Upregulation of Igf and Wnt signalling associated genes in pleomorphic adenomas of the salivary glands in *PLAG1* transgenic mice

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Abstract. The Pleomorphic adenoma gene 1 (PLAG1) is involved in various human neoplasias, including pleomorphic adenomas of the salivary glands. Moreover, the oncogenic role of PLAG1 was clearly demonstrated in two independent PLAG1 transgenic mouse founders, in which PLAG1 expression could be targeted to different tissues using the Cre/loxP system. MMTV-Cre-mediated targeted overexpression of PLAG1 in the salivary glands of double transgenic offspring mice, referred to as P1-MCre and P2-MCre mice, induced pleomorphic adenomas in this organ. Igf2, a genuine PLAG1 target gene, was highly upregulated in those tumours as well as in human pleomorphic adenomas of the salivary glands. These and previous observations in other PLAG1-induced tumours e.g. breast adenomyoepitheliomas emphasize the importance of Igf upregulation in such tumours. In this study, further evidence for the role of *Igf2* in PLAG1induced tumourigenesis, is reported. Inactivation of Igf2 in P1-MCre mice leads to a significant delay in tumour development. Since tumour development is not fully abrogated by inactivation of Igf2, other signalling pathways are likely to contribute to PLAG1-induced tumourigenesis as well. Further studies revealed that several genes such as H19, Dlk1, Gtl2, Igfbp2, Igfbp3 and genes involved in Wnt signalling, such as Wnt6, Cyclin D1 and β -catenin are upregulated in P1-MCre mice in which Igf2 is inactivated. In conclusion, we clearly demonstrate upregulation of several genes associated with Igf and Wnt signalling in PLAG1-induced pleomorphic adenomas. Furthermore, inactivation of Igf2 does not affect upregulation of genes associated with Wnt signalling, which might suggest that both signalling pathways are involved.

Introduction

Pleomorphic adenoma is the most common tumour in human salivary glands, accounting for about half of all neoplasms in this organ (1). About 84% of the pleomorphic adenomas occur in the parotid glands, 8% in the submandibular glands, 6.5% in the minor glands, and 0.5% in the sublingual glands (2).

Pleomorphic adenomas are slow growing, painless, encapsulated tumours that may become large if untreated. Larger lesions can have sites of necrosis, haemorrhage, focal calcification or occasionally ossification (3). Although these tumours are usually benign, they have the tendency to recur when inadequately excised. Moreover, 2-17% of the tumours can progress to malignancy and give rise to carcinoma ex pleomorphic adenoma (4-6).

Cytogenetically, pleomorphic adenomas of the salivary glands are well characterized, with several hundreds already karyotyped (7,8). Four major cytogenetic subgroups can be distinguished (9). The first consists of tumours with 8q12 rearrangements (39%). The second is composed of tumours with translocations involving chromosomal region 12q14-15 (8%). The third is composed of tumours with various nonrecurrent translocations (23%) not involving chromosomal region 8q12 or 12q14-15. The last subgroup consists of tumours with an apparently normal karyotype (30%). It is clear that the translocations involving 8q12 and 12q14-15 are frequently encountered in pleomorphic adenomas of the salivary glands. By positional cloning, we identified the genes involved in those translocations. The high mobility group protein C (HMGI-C, now known as HMGA2) gene was found to be affected in tumours with 12q14-15 translocations (10) whereas the Pleomorphic adenoma gene 1 (PLAG1) was found to be affected in tumours with 8q12 translocations (11). The most common abnormality in the latter cases is a t(3;8)(p21;q12) translocation, found in almost half of these. The translocation results in promoter swapping between PLAG1 and CTNNB1 (the gene for ß-catenin). As a result of the t(3;8)(p21;q12) translocation, the coding sequences of *PLAG1* are brought under the control of the 5' regulatory sequences of the CTNNB1 gene, and vice versa. The regulation of the expression of both genes is very different. Whereas, the CTNNB1 gene is highly, ubiquitously, and constitutively expressed, PLAG1 has high overall developmental expression

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levels, which drop shortly after birth (12). As a consequence, the above-sited t(3:8) translocation leads to an aberrant activation of PLAG1. In addition to the CTNNB1-PLAG1 fusion gene, three alternative fusion genes have been identified in pleomorphic adenomas. LIFR-PLAG1 is found in tumours with t(5;8)(p13;q12) (13), whereas TCEA1-PLAG1 (also known as SII) (14) and CHCHD7-PLAG1 (15) both result from cryptic rearrangements in tumours with a normal karyotype. Analysis of the structure and function of the PLAG1 fusion partners have not revealed any obvious similarities besides their constitutive expression pattern, or at least their expression in the cells or tissues from which the tumours are thought to originate. Therefore, it has been suggested that the most important function of the fusion partner genes is most likely to provide an active promoter that induces ectopic expression of PLAG1 (9).

