Krox20 Regulates Endothelial Nitric Oxide Signaling in Aortic Valve Development and Disease
Gaelle Odelin, Emilie Faure, Corinne Maurel-Zaffran, Stéphane Zaffran

To cite this version:
Gaelle Odelin, Emilie Faure, Corinne Maurel-Zaffran, Stéphane Zaffran. Krox20 Regulates Endothelial Nitric Oxide Signaling in Aortic Valve Development and Disease. Journal of Cardiovascular Development and Disease, MDPI, 2019, 6 (4), pp.39. 10.3390/jcdd6040039. hal-02441235

HAL Id: hal-02441235
https://hal-amu.archives-ouvertes.fr/hal-02441235
Submitted on 15 Jan 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Distributed under a Creative Commons Attribution 4.0 International License
Krox20 Regulates Endothelial Nitric Oxide Signaling in Aortic Valve Development and Disease

Gaëlle Odelin \(^1\), Emilie Faure \(^1\), Corinne Maurel-Zafran \(^2\) and Stéphane Zafran \(^1,\ast\)

\(^1\) Aix Marseille University, INSERM, Marseille Medical Genetics, U1251, 13005 Marseille, France; gaelle.odelin@univ-amu.fr (G.O.); emilie.faure@univ-amu.fr (E.F.)

\(^2\) Aix Marseille University, CNRS UMR7288, IBDM, 13009 Marseille, France; corinne.maurel-zaffran@univ-amu.fr

\ast\ Correspondence: stephane.zafran@univ-amu.fr; Tel.: +33-491-324936

Received: 10 September 2019; Accepted: 31 October 2019; Published: 2 November 2019

Abstract: Among the aortic valve diseases, the bicuspid aortic valve (BAV) occurs when the aortic valve has two leaflets (cusps), rather than three, and represents the most common form of congenital cardiac malformation, affecting 1–2% of the population. Despite recent advances, the etiology of BAV is poorly understood. We have recently shown that Krox20 is expressed in endothelial and cardiac neural crest derivatives that normally contribute to aortic valve development and that lack of Krox20 in these cells leads to aortic valve defects including partially penetrant BAV formation. Dysregulated expression of endothelial nitric oxide synthase (Nos3) is associated with BAV. To investigate the relationship between Krox20 and Nos3 during aortic valve development, we performed inter-genetic cross. While single heterozygous mice had normal valve formation, the compound Krox20\(^{+/−}\); Nos3\(^{+/−}\) mice had BAV malformations displaying an in vivo genetic interaction between these genes for normal valve morphogenesis. Moreover, in vivo and in vitro experiments demonstrate that Krox20 directly binds to Nos3 proximal promoter to activate its expression. Our data suggests that Krox20 is a regulator of nitric oxide in endothelial-derived cells in the development of the aortic valve and concludes on the interaction of Krox20 and Nos3 in BAV formation.

Keywords: cardiac development; Krox20; nitric oxide synthase; heart; mouse; bicuspid aortic valve

1. Introduction

The bicuspid aortic valve (BAV) is a congenital defect found in 1–2% of the population and is the most common valve malformation [1]. A bicuspid valve is comprised of two rather than three semilunar leaflets (cusps). In humans, most BAVs result from fusion of either the right-coronary and left-coronary leaflets (R-L) or the right-coronary and non-coronary leaflets (R-N) [2]. BAV formation is considered to be an abnormal fusion of the aortic valve leaflets occurring during development [3,4]. Early valve development is a complex process involving the interplay of multiple cell lineages. In the mouse, valve morphogenesis occurs around the embryonic day (E) 9.5 (3 weeks gestation in human) with the formation of endocardial cushions in the outflow tract (OFT) and atrio-ventricular canal (AVC) regions. Development of endocardial cushions initiates with expansion of the cardiac jelly, the extracellular matrix (ECM) between the myocardium and endocardium, followed by endothelial-to-mesenchymal transformation (EndMT) of endocardial cells [5,6]. In the OFT, part of mesenchymal cells colonizing the cushions derive from the neural crest [7,8]. Thus, both endocardial and neural crest derivatives contribute to the development of the aortic and pulmonary valves. At birth, valves continue to develop through apoptosis and remodeling of the ECM [9]. The actual processes that lead to abnormal valvulogenesis and the formation of a BAV are still unclear. However, recent studies have proposed that ECM is crucial for normal development of the aortic valve leaflets [10–12].
Neural crest populating the OFT cushions are important for ECM production and late remodeling [13]. We have recently identified a sub-population of the neural crest that contribute to arterial valve development [4]. Neural crest cells are essential for positioning the OFT cushions and patterning the arterial valve leaflets [14]. It is also possible that the valvular endothelium is responsible for transducing luminal events, such as hemodynamic shear stress and generating signals that regulates the developmental program of valvulogenesis. Expression and activity of endothelial nitric oxide synthase (Nos3) in aortic endothelial cells are controlled by hemodynamic shear stress [15]. Endothelial Nos3 plays an important role in arterial valve development, as shown by the presence in Nos3−/− mice of partially penetrant R-N BAVs [16] and a study has presented a significant decrease in Nos3 protein amount in BAV compared to tricuspid aortic valve (TAV) human tissues [17]. More recently, second heart field cells have been proposed to contribute to intercalated cushion formation from which the non-coronary leaflet arises [18–20]. These studies have indicated that the distribution of second heart field derived cells is affected in Nos3−/− and that Notch signaling plays a critical role in the formation of the intercalated cushion. Interestingly, the nitric oxide and Notch signaling pathways genetically interact in vivo [21]. Therefore, anomalous in coordination of these distinct cell types during arterial valve formation might be involved in BAV.

