2 is dispensable for FGF signaling.

The PhosphoSitePlus database indicates that Grb2 still possesses a less frequently phosphorylated Y160 site, which has also been previously implicated in FGF signaling (Ahmed et al., 2015). To rigorously assess the potential impact of Shp2-mediated Grb2 dephosphorylation, we developed a *Shp2*^{CS} mouse model by substituting the cysteine residue at position 463 (C459 in humans) with alanine in Shp2's catalytic domain, effectively abolishing its enzymatic activity (**Fig. 6E** and **F**). Unlike the earlier *Shp2* null mutants that perished by E7.5 (Yang et al., 2006), *Shp2*$^{CS/CS}$ embryos exhibited stunted growth but survived until E9.5, indicating that the *Shp2*^{CS}mutation doesn't entirely abrogate Shp2's function (**Fig. 6G**).

Moreover, after removing the *flox* allele using Cre-expressing adenovirus, the *Shp2*$^{f/CS}$ MEF cells still retained considerable pERK activity in response to FGF stimulation (**Fig. 6H**). This was mirrored in vivo, with pERK detection in the *Le-Cre;Shp2*$^{f/CS}$lens but not in the *Le-Cre;Shp2*$^{f/f}$ mutants (**Fig. 6I**). Consequently, lens epithelial cells in *Le-Cre;Shp2*$^{f/f}$ mutants migrated to the posterior pole with reduced p57 and Jag1 expression, indicating impaired differentiation, but *Le-Cre;Shp2*$^{f/CS}$ lens epithelial cells showed proper p57-mediated cell cycle exit at the lens equator and initiated timely expression of Jag1 (**Fig. 6J**). However, these lenses showed normal proliferation (Ki67) but increased cell death (TUNEL), resulting in a smaller size (**Supplementary Fig. 2**). Moreover, the development of the FGF signaling-sensitive lacrimal gland was blocked in both *Le-Cre;Shp2*$^{f/f}$ and *Le-Cre;Shp2*$^{f/CS}$ mutants, a more pronounced effect than the modest reduction in lacrimal gland buds observed in *Shp2*$^{YF/YF}$ mutants (**Fig. 6I**). This suggests that inhibiting Shp2's phosphatase activity more significantly affects FGF signaling compared to obstructing its adaptor function, yet doesn't completely abolish FGF signaling.

Shc1 cooperates with Frs2 and Shp2 to promote lens development

The mild lens defects observed in *Shp2* mutants lacking either adaptor or phosphatase function led us to investigate alternative mechanisms for Grb2 recruitment to the FGFR complex. Given the distinct lens phenotypes in *Le-Cre;Fgfr1*$^{f/f}$*;Fgfr2*$^{f/LR}$ and *Le-Cre;Fgfr1* $^{f/\Delta Frs}$*;Fgfr2*$^{f/f}$ mutants (**Fig. 7A**), we hypothesized that FGF might activate unidentified factor(s) in *Fgfr1*$^{f/f}$*;Fgfr2*$^{f/LR}$ MEF cells but not in *Fgfr1* $^{f/\Delta Frs}$*;Fgfr2*$^{f/f}$ cells following the excision of flox alleles by Cre-expressing adenovirus, mirroring the observed pattern of pERK activation. Interestingly, FGF stimulation was ineffective in raising pFrs2 and pShp2 levels in both sets of MEF cells and did not alter the phosphorylation states of Crk and Gab1, both recognized adaptors in FGF signaling (Collins *et al*., 2018; Hadari *et al*., 2001; Li *et al*., 2014). However, a key difference emerged – Shc phosphorylation was lost in *Fgfr1* $^{f/\Delta Frs}$*;Fgfr2*$^{f/f}$cells but persisted in *Fgfr1*$^{f/f}$*;Fgfr2*$^{f/LR}$mutants (**Fig. 7A**). This observation was further supported by in vivo data, which showed that pShc was detectable in both wild-type and *Le-Cre;Fgfr1*$^{f/f}$*;Fgfr2*$^{f/LR}$ lens vesicles, but not in *Le-Cre;Fgfr1* $^{f/\Delta Frs}$*;Fgfr2*$^{f/f}$ mutants (**Fig. 7B**, arrowhead). These findings suggest that Shc can be activated by the FGFR independently of its Frs2 binding site, potentially serving as an alternate route for Grb2's engagement.

Among the four *Shc* genes present in the mammalian genome, *Shc1* is the most abundant in the lens (**Fig. 7C**). This led us to ablate *Shc1* in the lens to determine its function in FGF signaling. However, *Le-Cre;Shc1*$^{f/f}$ lenses displayed only minor reductions in pERK staining and size, suggesting potential redundancy with other Shc proteins or compensatory mechanisms involving Frs2 and Shp2. To investigate this further, we created compound mutants involving these genes. We have previously reported that the deletion of *Frs2* or *Shp2* alone led to a modest diminution in lens size, akin to the *Shc1* deletion effect. However, the combined knockout of *Frs2* and *Shp2* (*Le-*