In addition to pleomorphic adenomas, ectopic expression of PLAG1 is also found in lipoblastomas (16-18), hepatoblastomas (19), and AML (20,21). The oncogenic capacity of PLAG1 has been demonstrated in vitro, i.e. in cell lines that were retrovirally transduced with PLAG1 (22), and recently, in vivo in mouse models (23,24). Whereas Zhao and co-workers generated classical, non-conditional transgenic mouse strains (24), we developed two independent PLAG1 transgenic mouse strains, PTMS1 and PTMS2, in which activation of overexpression of the transgene as well as the tissue distribution of such overexpression can be manipulated, by Cre-mediated activation and targeted expression, respectively (23). To study the consequences of genetically engineered PLAG1 expression in the salivary glands, the two independent PLAG1 transgenic mouse strains were intercrossed with B6129-Tgn(MMTV-LTR/Cre)1Mam (MMTV-Cre) transgenic mice (25,26). The resulting double transgenic offspring mice, referred to as P1-MCre and P2-MCre mice, developed pleomorphic adenomas of the salivary glands with a prevalence of 100% (within 5 weeks) and 6% (after several months), respectively (23).

Previous microarray studies, including comparative gene expression profiling in human and mouse salivary gland tumours (27), revealed genes that are consistently induced by PLAG1. Of interest to note is the upregulation of genes functioning in Igf (mouse) and IGF (human) signalling. In validation experiments, it has already been proven for instance for IGF-II that it constitutes a genuine direct target gene of PLAG1 (28).

The upregulation of Igf2 in pleomorphic adenomas of the salivary glands thus suggests a contributing role of Igf2 in the *PLAG1*-induced tumourigenesis. To study the precise impact of Igf2 upregulation on *PLAG1*-induced tumour formation, we intercrossed P1-MCre mice with Igf2 knockout mice (29,30). The investigation focused on monitoring tumour development, histological analysis of tumour lesions, and upregulation of expression of genes associated with signalling pathways.

Materials and methods

Generation of P1-MCre and various P1-MCre-Igf2 compound transgenic/knockout mice. The generation of the PLAG1 transgenic founder line, PTMS1, has been reported previously (23). To target PLAG1 expression to the salivary glands, this founder was crossed with B6129-Tgn(MMTV-LTR/Cre)1Mam transgenic mice (*MMMTV-Cre*) (Jackson's Laboratories, USA) (25), resulting in P1-MCre offspring. In order to generate compound transgenic/knockout mice involving *PLAG1*, *Cre*, and *Igf2*, *Igf2^{p-/m-}* mice (29,30) were crossed with PTMS1 mice, and *MMTV-Cre* mice with *Igf2^{p-/m-}* mice to generate *P1-Igf2^{p-/m+}* and *MMTV-Cre-Igf2^{p-/m+}* offspring, respectively. Mating of those compound heterozygous offspring yielded various genotypes, including *P1-MCre-Igf2^{p-/m+}*, *P1-MCre-Igf2^{p-/m+}* mice. These offspring mice were used in further breedings to expand colonies, necessary for further analysis of the impact of *Igf2* inactivation on tumour formation.

Genotyping of genetically modified mice by PCR analysis. Genotyping of candidate PLAG1 founders was performed by PCR analysis of tail DNA using oligonucleotide primers POS-1599 (5'-TTCTCAAGCATCGTCATCAT-3') and β-globin (5'-AAAATTCCAACACACTATTGC-3'). For genotyping of the various genetically modified mice, gene-specific primers were designed for the following genes: Cre (forward: 5'-CCTG TTTTGCACGTTCACCG-3' and reverse: 5'-ATGCTTCTG TCCGTTTGCCG-3'), Igf2 wild-type allele (forward: 5'-GTA CCAATGGGGATCCCAGTG-3' and reverse: 5'-GCGGTC CGAACAGACAAACTG-3') and the Igf2 knockout allele (forward: 5'-TGCTCTGATGCCGCCGTGTT-3' and reverse: 5'-GTGCACTCTCAACCTGGCTGA-3'). All PCR reactions were performed at an annealing temperature of 58°C and involved 35 cycles except for the Igf2 knockout allele, which involved 30 cycles. The annealing time was 40, 30, 30, and 50 sec for PLAG1, Cre, the Igf2 wild-type allele, and Igf2 knockout allele, respectively.