We have recently shown that the transcription factor Krox20 (also called Egr2) plays an important role in aortic valve formation [4,12,22]. Indeed, Krox20−/− mice develop aortic insufficiency associated with partially penetrant R-N BAVs. Similar defect is observed when Krox20 expression is inactivated in neural crest or endothelial lineages indicating that Krox20 functions in different cell types during valve development. BAV has also been found in mice deficient in Nkx2-5, Hoxa1, Gata5, Gata6, slit/robo, Notch1, and Nos3 [16,23–27]. Recently, BAV phenotype in Nos3−/− has been associated to a small deviation in the distribution of distinct valvular cell types [20]. Here, we show that Krox20 and Nos3 genetically interact in vivo as compound heterozygous Krox20;Nos3 mutant mice display BAV malformations whereas single heterozygous mutant mice have normal aortic valves. We further demonstrate that Krox20 regulates Nos3 expression by direct activation of Nos3 proximal promoters during arterial valve development. We used aortic valve interstitial cells (AVICs) in vitro model to confirm this activation. Conversely, we found normal contribution of Krox20-Cre labeled cells in Nos3 mutant mice. Our study thus provides new mechanistic insights into the regulation of nitric oxide activity during the formation of the aortic valve and disease such as BAV.

2. Materials and Methods

2.1. Mice

All animal procedures were carried out under protocols approved by a national appointed ethical committee for animal experimentation (Ministère de l’Éducation Nationale, de l’Enseignement Supérieur, de la Recherche et de l’innovation; APAFIS #2931-2015113016228473) and conformed to Directive 2010/63/EU of the European Parliament. Genotyping of Nos3+/− and Krox20+/− mice was performed as previously described [28,29]. Compound mutant mice were obtained by intercross Krox20+/− with Nos3+/− mice. The Krox20Cre and Krox20lox alleles and Tie2-cre, Wnt1-cre, −31/−23.5 Krox20/LacZ, and Gt(Rosa)26Sor(lacZ)tm1(CAG-tdTomato)Hze (Rosa tedTomato) transgenic mice have been previously described [4].

2.2. Real-Time qRT-PCR

The OFT and aortic valve leaflets were manually dissected from E13.5 and 18.5 mutant embryos. After genotyping, samples from 5 mice of the same genotype were used and RNA isolated using NucleoSpin RNA/Protein kit (Macherey-Nagel, Düren, Germany) per manufacturer’s instructions. Reverse transcriptions were performed by using first strand cDNA synthesis kit (Roche, Basel, Switzerland) per manufacturer’s instructions. LightCycler 480 SYBR Green I Master mix (Roche, Basel, Switzerland) was used for quantitative real-time qRT-PCR analysis with a LightCycler
480 (Roche, Basel, Switzerland) following the manufacturer’s instructions. Gene-specific primers used in this study are listed in Table 1. Each experiment was performed in triplicate for each genotype. Samples were normalized to endogenous housekeeping gene (TBP gene). Level changes were calculated by the comparative cycle threshold (ΔΔCT) method. Normalized expression levels in the control were set to 1.0 for each gene.

2.3. Histological and Immunostaining

Staged mouse hearts were fixed 1 h in 4% paraformaldehyde, washed in phosphate buffered saline, and then paraffin embedded, sectioned at 8-µm, and then processed as previously described [4]. Sections were stained with hematoxylin & eosin (H & E) (Sigma-Aldrich, St. Louis, MO, USA) according to the manufacturer’s instruction. X-gal staining was performed as previously described [4]. Sections or whole-mount embryos were examined using an Axio Zoom. V16 (Zeiss, Oberkochen, Germany) was photographed with an Axiocam digital camera (Zen 2011, Zeiss).

Polyclonal anti-Nos3 antibody was purchased from Microm (Rabbit, 1:50) and used on OCT embedded and cryo-sectioned fixed tissue. The anti-Pecam (CD31, Rat, 1:100) antibody was purchased from BD-Pharmingen (BD Biosciences, San Jose, CA, USA). The Alexa fluorescent-conjugated antibody (Life Technologies, Thermo Fischer Scientific, Carlsbad, CA, USA) was used at 1:500. Images were taken with DM5000 microscope with LAS software (Leica Microsystems, Wetzlar, Germany). For each experiment, a minimum of 3 embryos of each genotype was scored.