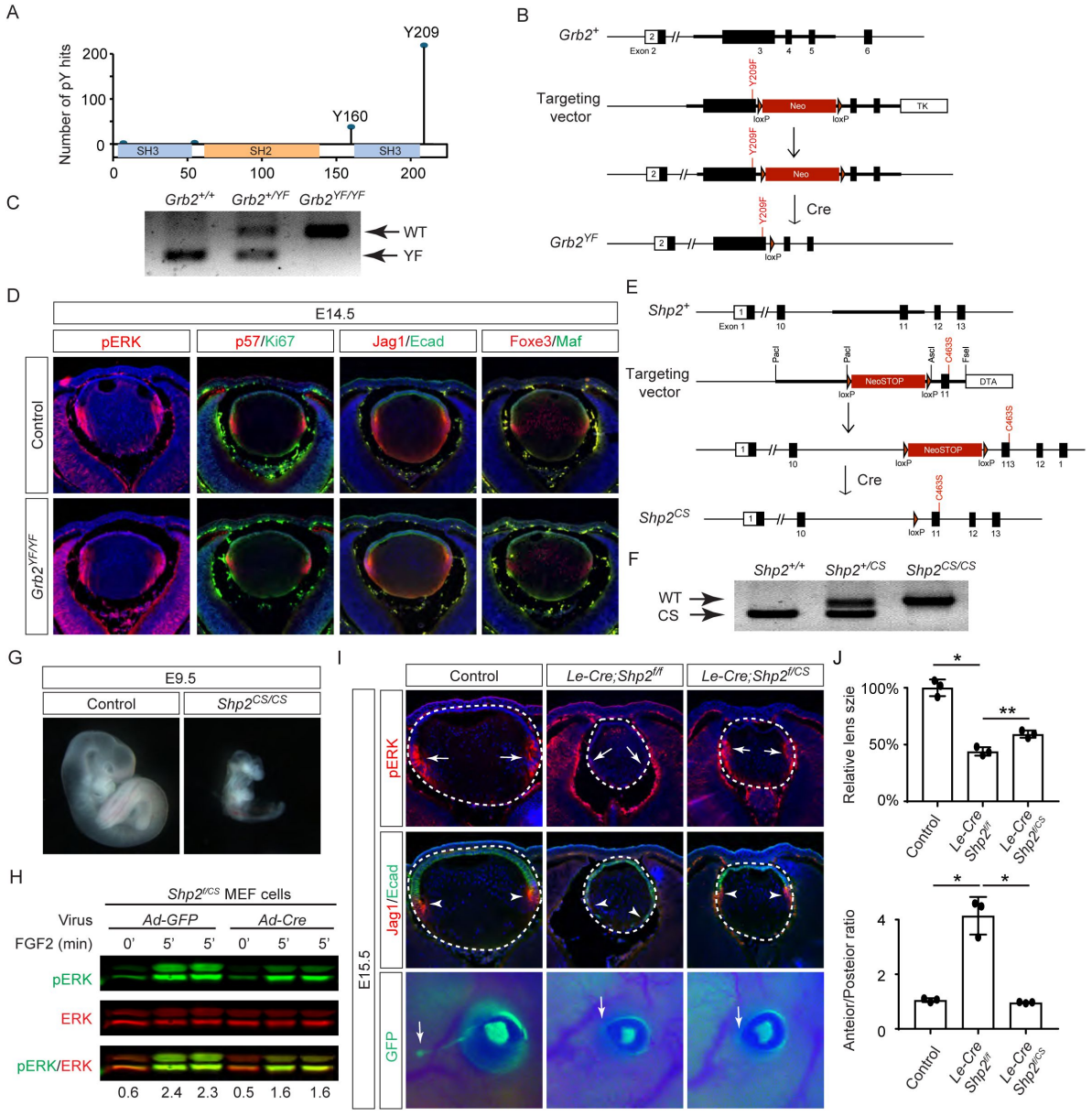


Figure 6.

Shp2 phosphatase activity is partially required for FGF signaling independently of Grb2 dephosphorylation.

(A) PhosphositePlus database indicates that Grb2 predominantly undergoes phosphorylation at Y209 and less frequently at Y160. **(B)** The *Grb2*^{YF} allele was constructed by homologous recombination to integrate a *loxP*-flanked *Neo* cassette and a Y209F point mutation into the *Grb2* locus. **(C)** PCR genotyping confirmed the presence of the *Grb2*^{YF} allele. **(D)** *Grb2* mutant lens typical expression patterns of pERK, cell cycle markers p57 and Ki67 and differentiation markers Foxe3, Maf and Jag1. **(E)** The *Shp2*^{CS} allele was generated by inserting the C459S mutation into the Shp2 locus by homologous recombination, followed by Cre-mediated removal of the *loxP*-flanked *Neo* cassette. **(F)** *Shp2*^{CS} allele validated by PCR genotyping. **(G)** *Shp2*$^{CS/CS}$ mutants exhibited growth retardation and died at E9.5. **(H)** *Shp2*$^{f/CS}$MEF cells retained a significant capacity to activate pERK upon FGF stimulation after Cre virus infection. **(I)** *Le-Cre;Shp2*$^{f/f}$ mutants exhibited loss of pERK and Jag1 staining at the lens transition zone (arrowheads), which also shifted posteriorly. *Le-Cre;Shp2*$^{f/CS}$ mutant lens, in contrast, maintained staining at the equatorial region. Notably, both mutant types lacked lacrimal gland buds (arrows). **(J)** Quantification of the lens size. One-way ANOVA n=3, *P<0.0001, **P<0.001. **(K)** Quantification of the lens perimeter spanning the anterior epithelium versus that of the posterior lens fiber. One-way ANOVA n=3, *P<0.001.