Real-time quantitative PCR (QRT-PCR). Total RNA from selected tissue specimens from normal tissue and tumours of the salivary glands was prepared using the NucleoSpin® RNA L kit, as described by the manufacturer, Macherey-Nagel. Total RNA (5 μ g) was reverse transcribed using random hexamer primers and M-MLV reverse transcriptase from Invitrogen (Merelbeke, Belgium). QRT-PCR was performed with the MyIQ system (Biorad). In all cases, 40 cycles of annealing/extension for 1 min at 60°C were performed. QRT-PCR products were detected using SYBERGreen. QRT-PCR for mt-Atp6 was used as a reference to correct for sample quantity (forward primer: 5'-AAGCTCACTTGCCCAC TTCCTT-3' and reverse primer: 5'-GCTGTAAGCCGGA CTGCTAATG-3'). Gene-specific primers were designed for the following genes; PLAG1 (forward: 5'-CCACGTTTCCA TCAAGCTTTTC-3' and reverse: 5'-AGGCAGCCTGC ACCTGAG-3'), Igf2 (forward: 5'-TGTCTGTTCGGACC GCG-3' and reverse: 5'-GTTGGCACGGCTTGAAGG-3'), H19 (forward: 5'-AAGAGCTCGGACTGGAGACTAGG-3' and reverse: 5'-GGCACATCCACCTCTGCTG-3'), Dlk1 (forward: 5'-TGCGCGTCCTCTTGCTC-3' and reverse: 5'-CATTCAGCCCCATAGGTGCT-3'), Gtl2 (forward: 5'-CTCCAACCCACTGCTTCCTG-3' and reverse: 5'-AGCGA GAGCCGTTCGATG-3'), Igfbp2 (forward: 5'-CCAACTGT GACAAGCATGGC-3' and reverse: 5'-GAGACATCTT GCACTGCTTAAGGTT-3'), Igfbp3 (forward: 5'-GCAGG CAGCCTAAGCACC-3' and reverse: 5'-GATGTTTCCT GGAGCAGGTTG-3'), Cyclin D1 (forward: 5'-CGAGGAG

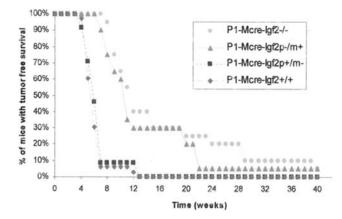


Figure 1. Percentage of *PLAG1/lgf2* genetically modified mice with tumourfree survival as detected by the absence of a macroscopically visible tumour mass in the ventral neck region in function of time. At least 20 mice were studied for each genotype.

CTGCTGCAAATG-3' and reverse: 5'-TTCCACTTGAG CTTGTTCACCA-3'), *Wnt6* (forward: 5'-TGTCAGTTCCA GTTCCGTTTCC-3' and reverse: 5'-GCTGCGGTGATTG CAAACA-3') and β -catenin (forward: 5'-TTCAGATCTTA GCTTATGGCAATCAA-3' and reverse: 5'-TGGCCAGA ATGATGAGCTTG-3').

Western blot analysis. Salivary gland tumours of 8- and 12-week-old P1-MCre mice, control littermate MMTV-Cre mice, and 30- and 37-week-old P1-MCre-Igf2^{p-/m-} mice were snap-frozen and stored at -80°C. Cryo-frozen tissue samples were homogenized in 5 volumes of suspension buffer, prepared by combining 0.1 M NaCl, 0.01 M Tris/HCl pH 7.5, 1 mM EDTA pH 8.0 and protease inhibitors cocktail EDTA-free (Roche). An equal volume of 2X SDS sample buffer, prepared by combining 20 ml 10% SDS, 10 ml glycerol, 10 ml 0.5 M Tris/HCl pH 6.8, 60 ml H_2O , was added and the samples were heated for 10 min at 95°C. The total protein concentration was determined using the BCA method and equal amounts of proteins were size-fractionated by SDS-Page. The proteins were transferred to a nitrocellulose membrane and Western blot analysis was performed, as described previously (23). Active-ß-catenin and total ß-catenin were detected with highly specific antibodies, clone 8E7 (Upstate) to detect active dephosphorylated ß-catenin and antibody 610154 (BD Bioscience) to detect total ß-catenin. As control for equal loading, actin was visualized using antibody A 5060 (Sigma).

Results

Evaluation of the role of Igf2 in PLAG1-induced tumour development in P1-MCre mice. Previously, we generated two independent PLAG1 transgenic mouse lines, in which activation of overexpression of the transgene as well as the tissue distribution of such overexpression can be manipulated by Cre-mediated activation and targeted expression, respectively. These founder lines were intercrossed with MMTV-Cre mice to target the expression of the transgene mainly to the salivary glands. P1-MCre mice (100%) developed pleomorphic adenomas of the salivary glands at ~5-6 weeks. In contrast, only 6% of the P2-MCre mice

Table I. Upregulation of PLAG1 target genes in pleomorphic adenomas of the salivary glands.