2.4. DNA-Binding Assay

For electrophoretic mobility shift assays (EMSA), the Krox20 protein was produced with the TNT (T7)-coupled in vitro transcription/translation system (Promega, Madison, WI, USA) as previously described [12]. The Probes used for KROX binding corresponded to the -513 and -136 KROX binding sites (Table 1). For EMSA, 3 or 9-µL of in vitro translated Krox20 protein were mixed in 20-µL binding reaction containing 20% glycerol, 50 mM Tris-HCl pH 7.5, 250 M NaCl, 2.5 mM EDTA, 2.5 mM DTT, and 5 mM MgCl2. The reactions were incubated on ice for 10 min before the addition of 10,000 counts/min [α-32P]dATP-labeled oligonucleotides. Mixtures were further incubated on ice for 30 min before being loaded on a 0.5× Tris-boric acid-EDTA buffer-4% polyacrylamide gel, and then electrophoresis was carried out at 250 V for 1.5 h at 4 °C. The gel was dried and exposed to a Kodak autoradiography film overnight at −80 °C.

2.5. Chromatin Immunoprecipitation (ChIP)

For ChIP experiments, hearts at stage E13.5 were collected and dissected in cold PBS. Freshly dissected OFT and left ventricles were lysed in trypsin solution and homogenized in cold PBS containing a protease inhibitor cocktail (Roche, Basel, Switzerland). Tissues were fixed in 1% formaldehyde for 15 min at RT and 40 min at 4 °C on a shaking platform. Formaldehyde cross-linking was stopped by adding Glycine to a final concentration of 0.125 M and incubated for 5 min at RT. Tissues were then lysed in lysis buffer (0.5% NP-40, 5 mM PIPES pH 8.0, 85 mM KCl) containing a protease inhibitor cocktail and then homogenized using dounce homogenizer. Nuclei lysates were collected, lysed in Nuclei lysis buffer (1% SDS, 50 mM Tris-HCl pH 8.0, 10 mM EDTA) containing a protease inhibitor cocktail and then sonicated to obtain chromatin fragments <1 kb. Chromatin was diluted 1:10 with ChIP Solution (1% Triton-X100, 0.01% SDS, 1.2 mM EDTA, 167 mM NaCl, and 16.7 mM Tris-HCl pH 8.0) containing protease inhibitor cocktail and precleared with 50% salmon sperm DNA/protein-A sepharose slurry (Sigma-Aldrich, St. Louis, MO, USA). Chromatin fragments were incubated with one of the following antibodies at 4 °C on a rotating platform: 5 µg of rabbit polyclonal anti-Histone H3 (Millipore, Burlington, MA, USA) and 10 µg of rabbit polyclonal anti-Krox20 (Covance, Princeton, NJ, USA). Magna ChIP™ Protein A Magnetic Beads (Millipore) (25 µL) were then added and incubated for 1 h at 4 °C. Immunoprecipitated pellets were washed once with a “low salt” solution (0.1% SDS, 1% Triton-X100, 2 mM EDTA, 20 mM Tris-HCl (pH 8.0) and 150 mM NaCl), once with a “high salt”
solution (0.1% SDS, 1% Triton-X100, 2 mM EDTA, 20 mM Tris-HCl (pH 8.0), and 500 mM NaCl) and
once with 0.25 M LiCl, 1% Nonidet P-40, 1% sodium deoxycholate, 1 mM EDTA and 10 mM Tris-HCl,
pH 8.0 and twice 10 mM Tris-HCl (pH 8.0) and 1 mM EDTA. Chromatin was eluted from the beads
with 250 µL 1% SDS and 0.1 M NaHCO₃. Crosslinks were reversed for 4 h at 65 °C after addition
of 20 µL of 5 M NaCl. Samples were supplemented with 20 µL of 1 M Tris-HCl (pH 7.0), 10 µL of
0.5 M EDTA, and 40 µg of proteinase K and incubated for 1 h at 45 °C. DNA was then recovered
by phenol/chloroform extraction and ethanol precipitation. For total DNA samples (Input), aliquots
responding to 1:10 dilution of the amount lysate used in the immunoprecipitation were processed
along the rest of samples at the step of reversing the crosslink. DNA samples were quantified using
the NanoDrop ND-1000 spectrophotometer (NanoDrop Technologies LLC, Wilmington, DE, USA).
The presence of individual Krox20 consensus binding site on Nos3 promoters was analyzed by qPCR
using LightCycler 480 SYBR Green I Master mix (Roche, Basel, Switzerland) on a LightCycler480
(Roche, Basel, Switzerland) following manufacturer’s instructions. The Histone H3 antibody was
used as positive control of immunoprecipitation and a set of primers for Nos3 corresponding to a
coding region without consensus binding site were used as negative control. Relative quantities of
each chromatin bound fragment expression were calculated using the comparative cycle threshold
(ΔΔCT) method and were normalized to the amount of input DNA (in the same amount of chromatin
before immunoprecipitation, quantified with the same PCR), and to the level of TBP gene. Primers
used in this experiment were listed in Table 1.