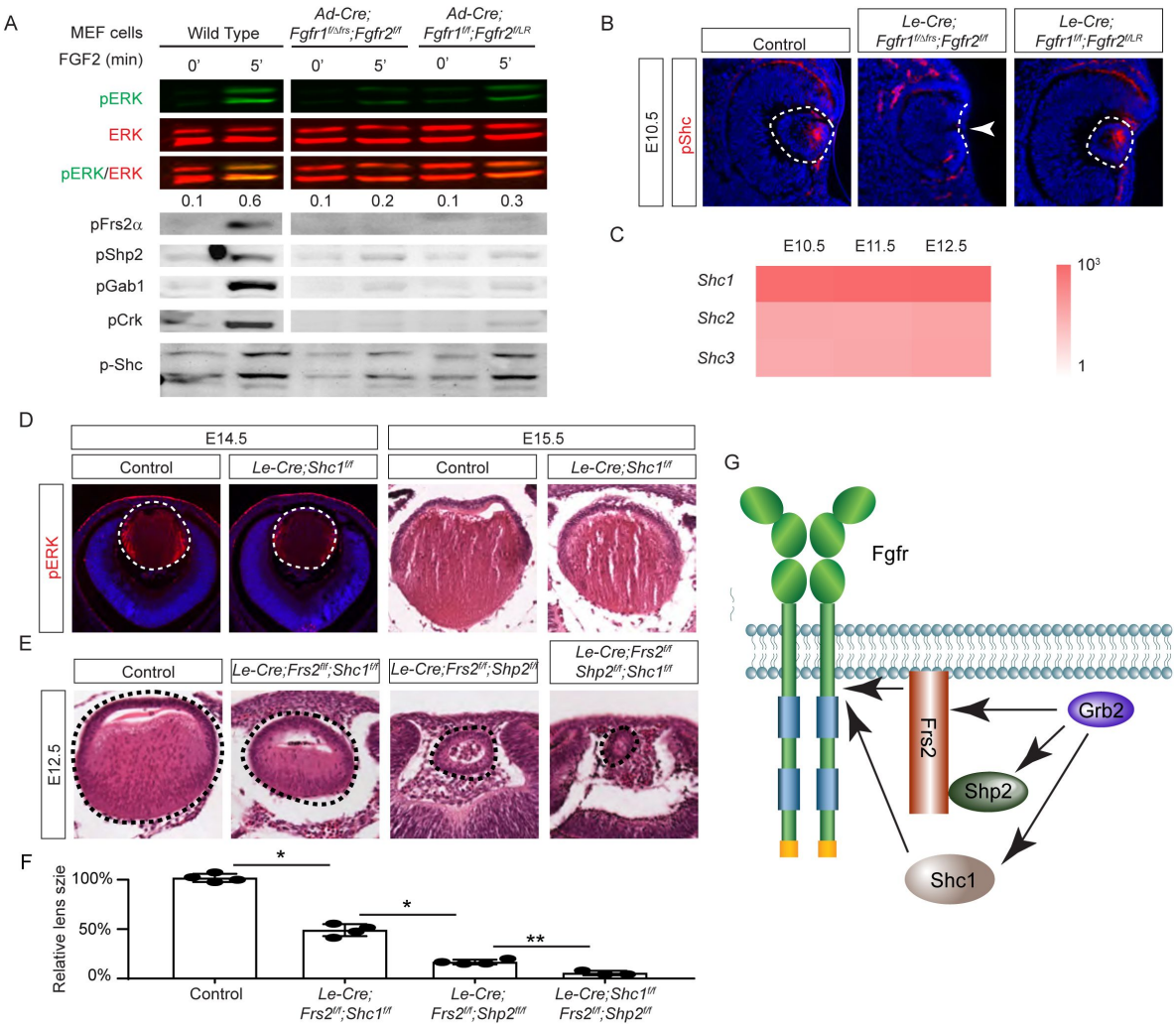
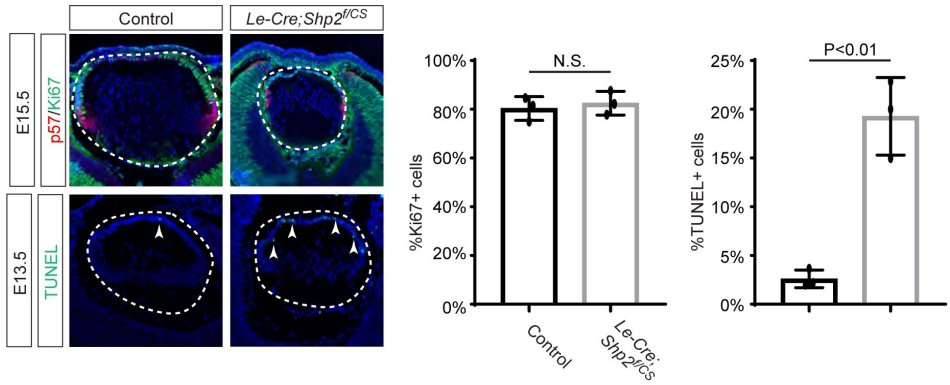


Figure 7.

Shc1 complements Frs2 and Shp2 in mediating FGF signaling in lens development.

(A) *Fgfr1*$^{f/f}$*;Fgfr2*$^{f/LR}$ infected with Cre virus showed stronger pERK and pShc activation than *Fgfr1* $^{f/\Delta Frs}$*;Fgfr2*$^{f/f}$ MEF cells, despite both losing Frs2, Shp2, Gab1, and Crk phosphorylation. **(B)** pShc staining was lost in *Le-Cre;Fgfr1* $^{f/\Delta Frs}$*;Fgfr2*$^{f/f}$mutant lens (arrowhead) but preserved in *Le-Cre;Fgfr1*$^{f/f}$*;Fgfr2*$^{f/LR}$ lens. **(C)** Heatmap showing Shc expression levels during lens development. **(D)** *Shc1*-deficient lenses showed a slight decrease in both pERK staining intensity and overall lens size. **(E)** E12.5 Frs2/Shc1 mutant lenses were smaller than controls, while lenses from Frs2/Shp2 mutants showed a pronounced hollow vesicle structure, a condition that worsened in Frs2/Shp2/Shc1 triple mutants. **(F)** Quantification of the lens size. One-way ANOVA n=4, *P<0.001, **P<0.05. **(G)** Model of FGF signaling network. Frs2 recruits Grb2 directly and indirectly through Shp2, while Shc1 provides an alternate Grb2 recruitment route independent of Frs2.



Supplementary Figure 2.

Cell proliferation and apoptosis in *Shp2*^{CS}mutants.

Le-Cre;Shp2$^{f/CS}$ lens exhibits normal expression of proliferation marker Ki67, but there is a significant increase in TUNLE+ cells (arrowheads). Student's t-test, N.S. (not significant) for %Ki67+ cells and P<0.01 for %TUNEL+ cells in the lens epithelium.

Cre;Frs2$^{f/f}$*;Shp2*$^{f/f}$) resulted in hollow lens vesicles, highlighting a synergistic interaction between these two genes (Li *et al*., 2014). While the *Le-Cre;Frs2*$^{f/f}$*;Shc1*$^{f/f}$compound mutant did not exhibit as severe abnormalities, introducing the *Shc1* knockout into the *Le-Cre;Frs2*$^{f/f}$*;Shp2*$^{f/f}$ background further diminished the lens size, suggesting that Shc1 contributes an additive role alongside Frs2 and Shp2 in modulating lens development. These findings collectively showed that Shc1 functions independently of Frs2 and Shp2 to transmit FGF signaling in lens development.

Discussion

This study used lens development as a model system to dissect the intricate mechanisms of FGF signaling. By systematically disrupting FGF signaling components, it unveiled a previously unappreciated dependency on precise FGF dosage for each developmental stage. Genetic rescue experiments and targeted manipulation of tyrosine phosphorylation further demonstrated that FGF signaling relies only partially on Frs2 and Shp2 for Grb2 recruitment, ultimately activating Ras and preventing cell death. Contrary to prevailing expectations, while both the adaptor function and the phosphatase activity of Shp2 are vital for embryonic survival, they play a surprisingly modest role in lens development, challenging the current understanding of Shp2 signaling mechanism. Notably, our research suggests that Shc may provide an alternative pathway for Grb2 recruitment and subsequent Ras activation. Although various adaptor proteins like Frs2, Crk, Shb, and Gab have been recognized for their roles in FGF signal transduction, recent findings suggest that mutations in their binding sites on FGF receptors have a significantly lesser impact compared to *Fgfr* null mutations (Brewer *et al*., 2015; Klint and Claesson-Welsh, 1999). Our data propose that Shc1 serves as an alternative route for FGF signal transmission, thereby adding a new dimension to our understanding of FGF signaling dynamics.

Lens induction, the pivotal event in eye development, has captivated developmental biologists since Hans Spemann's seminal discovery over a century ago, which identified the optic vesicle's role in triggering the overlying head ectoderm to differentiate into the lens (Spemann, 1901). However, the nature of the lens inductive signal has remained elusive (Makrides et al., 2022; Robinson, 2006). Previous studies suggested that FGF signaling might not be essential, as deleting Fgfr1/2 in the head ectoderm did not affect the expression of the early lens determination gene, Foxe3 (Garcia *et al*., 2011). Contrary to this notion, we have ablated all FGFRs present in the surface ectoderm, which led to a complete loss of pERK, confirming the absence of FGF signaling activity. Although the mutant ectoderm still expressed Pax6, it failed to upregulate Sox2 and Foxe3, the definitive markers of the lens induction. Moreover, the disruption of FGF signaling prevented the apical confinement of F-actin, impeding lens placode invagination driven by apical constriction (Chauhan *et al*., 2011). Considering the concomitant expression of FGF ligands in the optic vesicle, our findings suggest that FGF signaling is an indispensable factor in lens induction.

The role of Shp2 phosphatase in enhancing Receptor Tyrosine Kinase (RTK) signaling pathways is well established, yet its molecular mechanism remains largely resolved (Neel et al., 2003). The prevailing model posits that Shp2 functions by dephosphorylating key tyrosine residues on target proteins, thereby activating Ras signaling. However, it has also been suggested that Shp2 itself can undergo C-terminal phosphorylation, potentially serving as a docking platform for other signaling molecules. Through targeted mutagenesis of these putative phosphorylation sites (*Shp2*^{YF}), we demonstrate the critical role of Shp2 phosphorylation in placental formation and neonatal survival. Biochemical analyses revealed distinct cellular responses to FGF and PDGF stimulation in *Shp2*^{YF} mutants, suggesting context-dependent functions for these C-terminal modifications, which may explain the narrow phenotypic spectrum associated with the *Shp2*^{YF} mutation. Intriguingly, the inactivation of Shp2 phosphatase activity via the *Shp2*^{CS}mutation also resulted in minimal disruption of FGF signaling in lens development, unlike the control *Le-Cre; Shp2*$^{f/f}$ mutant, which showed a significant reduction in pERK levels and subsequent lens differentiation defects. This

lack of a robust phenotype cannot be attributed to residual protein activity following Cre-mediated gene deletion due to the systemic nature of the $Shp2^{CS}$ mutation. While Shp2 phosphatase deficiency did cause early embryonic lethality and abrogated the development of the more FGF-sensitive lacrimal gland, the absence of a pronounced lens phenotype calls into question the essentiality of Shp2 phosphatase activity for its overall function. Given the distinct phenotype observed in the $Shp2^{YF}$ mutant, it is plausible that Shp2 fulfills dual roles as both an adaptor and a phosphatase in certain signaling contexts, challenging existing paradigms and inviting further investigation into its multifaceted biological functions.