2.6. Luciferase Assay

The Krox20 expression plasmid (CMV-Krox20) has been previously described [12]. The Nos3
constructs were derived from the pXP2 reporter constructs (kindly provided by Pr. Mona Nemer) [24].
The pXP2-Nos3-1522 and pXP2-Nos3-265 reporter constructs contain a segment extending from the bp
+1 to −1522, and bp +1 to −265 of the Nos3 proximal promoter cloned upstream the luc gene in the
pXP2. To generate the mutated Krox20 reporter constructs, one consensus Krox20 binding site in the
Nos3 promoter (bp +1 to −1522) was changed by PCR (K2; GTGTGGGAC to mutated K2; GTGagtcAC).
Cos7 cells were transiently co-transfected using the Promofectin (Promocell, Heidelberg, Germany)
according to the manufacturer’s instructions with 200 ng of indicated constructs and 10 ng of control
pXP22 vector and various amounts (0 ng, 50 ng, 150 ng, and 300 ng) of CMV-Krox20 expression vector
or of CMV-control. Then, 24 h after transfection, cells were lysed, and luciferase activity was measured
using the Dual-Luciferase® Reporter Assay System (Promega, Madison, WI, USA). All the transfection
experiments were done in triplicate and repeated at least three times. Luciferase activities were read
using a GloMax® Multi Microplate Multimode Reader and were normalized to Renilla luciferase to
compensate for variations in transfection efficiency. Results are presented as fold activation of the
relative luciferase activities over the CMV control.

2.7. Rat Aortic Valve Interstitial Cell Culture and Transfection

Rat aortic valve interstitial cells (AVICS) were collected from aortic valve of 10-week-old Sprague
Dawley females. AVICS were isolated as previously described by Gould et al., 2010 [30]. Briefly,
valves leaflets were isolated and submitted to collagenase type II digestion. To isolate AVIC, leaflets were
cut into small pieces and placed into collagenase solution during 8 h at 37 °C. After isolation, AVICS were
cultured in DMEM-GlutamaX (Invitrogen, Thermo Fisher Scientific, Carlsbad, CA, USA) supplemented
with 10% FCS (Invitrogen). AVICS were used between passage 3 and 7 for this study. AVIC were
seeded into 6-well plates at 200,000 cells of density and 500 ng of CMV-Krox20 or CMV-GFP were
transfected using Promofectin (Promocell, Heidelberg, Germany). Cells were lysed 24 h, 48 h,
or 72 h after transfection, and RNA was isolated using NucleoSpin RNA/Protein kit (Macherey-Nagel,
Düren, Germany).


Table 1. Primers qPCR, ChIP and EMSA.

<table>
<thead>
<tr>
<th>Name</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alk2</td>
<td>Forward 5′- GAAGATGACGTGTAAGACCCC - 3′</td>
</tr>
<tr>
<td></td>
<td>Reverse 5′- ATAAGGCCAATTCCAGGTG - 3′</td>
</tr>
<tr>
<td>Gata5</td>
<td>Forward 5′- CTAATCTATCGACATTCCCTGCG - 3′</td>
</tr>
<tr>
<td></td>
<td>Reverse 5′- CAGTATGGCACTGGGCGACAG - 3′</td>
</tr>
<tr>
<td>NOS3</td>
<td>Forward 5′- CCTAGAGCAGACGCCACTG - 3′</td>
</tr>
<tr>
<td></td>
<td>Reverse 5′- GTTGTAGGGGCTGCATTTT - 3′</td>
</tr>
<tr>
<td>Notch1</td>
<td>Forward 5′- CAAGAGGCTTGAGATGCTCC - 3′</td>
</tr>
<tr>
<td></td>
<td>Reverse 5′- AAGGATGAGTCTGCCACAT - 3′</td>
</tr>
<tr>
<td>Hey1</td>
<td>Forward 5′- ATGCTCAGATAACGGGCAAC - 3′</td>
</tr>
<tr>
<td></td>
<td>Reverse 5′- CACCTGAAAATGCTGCACAC - 3′</td>
</tr>
<tr>
<td>Hey2</td>
<td>Forward 5′- TGAGAGTGGGTGGTTCTCT - 3′</td>
</tr>
<tr>
<td></td>
<td>Reverse 5′- AAGAGCATGGGCATCAAAGT - 3′</td>
</tr>
<tr>
<td>TBP</td>
<td>Forward 5′- CCCACAATCCCTCCATTCT - 3′</td>
</tr>
<tr>
<td></td>
<td>Reverse 5′- GCAGGAGTGGGTGGCTCAT - 3′</td>
</tr>
<tr>
<td>NOS3 (rat)</td>
<td>Forward 5′- GCAGTAACGACGGGCAAGGA - 3′</td>
</tr>
<tr>
<td></td>
<td>Reverse 5′- ACGGCCACGGCTGCTCC - 3′</td>
</tr>
<tr>
<td>TBP (rat)</td>
<td>Forward 5′- ACCCCACAATCTCTCCATTC - 3′</td>
</tr>
<tr>
<td></td>
<td>Reverse 5′- GGGTCATAGGAGTGGTG - 3′</td>
</tr>
<tr>
<td>NOS – postATG</td>
<td>Forward 5′- CTGGGTATGAGGCTGTC - 3′</td>
</tr>
<tr>
<td></td>
<td>Reverse 5′- CTGGGTATGAGGCTGCTTG - 3′</td>
</tr>
<tr>
<td>NOS3-K1</td>
<td>Forward 5′- CTCTATCTGACATGGGTC - 3′</td>
</tr>
<tr>
<td></td>
<td>Reverse 5′- TCTATCCAGATCTTACCTTC - 3′</td>
</tr>
<tr>
<td>NOS3-K2</td>
<td>Forward 5′- TCGGTTCCACACTCATTGCTGC - 3′</td>
</tr>
<tr>
<td></td>
<td>Reverse 5′- CCTTTCAATGGGAAGCCAAGGGA - 3′</td>
</tr>
</tbody>
</table>

**EMSA**

| K1       | Wild-type 5′- tGAGTCATGGCTGGTGGTGGTTTCAGGAAAATTGAGAT - 3′ |
|          | Mutated 5′- tGAGTCATGGCTGGTGGTGGTTTCAGGAAAATTGAGAT - 3′   |
| K2       | Wild-type 5′- tCCTGTCCCATTGTGTGGGAAGCGGGCGGGCGGCG - 3′   |
|          | Mutated 5′- tCCTGTCCCATTGTGTGGGAAGCGGGCGGGCGGCG - 3′    |

3. Results

3.1. Expression of Genes Associated with BAVs

We have previously reported that Krox20 is expressed in valvular cell populations contributing to arterial valve development including endothelial and neural crest derivatives [4,12]. Consistently, Krox20−/− mice are predisposed to develop a BAV (27%) (Figure 1A–C). Interestingly, conditional deletion of Krox20 in the endothelial-, or neural crest cell-lineage led to BAV phenotype indicating that Krox20 is required in both lineages (Figure 1A). Several studies have shown that defective function of Notch1, Gata5, Alk2, and Nos3 leads to BAV development [16,23–25]. To determine if the transcription factor Krox20 is playing a role in the activation of these genes, we analyzed their transcriptional levels in Krox20−/−. Expression of Alk2 and Gata5 are unchanged in Krox20−/− aortic valves (Figure 1D). However, a significant reduction of the mRNA levels of Nos3 is observed in Krox20 mutant embryos at
E18.5 (Figure 1D). Interestingly, expression of Notch1, which is regulated by Nos3 signaling in aortic valve disease [21], is also reduced in Krox20−/− embryos. We also examined expression of Notch1 target genes, Hey1, Hey2. While mRNA levels of Hey1 are unchanged in Krox20 mutant (Figure 1D), we found a significant reduction of Hey2 expression in the aortic valve from Krox20−/− compared to the littermates (Figure 1D). These findings indicate a down-regulation of genes previously associated with aortic valve disease and BAV in Krox20−/− mice.

### Table 1

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Total mice</th>
<th>Mice with BAV</th>
</tr>
</thead>
<tbody>
<tr>
<td>Krox20+/+</td>
<td>20</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Krox20+/−Tie2-cre</td>
<td>22</td>
<td>6 (27%)</td>
</tr>
<tr>
<td>Krox20−/−Tie2-cre</td>
<td>22</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Tie2Cre;Krox20+/+</td>
<td>20</td>
<td>2 (10%)</td>
</tr>
<tr>
<td>Wnt1Cre;Krox20+/+</td>
<td>19</td>
<td>2 (10.5%)</td>
</tr>
</tbody>
</table>

3.2. Krox20 Interacts In Vivo with Nos3

Since Nos3 is required for normal aortic valve development, and is associated with aortic valve disease including BAV, specifically in the fusion of the right-coronary and non-coronary leaflets, we examined if Krox20 and Nos3 signaling pathways exhibited an in vivo genetic interaction in aortic valve development. As previously shown [16], at E18.5, Nos3−/− embryos (n = 8) are observed at the expected mendelian ratio with a partially penetrance of BAV (28%), whereas all Nos3+/− embryos (n = 21) have normal aortic valve (Figure 2A,B). Krox20 heterozygous embryos are observed at the expected mendelian ratio with no evidence of BAV (Figure 2A,C). We bred Krox20+/− mice with