Previous studies have identified FGFR as a docking station for various signaling adaptor proteins, including Frs2, Plcg, Crk, Grb14 and Shb. In a heroic effort, Soriano and colleagues have eliminated these binding sites, both individually and collectively, but the outcomes were unexpectedly mild compared to the more severe phenotypes observed in the corresponding null mutants (Brewer *et al*., 2015; Clark and Soriano, 2024). For instance, whereas the *Fgfr1* null mutant is lethal by E6.5, mutants lacking the ability to bind Frs2, CrkL and Plcg/Shb/Shc/Grb14 survive until E10.5. More strikingly, *Fgfr2* null mutants typically succumb by E10.5 due to widespread organ development failures, yet mutants deficient in these specific binding sites can reach adulthood with minimal apparent defects. The fact that combining *Fgfr1/2* signaling mutations does not mimic the null phenotype further suggests that these mild mutant phenotypes are not simply a result of compensatory actions by other FGF receptors. This discrepancy highlights a crucial gap in our understanding of FGF signaling, implying the existence of unidentified factors that can compensate for the loss of Frs2 and other adaptors. Our study proposes Shc1 as a potential player in this complex signaling web, which is consistent with the observations that Shc1 can be phosphorylated in association with FGF receptors at sites known to facilitate Grb2 binding (Klint et al., 1995; Schuller et al., 2008), indicating an alternative route for signal propagation. Although *Shc1* knockout models exhibit relatively mild lens phenotypes, which may be attributed to the redundancy among Shc family proteins and potential compensation by Frs2, simultaneous deletion of *Shc1*, *Frs2* and *Shp2* further worsened lens development defects. These findings point towards a robust and adaptable FGF signaling network, capable of engaging alternative pathways through Frs2, Shc, and other adaptor proteins, thereby maintaining its function despite significant genetic disruptions. These insights underscore the complexity and resilience of cellular signaling networks, understanding which is important for developing strategies to manipulate them in developmental and disease contexts.

Methods and materials

Mice

All procedures related to animal care and experimentation were conducted in adherence to the protocols and guidelines approved by the Institutional Animal Care and Use Committee at Columbia University. We obtained $Fgfr1^{\Delta Frs}$ from Dr. Raj Ladher (RIKEN Kobe Institute-Center for Developmental Biology, Kobe, Japan) (Hoch and Soriano, 2006), $Fgfr2^{LR}$ from Dr. Jacob V.P. Eswarakumara (Yale University School of Medicine, New Haven, CT) (Eswarakumar *et al*., 2006) and $Fgfr2^{flox}$ from Dr. David Ornitz (Washington University Medical School, St Louis, MO) (Yu et al., 2003). $Fgfr3^{flox}$from Dr. Xin Sun (University of California San Diego, La Jolla, CA) (Su et al., 2010), $Fgfr4^{-/-}$ from Dr. Chu-Xia Deng (National Institute of Health, Bethesda, MD) (Weinstein et al., 1998), $Frs2\alpha^{flox}$ from Fen Wang (Texas A&M, Houston, TX) (Lin et al., 2007), $Grb2^{flox}$ from Dr. Lars Nitschke (University of Erlangen-Nürnberg, Erlangen, Germany) (Ackermann et al., 2011), *Le-Cre* from Richard Lang (Children's Hospital Research Foundation, Cincinnati, OH) (Ashery-Padan *et al*., 2000), P6 5.0 *lacZ* (*Pax6-LacZ*) reporter transgenic mice from Dr. Paul A. Overbeek (Baylor College of Medicine, Houston, TX) (Makarenkova et al., 2000), $Shc1^{flox}$ from Tony Pawson (University of Toronto, Ontario, Canada) (Hardy et al., 2007), $Shp2^{flox}$ from Gen-sheng Feng (UCSD, Sad Diego, CA) (Zhang et al., 2004), $LSL\text{-}Kras^{G12D}$ mice was obtained from the

Mouse Models of Human Cancers Consortium (MMHCC) Repository at National Cancer Institute (Tuveson *et al*., 2004). *Bax*$^{flox/flox}$;*Bak*$^{KO/KO}$ (Stock No: 006329), *Fgfr1*^{flox} (Stock No: 007671), *Sox2Cre* (Stock No: 008454) mice were obtained from Jackson Laboratory. Animals were maintained on mixed genetic backgrounds. In all conditional knockout experiments, mice were maintained on a mixed genetic background and *Le-Cre* only or *Le-Cre* and heterozygous flox mice were used as controls. Mouse maintenance and experimentation were performed according to protocols approved by Columbia University Institutional Animal Care and Use Committee.

Shp2^{YF}, *Shp2*^{CS} and *Grb2*^{YF}targeting vectors were constructed using the recombineering method from C57BL/6 Bac clones (RP23-257E17 for *Shp2*, P23-2814 for *Grb2*, BACPAC Resources Center at Children's Hospital Oakland Research Institute) (Carbe et al., 2012). The *Shp2*^{YF}vector includes a neomycin resistance (*Neo*) cassette bordered by *loxP* sites, along with exon 14 of the *Shp2* gene harboring Y542F mutations and exon 15 with Y580F mutations. The *Shp2*^{CS} vector comprises a *NeoSTOP* cassette encased by *loxP* sites and exon 11 of the *Shp2* gene with the C483S mutation. Similarly, the *Grb2*^{YF} vector contains a *NeoSTOP* cassette flanked by *loxP* sites and exon 3 of the *Grb2* gene with the Y209F mutation. These targeting constructs, once linearized, were introduced into C57BL/6 and 129 hybrid ES cells via electroporation. *Shp2*^{YF} recombinant clones were screened by Southern blot analysis with 5' and 3' external probes after restriction digestion with *EvoR V*, while *Grb2*^{YF}and *Shp2*^{CS} clones were identified by long-range PCR before being injected into C57BL/6 blastocysts. Chimeras were further bred with C57BL/6 mice for germline transmission, verified through PCR genotyping with specific primers for each mutation: *Grb2*^{YF} *F*: 5'-TGGGGGTCAAAGTCAAAGAG -3'; *R*: 5'-CGGAGGGAGTGAGGTATGAG -3' (wild type: 179 bp, mutant: 270 bp), *Shp2*^{YF} *F*: 5'-AAAAAGAGGCTGCTCTGCAC -3'; *R*: 5'-TCTGCAGAATGAGGGAGGAC -3' (wild type: 195 bp, mutant: 250 bp) and *Shp2*^{YF} *F*: 5'-TGGGAAGACAGACTGCAGTC-3'; *R*: 5'-GAAGGAGCACCTGCCTGTTA-3' (wild type: 180 bp, mutant: 210 bp). The Neo cassette was subsequently excised by breeding with an *EIIa-cre* transgenic line (stock number 003724, Jackson Laboratory, Bar Harbor, ME).

Database Analysis

The cumulative references for each phosphorylation site, derived from both low-throughput (LTP) and high-throughput (HTP) experiments, were sourced from the PhosphositePlus database (*phosphosite.org*) and graphically represented along the amino acid sequence. The expression data for lens genes from embryonic days 10.5 to 12.5 was extracted from the iSyTE database (*https://research.bioinformatics.udel.edu/iSyTE/ppi/expression.php*) and visualized as heatmaps to illustrate the variations in expression levels over time.

Histology and immunohistochemistry

Histology and immunohistochemistry were performed on the paraffin and cryosections as previously described (Carbe *et al*., 2012; Carbe and Zhang, 2011). For hematoxylin and eosin (H&E) staining, 10 μM paraffin sections underwent deparaffinization with histosol wash, rehydration through decreasing concentrations of ethanol solutions, and final washing in water. The slides were immersed in hematoxylin for 3 minutes, followed by a 10-15 minute wash with tap water. Subsequently, they were decolorized with 1% acid alcohol for 30 seconds before treatment with eosin for 1 minute. Samples were dehydrated through increasing ethanol concentrations, transferred to histosol, and mounted using a Permount mounting medium. For X-gal staining, the mouse lacrimal gland was exposed by dissecting away the periocular skin and fixed in 4% paraformaldehyde at 4 °C overnight.

The antibodies used are phospho-ERK1/2 (#4370), phospho-mTOR (#2971), phospho-S6 (#5364), phospho-Shc (#2434), phospho-MEK1/2 (#2338), phospho-Smad1/5/9 (#13820), LEF1 (#2230), Cleaved caspase3 (#9662), cyclin D1 (#2926, discontinued), cyclin-D1 (#2978), cyclin-D3(#2936), N-cadherin (#13116) (all from Cell Signaling Technology), Fibronectin (AB2033) (from Millipore), Foxe3 (#377465), Jag1(#6011), Maf (#7866) (all from Santa Cruz), E-cadherin (#610181) and Ki67

(#550609) (both from BD Pharmingen), GFP (GFP-1010) (from Aves Labs), p57 (#75947) (from Abcam), Prox1 (PRB-238C) and Pax6 (PRB-278P) (both from Covance), Sox2 (14-9811-82) (from Thermo Fisher). Antibodies against α- and γ-crystallins were kindly provided by Sam Zigler (National Eye Institute, Bethesda, MD).

Phospho-ERK, phopho-MEK, phospho-mTOR, phosphor-Shc and phospho-Akt staining was amplified using a Tyramide Signal Amplification kit (TSATM Plus System, PerkinElmer Life Sciences, Waltham, MA). Alexa Fluor secondary antibodies and Alexa Fluor 488 phalloidin (A-12379) were ordered from Invitrogen. TUNEL staining was performed following the in situ cell death detection kit (Roche Applied Science, Indianapolis, IN). All commercial antibodies were validated by vendors. At least three embryos of each genotype were stained for each marker.

Cell culture and western blot

Primary mouse embryonic fibroblast (MEF) cells were generated according to a previously published protocol and cultured in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% FBS and 1% penicillin-streptomycin. Adenovirus expressing Cre recombinase (Ad-cre) (Gene Transfer Vector Core, University of Iowa, IA.) were applied to MEF cells carrying flox alleles for 5 days to achieve gene deletion, while adenovirus expressing GFP (Ad-GFP) served as a control treatment. To assess growth factor responses, MEF cells were starved overnight and then treated with either FGF2 (50 ng/μl) or PDGFA (20 ng/μl) (from R&D systems) for 5 mins. Cells were immediately washed with cold PBS and harvested in ice-cold CelLytic buffer (C2978, Sigma-Aldrich, St.Louis, MO) supplemented with protease and phosphatase inhibitor cocktails (Pierce, Rockford, IL). Extracted proteins were subjected to standard western blot analysis. The antibodies used include ERK1/2 (#4695), phospho-Shp2 (#15543), phospho-Crk(#3491), phospho-Gab1(#3234), phopho-Frs2 (#3861), phospho-Shc (#2434) (all from Cell Signaling Technology), along with phospho-ERK1/2 (#7383) from Santa Cruz Biotechnology.

Quantification and Statistical Analysis

The relative lens sizes were measured using Image J and normalized against the control. The anterior/posterior lens ratio was determined by comparing the length of the anterior epithelium, as measured in Image J, to the length of the posterior lens boundary. The percentage of TUNEL and cleaved-caspase3 positive cells were normalized against the total number of DAPI positive cells. Statistical analysis was performed using GraphPad Prism 7. Sample sizes were not predetermined. Data represent mean ± s.d. Statistical differences between two groups were assessed using an unpaired, two-tailed t-test, while comparisons among three or more groups employed one-way ANOVA followed by Tukey's multiple comparison test.