---

**Figure 1.** Modulation of gene expression in Krox20−/− embryos. (A) Table depicting penetrance of bicuspid aortic valve (BAV) in Krox20−/−, Tie2-cre;Krox20ff, and Wnt1-cre;Krox20ff mice. (B,C) Cross-sectional H&E images through the aortic valve of Krox20+/+ (B) and Krox20−/− (C) littermate embryos. At E18.5, left and right-coronary leaflets are observed in BAV of Krox20−/− (C) embryos. (D) Real-time qPCR analyses were performed from isolated aortic valve of Krox20+/+ (n = 5) and Krox20−/− (n = 5) embryos at E18.5. qPCR showing normal levels of Alk2, Gata5, and Hey1, and altered expression of Nos3, Notch1, and Hey2 in the aortic valve of Krox20−/− embryos at E18.5. qRT-PCR experiments were performed in triplicate and expressed as mean ±SEM (*p < 0.05 using Mann–Whitney test). Scale bars: 100 µm.
Nos3+/− or Nos3−/− mice and found low incidence of BAV in compound Krox20+/−;Nos3+/− embryos (8%; Figure 2A,D), suggesting a genetic interaction between these two genes. To test if transcriptional levels of Nos3 are affected in this context, we analyzed the Nos3 mRNA levels in single or compound mutants. Interestingly, significant decrease of Nos3 mRNA is observed in Krox20+/−;Nos3+/− mice (Figure 2E). We found a similar reduction of Nos3 mRNA in Krox20−/−, suggesting that Krox20 controls Nos3 mRNA expression.

Since Nos3 mRNA level is downregulated in Krox20−/− mice, we examined wild-type, single, and compound mutant hearts to determine whether there is a correlation with Nos3 protein expression. Therefore, we performed immunohistochemistry with anti-Nos3 and anti-Pecam on compound mutant hearts. Consistent with previous observation [11], we found Nos3 expression in the endothelial and mesenchyme of wild-type aortic valve leaflets at E18.5 (Figure 3A). As expected, no expression is detected in Nos3−/− embryos (Figure 3B). Although we did not observe a difference of Nos3 expression in the valvular endothelium in Krox20−/− mice, its expression is reduced in the mesenchyme of the aortic valve leaflets where Krox20 is normally expressed (Figure 3C). The expression of Nos3 is unaffected in Nos3+/− or Krox20+/− mice. Anti-Pecam immunostaining shows that integrity of the endothelium is maintained in all genotypes analyzed (Figure S1). Altogether, these data indicate that mesenchymal Nos3 expression is dependent on Krox20. To assess whether the Krox20-dependent Nos3-expressing mesenchyme cells are derived from the endothelial-, or neural crest cell-lineage,
we performed qPCR on aortic valves from Tie2-cre;Krox20ff and Wnt1-cre;Krox20ff mice (Figure S2). Transcriptional expression of Nos3 is reduced in both conditional mutant mice, suggesting that Nos3 is impaired in mesenchyme cells derived from both lineages.

3.3. Krox20 Activates Nos3 Promoter

Laforest and colleagues have identified conserved GATA binding sites in the murine −1.5-kb promoter of Nos3 and showed that Gata5 enhanced Nos3 promoter activity through these binding sites [24]. Based on these data, we examined the Nos3 promoter for conserved Krox20 binding sites. Bioinformatics analysis identified two evolutionary conserved Krox20-binding sites (K1 and K2) [31] in the Nos3 proximal promoter (Figure 4A). EMSA experiments showed that Krox20 is able to bind to these binding sites with a higher affinity for the K2 site (Figure 4B). Additionally, we carried out luciferase assays to show that overexpression of Krox20 in Cos7 cells increased the transcriptional activity of the −1500 bp region up to 2.5-fold but not the −265-bp Nos3 promoter (Figure 4C). Importance of K2 site is confirmed by luciferase assay, as mutation of this specific site abolished the activation of the −1500 bp promoter by Krox20. To confirm binding of Krox20, we performed chromatin immunoprecipitation (ChIP) experiments on freshly dissected OFT and ventricle tissues at E13.5. The amount of immunoprecipitated DNA relative to the input chromatin is determined by quantitative PCR using primers flanking Krox20-binding sites in the Nos3 (A and B regions) proximal promoters (Figure 4). Consistent with the high affinity of Krox20 for the K2 site and the transactivation results, ChIP qPCR demonstrated enrichment of binding only within the A region of Nos3 in the OFT extracts (Figure 4D). Furthermore, transfection of rat AVIC with Krox20 is sufficient to activate Nos3 expression (Figure 4E). Together, these results identified Krox20 as an activator of Nos3 promoter and suggest that reduction of Nos3 expression may be one of the leading causes of BAVs observed in Krox20 mutant mice.
At E9.5, we found no reduction of X-gal-positive cells in Nos3. Together, these results indicate that absence of Tomato expression (red), as an indicator of recombination, and Pecam (green) as an endothelial cell marker (Figure 5A). At E18.5, the number of recombined cells is comparable between Krox20 mutant mice. Thus, we used Nos3 mouse lines to perform lineage tracing experiments. Experiments were performed in triplicate and expressed as means ± SEM.