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Reviewer #1 (Public review):

Summary:

This manuscript uses the eye lens as a model to investigate basic mechanisms in the Fgf signaling pathway. Understanding Fgf signaling is of broad importance to biologists as it is involved in the regulation of various developmental processes in different tissues/organs and is often misregulated in disease states. The Fgf pathway has been studied in embryonic lens development, namely with regards to its involvement in controlling events such as tissue invagination, vesicle formation, epithelium proliferation, and cellular differentiation, thus making the lens a good system to uncover the mechanistic basis of how the modulation of this pathway drives specific outcomes. Previous work has suggested that proteins, other than the ones currently known (e.g., the adaptor protein Frs2), are likely involved in Fgfr signaling. The present study focuses on the role of Shp2 and Shc1 proteins in the recruitment of Grb2 in the events downstream of Fgfr activation.

Strengths:

The findings reveal that the juxtamembrane region of the Fgf receptor is necessary for proper control of downstream events such as facilitating key changes in transcription and cytoskeleton during tissue morphogenesis. The authors conditionally deleted all four Fgfrs in the mouse lens that resulted in molecular and morphological lens defects, most importantly, preventing the upregulation of the lens induction markers Sox2 and Foxe3 and the apical localization of F-actin, thus demonstrating the importance of Fgfrs in early lens development, i.e. during lens induction. They also examined the impact of deleting Fgfr1 and 2, on the following stage, i.e. lens vesicle development, which could be rescued by expressing constitutively active KrasG12D. By using specific mutations (e.g. Fgfr1ΔFrs lacking the Frs2 binding domain and Fgfr2LR harboring mutations that prevent binding of Frs2), it is demonstrated that the Frs2 binding site on Fgfr is necessary for specific events such as morphogenesis of lens vesicle. Further, by studying Shp2 mutations and deletions, the authors present a case for Shp2 protein to function in a context-specific manner in the role of

an adaptor protein and a phosphatase enzyme. Finally, the key surprising finding from this study is that downstream of Fgfr signaling, Shc1 is an important alternative pathway - in addition to Shp2 - involved in the recruitment of Grb2 and in the subsequent activation of Ras. The methodologies, namely, mouse genetics and state-of-the-art cell/molecular/biochemical assays are appropriately used to collect the data, which are soundly interpreted to reach these important conclusions. Overall, these findings reveal the flexibility of the Fgf signaling pathway and its downstream mediators in regulating cellular events. This work is expected to be of broad interest to molecular and developmental biologists.

Weaknesses:

A weakness that needs to be discussed is that Le-Cre depends on Pax6 activation, and hence its use in specific gene deletion will not allow evaluation of the requirement of Fgfrs in the expression of Pax6 itself. But since this is the earliest Cre available for deletion in the lens, mentioning this in the discussion would make the readers aware of this issue. Referring to Jag1 among "lens-specific markers" (page 5) is debatable, suggesting changing to the lines of "the expected upregulation of Jag1 in lens vesicle". The Abstract could be modified to clearly convey the existing knowledge gap and the key findings of the present study. As it stands now, it is a bit all over the place. Some typos in the manuscript need to be fixed, e.g. "...yet its molecular mechanism remains largely resolved" - unresolved? "...in the development lens" - in the developing lens? In Figure 4 legend, "(B) Grb2 mutants Grb2 mutants displayed...", etc.

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Reviewer #2 (Public review):

Summary:

I have reviewed a manuscript submitted by Wang et al., which is entitled "Shc1 cooperates with Frs2 and Shp2 to recruit Grb2 in FGF-induced lens development". In this paper, the authors first examined lens phenotypes in mice with Le-Cre-mediated knockdown (KD) of all four FGFR (FGFR1-4), and found that pERK signals, Jag1, and foxe3 expression are absent or drastically reduced, indicating that FGF signaling is essential for lens induction. Next, the authors examined lens phenotypes of FGFR1/2-KD mice and found that lens fiber differentiation is compromised and that proliferative activity and cell survival are also compromised in lens epithelium. Interestingly, Kras activation rescues defects in lens growth and lens fiber differentiation in FGFR1/2-KD mice, indicating that Ras activation is a key step for lens development. Next, the authors examined the role of Frs2, Shp2, and Grb2 in FGF signaling for lens development. They confirmed that lens fiber differentiation is compromised in FGFR1/3-KD mice combined with Frs2-dysfunctional FGFR2 mutants, which is similar to lens phenotypes of Grb2-KD mice. However, lens defects are milder in mice with Shp2YF/YF and Shp2CS mutant alleles, indicating that the involvement of Shp2 is limited for the Grb2 recruitment for lens fiber differentiation. Lastly, the authors showed new evidence on the possibility that another adapter protein, Shc1, promotes Grb2 recruitment independent of Frs2/Shp2-mediated Grb2 recruitment.

Strengths:

Overall, the manuscript provides valuable data on how FGFR activation leads to Ras activation through the adapter platform of Frs2/Shp2/Grb2, which advances our understanding of complex modification of the FGF signaling pathway. The authors applied a genetic approach using mice, whose methods and results are valid to support the conclusion. The discussion also well summarizes the significance of their findings.

Weaknesses:

The authors eventually found that the new adaptor protein Shc1 is involved in Grb2 recruitments in response to FGF receptor activation. however, the main data for Shc1 are histological sections and statistical evaluation of lens size. So, my major concern is that the authors need to provide more detailed data to support the involvement of Shc1 in Grb2 recruitment of FGF signaling for lens development.

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Reviewer #3 (Public review):

Summary:

The manuscript entitled "Shc1 cooperates with Frs2 and Shp2 to recruit Grb2 in FGF-induced lens development" by Wang et al., investigates the molecular mechanism used by FGFR signaling to support lens development. The lens has long been known to depend on FGFR signaling for proper development. Previous investigations have demonstrated that FGFR signaling is required for embryonic lens cell survival and for lens fiber cell differentiation. The requirement of FGFR signaling for lens induction has remained more controversial as deletion of both Fgfr1 and Fgfr2 during lens placode formation does not prevent the induction of definitive lens markers such as FOXE3 or αA-crystallin. Here the authors have used the Le-Cre driver to delete all four FGFR genes from the developing lens placode demonstrating a definitive failure of lens induction in the absence of FGFR signaling. The authors focused on FGFR1 and FGFR2, the two primary FGFRs present during early lens development, and demonstrated that lens development could be significantly rescued in lenses lacking both FGFR1 and FGFR2 by expressing a constitutively active allele of KRAS. They also showed that the removal of pro-apoptotic genes Bax and Bak could also lead to a substantial rescue of lens development in lenses lacking both FGFR1 and FGFR2. In both cases, the lens rescue included both increased lens size and the expression of genes characteristic of lens cells.

Significantly the authors concentrated on the juxtamembrane domain, a portion of the FGFRs associated with FRS2. Previous investigations have demonstrated the importance of FRS2 activation for mediating a sustained level of ERK activation. FRS2 is known to associate both with GRB2 and SHP2 to activate RAS. The authors utilized a mutant allele of Fgfr1, lacking the entire juxtamembrane domain (Fgfr1ΔFrs), and an allele of Fgfr2 containing two-point mutations essential for Frs2 binding (Fgfr2LR). When combining three floxed alleles and leaving only one functional allele (Fgfr1ΔFrs or Fgfr2LR) the authors got strikingly different phenotypes. When only the Fgfr1ΔFrs allele was retained, the lens phenotype matched that of deleting both Fgfr1 and Fgfr2. However, when only the Fgfr2LR allele was retained the phenotype was significantly milder, primarily affecting lens fiber cell differentiation, suggesting that something other than FRS2 might be interacting with the juxtamembrane domain to support FGFR signaling in the lens. The authors also deleted Grb2 in the lens and showed that the phenotype was similar to that of the lenses only retaining the Fgfr2LR allele, resulting in a failure of lens fiber cell differentiation and decreased lens cell survival. However, mutating the major tyrosine phosphorylation site of GRB2 did not affect lens development. The author additionally investigated the role of SHP2 lens development by making by either deleting SHP2 or by making mutations in the SHP2 catalytic domain. The deletion of the SHP2 phosphatase activity did not affect lens development as severely as the total loss of SHP2 protein, suggesting a function for SHP2 outside of its catalytic activity. Although the loss of Shc1 alone has only a slight effect on lens size and pERK activation in the lens, the authors showed that the loss of Shc1 exacerbated the lens phenotype in lenses

lacking both Frs2 and Shp2. The authors suggest that SHC1 binds to the FGFR juxtamembrane domain allowing for the recruitment of GRB2 independently of FRS2.

Strengths:

(1) The authors used a variety of genetic tools to carefully dissect the essential signals downstream of FGFR signaling during lens development.

(2) The authors made a convincing case that something other than FRS2 binding mediates FGFR signaling in the juxtamembrane domain.

(3) The authors demonstrated that despite the requirement of both the adaptor function and phosphatase activity of SHP2 are required for embryonic survival, neither of these activities is absolutely required for lens development.

(4) The authors provide more information as to why FGFR loss has a phenotype much more severe than the loss of FRS2 alone during lens development.

(5) The authors followed up their work analyzing various signaling molecules in the context of lens development with biochemical analyses of FGF-induced phosphorylation in murine embryonic fibroblasts (MEFs).

(6) In general, this manuscript represents a Herculean effort to dissect FGFR signaling in vivo with biochemical backing with cell culture experiments in vitro.

Weaknesses:

(1) The authors demonstrate that the loss of FGFR1 and FGFR2 can be compensated by a constitutive active KRAS allele in the lens and suggest that FGFRs largely support lens development only by driving ERK activation. However, the authors also saw that lens development was substantially rescued by preventing apoptosis through the deletion of BAK and BAX. To my knowledge, the deletion of BAK and BAX should not independently activate ERK. The authors do not show whether ERK activation is restored in the BAK/BAX deficient lenses. Do the authors suggest the FGFR3 and/or FGFR4 provide sufficient RAS and ERK activation for lens development when apoptosis is suppressed? Alternatively, is it the survival function of FGFR-signaling as much as a direct effect on lens differentiation?

(2) The authors make the argument that deleting all four FGFRs prevented lens induction but that the deletion of only FGFR1 and FGFR2 did not. Part of this argument is the retention of FOXE3 expression, αA-crystallin expression, and PROX1 expression in the FGFR1/2 double mutants. However, in Figure 1E, and Figure 1F, the staining of the double mutant lens tissue with FOXE3, αA-crystallin, and PROX1 is unconvincing. However, the retention of FOXE3 expression in the FGFR1/FGFR2 double mutants was previously demonstrated in Garcia et al 2011. Also, there needs to be an enlargement or inset to demonstrate the retention of pSMAD in the quadruple FGFR mutants in Figure 1D.

(3) Do the authors suggest that GRB2 is required for RAS activation and ultimately ERK activation? If so, do the authors suggest that ERK activation is not required for FGFR-signaling to mediate lens induction? This would follow considering that the GRB2 deficient lenses lack a problem with lens induction.

(4) The increase in p-Shc is only slightly higher in the Cre FGFR1f/f FGFR2r/LR than in the FGFR1f/Δfrs FGFR2f/f. Can the authors provide quantification?

(5) The authors have not shown directly that Shc1 binds to the juxtamembrane region of either Fgfr1 or Fgfr2.

(6) The authors have used the Le-Cre strain for all of their lens deletion experiments. Previous work has documented that the Le-Cre transgene can cause lens defects independent of any floxed alleles in both homozygous and hemizygous states on some genetic backgrounds (Dora et al., 2014 PLoS One 9:e109193 and Lam et al., Human Genomics 2019 13(1):10. Are the controls used in these experiments Le-Cre hemizygotes?

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