3.4. Krox20 Is Not Affected in Nos3 Mutant Mice

To determine whether nitric oxide is regulating Krox20, we examined the Krox20-labeled cells in Nos3 mutant mice. Thus, we used Krox20Cre mouse line to perform lineage tracing experiments. Experiments were performed in triplicate and expressed as means ± SEM.
This study also revealed an in vivo genetic interaction between patients with BAV display decreased levels of valve, as their dysfunction has been associated to BAV. Mice lacking functional Nos3 demonstrated a partially penetrance of BAV phenotype [3,16]. This observation is supported by a study showing that patients with BAV display decreased levels of Nos3 [17]. While, molecular basis of BAV in Nos3−/− mice is still unknown, it has been showed that EndMT is impaired in the AVC cushions of Nos3−/− embryos at E12.5 [32]. However, its function in the OFT cushions has not yet been reported. Interestingly, a recent study uncovered a novel mechanism by which nitric oxide modulates gene expression in neighboring cells, including expression of Hey1, a downstream mediator of Notch1 signaling [21]. This study also revealed an in vivo genetic interaction between Nos3 and Notch1, which has already been associated with BAVs in humans and mice [23]. Interestingly, expression of Notch1 and its

![Figure 5](image_url)

**Figure 5.** Absence of Nos3 does not affect Krox20 contribution. (A,B) Embryos were harvested from Krox20Cre+;Rosa26Tomato mice at E18.5 and immunohistochemistry is performed to detect Tomato expression (red) as an indicator of recombination, while Pecam (green) identifies endothelial cells in the aortic valve. No major difference is observed between Nos3−/− and control littermate embryos. (C–F) X-gal staining was performed on −31/−23.5 Krox20/LacZ transgenic mice to follow the Krox20-expressing cells at E9.5 (C,D), and E13.5 (E,F) stages. (C,D) At E9.5, β-galactosidase (β-gal) activity is detected in migratory neural crest cells. No defect is observed in Nos3−/− compared with control embryos (compared D with C). (E,F) Transverse section through the outflow tract cushions at E13.5 showing β-gal-positive cells in the arterial valve leaflets. AoV, aortic valve; ba1, branchial arch 1; PV, pulmonary valve; NCC, neural crest cells. Scale bars: 100 μm (A,B); 50 μm (C–F).

4. Discussion

Here, we report BAV phenotype in compound heterozygous Krox20;Nos3 mice, and show a direct activation of Nos3 expression by Krox20, demonstrating a genetic link between these two genes already known to be implicated in aortic valve disease including BAV [4,17]. We have previously shown that Krox20 is expressed in mesenchymal cells of the aortic valve leaflets, and that its function is required in both endothelial and neural crest derivatives to form normal aortic valves [4,12,22]. Aortic valve endothelial and interstitial cells play important roles in the development and remodeling of the aortic valve, as their dysfunction has been associated to BAV. Mice lacking functional Nos3 demonstrated a partially penetrance of BAV phenotype [3,16]. This observation is supported by a study showing that patients with BAV display decreased levels of Nos3 [17]. While, molecular basis of BAV in Nos3−/− mice is still unknown, it has been showed that EndMT is impaired in the AVC cushions of Nos3−/− embryos at E12.5 [32]. However, its function in the OFT cushions has not yet been reported. Interestingly, a recent study uncovered a novel mechanism by which nitric oxide modulates gene expression in neighboring cells, including expression of Hey1, a downstream mediator of Notch1 signaling [21]. This study also revealed an in vivo genetic interaction between Nos3 and Notch1, which has already been associated with BAVs in humans and mice [23]. Interestingly, expression of Notch1 and its
downstream effector Hey2 are reduced in Krox20+/− mice, indicating that absence of Krox20 affects both nitric oxide and consequently Notch signaling during aortic valve formation. While we have no evidence for a direct regulation of Notch1 expression, our data supports a direct activation of Nos3 by Krox20. First, our findings revealed an in vivo genetic interaction between Krox20 and Nos3 mutant alleles, as BAV phenotype is detected in compound heterozygous but not in single heterozygous mutant mice. Second, the absence of Krox20 activity affects transcriptional levels of Nos3 at E18.5 when BAVs are observed. Third, the 1.5-kb proximal promoter of Nos3, contains multiple conserved sequences that constitute putative sites for Krox20 binding. EMSA shows that Krox20 can bind K2 site with better affinity than K1 site, a result confirmed by in vivo quantitative ChIP analysis notably in the OFT, where Krox20 is strongly bound to region A of the Nos3 promoter. Fourth, transient transfection experiments displayed that overexpression of Krox20 has transactivation effects on reporter constructs containing −1.5-kb 5′ to the Nos3 promoter and that Nos3 expression is increased in AVIC after Krox20 transfection. Consistently, when a shorter version of Nos3 promoter is used, or when K2 motifs are mutated, transactivation is significantly decreased for Nos3 promoter. Finally, Nos3 expression is upregulated in AVICs after Krox20 transfection. These findings identify Nos3 as a Krox20 target and suggest that reduction in Nos3 activation may be a contributing mechanism to BAV in Krox20 mutant mice. A previous study has reported that Gata5 regulates Nos3 expression during aortic valve formation [24]. Interestingly, GATA binding sites are located next to those of Krox20. This observation suggests that Krox20 may interact with other factors to activate Nos3 and promote nitric oxide activity during the valvulogenesis. It has been shown that BAV is highly heritable, but with reduced penetrance and variable expressivity [33]. The high heterogeneity of BAV is probably the result of a combination of genetic, functional, and hemodynamic factors acting as modulators on the phenotype [34–36]. Therefore, the low percentage of BAV observed in the compound Krox20+/−;Nos3+/− mice suggests that the combination of the two alleles would favor the appearance of this defect. It would be interesting to study the influence of hemodynamic forces on the penetrance of BAV defect.

Because valves are constantly exposed to hemodynamic forces, it is critical to understand how shear stress is associated to valve remodeling [37]. The blood flow mediates nitric oxide production through influencing Nos3 expression and activity [38]. Nos3 is abundantly expressed in the valve endothelial cells but nitric oxide is also known to regulate VIC phenotypic expression in the aortic valve [39]. Moreover, porcine AVICs treated with agonist or antagonist of Nos3 demonstrated that nitric oxide activity impact AVIC phenotype [21,40]. Here, we show that Nos3 is expressed in the mesenchymal cells (or VICs) during development of the aortic valves, and that transient transfection of Krox20 in rat AVICs activates Nos3 expression (Figure 4E). This observation is consistent with another study which has reported Nos3 expression in the mesenchyme of the aortic valve [11]. The decrease of Nos3 expression in Krox20 mutant mice may impact mesenchymal differentiation and the remodeling of the aortic valve. We recently observed that Krox20 expression is modulated in AVICs in response to different shear stress forces (unpublished data). These observations suggest that Krox20 may participate to the regulation of nitric oxide during aortic valve leaflet development. A potent activator of the AVICs is the transforming growth factor-β1 (TGF-β1) [41]. TGF-β1, as well as other inflammatory cytokines, regulates the activation of nitric oxide in normal and pathological valves. Further investigation is required to determine if Krox20 interacts with other pathways to regulate the nitric oxide in response to normal and pathological blood flow patterns at the surface of the aortic valve leaflets.

In Krox20 mutant mice, aortic valve leaflets are misshaped due to an excess of neural crest derivatives [4]. This enlargement blocks normal valvulogenesis and results in BAV in 30% of Krox20+/− mice. The BAV in Krox20+/− mice results from fusion of either the right or left-coronary and non-coronary leaflets (R-N). This fusion pattern is consistent with the Nos3 deficient mouse model of BAV where endothelial–mesenchymal signaling is impaired [3]. Our previous study indicates that Krox20 is required within the endothelial-derived cells for proper aortic valve remodeling [12]. Krox20 is also required in neural crest-derived cells as demonstrated by the BAV observed in Wnt1-cre;Krox20ff mice (Figure 1A) [4]. However, the bicuspid phenotype obtains in Tie2-cre;Krox20ff mice is different
from those observed in Krox20\(^{-/-}\) or Wnt1-cre;Krox20\(^{ff}\) mice as the BAV is formed by equal-sized leaflets. These results suggest that Krox20 plays multiple roles during the development and remodeling of the aortic valves.

5. Conclusions

In conclusion, the data presented here are consistent with a crucial role for Krox20 in aortic valve development and suggest that Krox20 may be related to aortic valve disease in human. Observations that Krox20 regulates nitric oxide activity through activation of Nos3 proximal promoter in vivo and in vitro suggest that interaction between different pathways may be implicated in aortic valve disease such as BAV. Future studies aimed at elucidating the downstream targets of Krox20 in valve cells will contribute to understanding molecular mechanics in aortic valve development as well as BAV.


Author Contributions: Conceptualization, G.O., E.F., C.M.-Z. and S.Z.; validation, G.O., E.F. and C.M.-Z.; formal analysis, G.O.; investigation, S.Z.; writing—original draft preparation, S.Z.; writing—review and editing, S.Z.; visualization, X.X.; supervision, S.Z.; funding acquisition, S.Z.

Funding: This research was funded by the “Association Français contre les Myopathies” (NMH-Decrypt and TRIM-RD Projects), the “Fondation pour la Recherche Médicale” (DPC20111123002), and the “Institut National de la Santé et de la Recherche Médicale” to S.Z. G.O. received fellowships from the “Fondation pour la Recherche Médicale”, the “Institut National de la Santé et de la Recherche Médicale”, the “Fondation Lefoulon Delalande”. E.F received a postdoctoral fellowship from the “Association Française contre les Myopathies”.

Acknowledgments: We are grateful to Patrick Charnay and Piotr Topilko for the Krox20 mouse lines, and Adeline Gatha and Elise Plaindoux for their technical assistance.

Conflicts of Interest: The authors declare no conflict of interest. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

References


30. Gould, R.A.; Butcher, J.T. Isolation of valvular endothelial cells. J. Vis. Exp. 2010, 46, e2158. [CrossRef]


© 2019 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (http://creativecommons.org/licenses/by/4.0/).