Genes	P1-MCre-Igf2+/+	P1-MCre-Igf2-/-
Igf2	3422±1212	0
H19	948±328	276±69
Dlk1	6165±1190	3337±1180
Gtl2	79.5±0.3	78.8±14
Igfbp2	17.4±4.6	11.4±3.5
Igfbp3	16.5±4.4	18.8±4.9
Cyclin D1	3.7±0.6	3.2±0.7
Wnt6	46.8±10.8	43.2±15.1
β-catenin	2.1±0.4	1.7±0.6 ^a

Mean values ± SEM of the fold upregulation of PLAG1 target genes in pleomorphic adenomas of the salivary glands of 5 *P1-MCre-* $Igf2^{p+/m+}$ and 5 *P1-MCre-Igf2^{p-/m-}* mice as compared to normal salivary gland tissue of 5 *MMTV-Cre* and 5 *MMTV-Cre-Igf2^{p-/m-}* littermates, respectively. P-values are <0.05, except for ^aP=0.2.

developed similar tumours after several months. *Igf2* was highly upregulated in those PLAG1-induced pleomorphic adenomas of the salivary glands. Similarly, *IGF-II* was upregulated in human pleomorphic adenomas that expressed *PLAG1* (28). IGF signalling is also implicated in many tumour types including, breast (31-33), colon (34) and liver (35). Altogether, those data indicate the Igf signalling might be important in PLAG1-induced tumourigenesis.

In this study, the role of Igf2 on PLAG1-induced tumourigenesis is further investigated. Due to the low tumour incidence and the long latency period in P2-MCre mice, we decided to investigate the role of Igf2 in PLAG1-induced tumourigenesis only in P1-MCre mice. Therefore, P1-MCre mice were crossed with *Igf2* knockout mice (29,30). Due to imprinting, only the paternal allele of *Igf2* is active, whereas the maternal allele is normally silenced via methylation. P1-MCre offspring, in which the paternal *Igf2* allele is knocked out or both *Igf2* alleles are knocked out, show a significant delay in the development of salivary gland tumours. This was assessed by determing the presence of macroscopically visible tumour masses in the ventral neck region (Fig. 1). As can be deduced from Fig. 1, for example 50% of the P1-MCre-Igf2^{p-/m-} mice and P1-MCre-Igf2^{p-/m+} mice developed large salivary gland tumours at ~11-12 weeks after birth. In contrast, 50% of the *P1-MCre-Igf2*^{p+/m-} and*P1-MCre-Igf2*^{<math>p+/m+} mice showed macro-</sup></sup> scopically visible tumour masses already at ~6 weeks after birth (Fig. 1).

We have performed comparative histopathological studies to investigate whether or not particular differences could be found in tumour lesions with and without *Igf2* expression. These studies indicated that the histopathological features of the salivary gland tumours of *P1-MCre-Igf2^{p-/m-}* mice were similar to those observed in corresponding *P1-MCre-Igf2^{p+/m+}* mice (Fig. 2). The salivary gland tumours studied all showed typical characteristics of pleomorphic adenomas. An overview of the pleomorphic character of the tumours of *P1-MCre-Igf2^{p-/m-}*

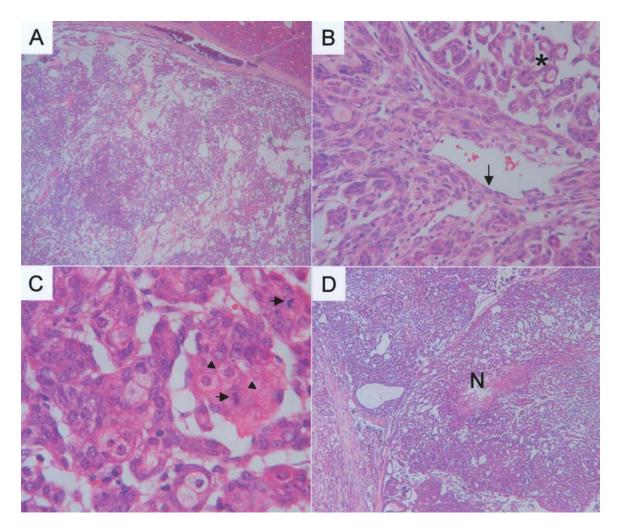
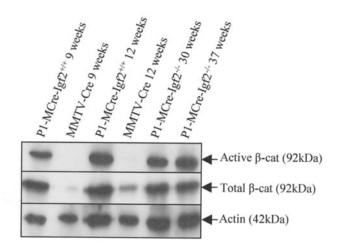


Figure 2. (A) Overview figure of a pleomorphic adenoma of a 12-week-old P1-MCre- $Igf2^{p-/m}$ mouse, demonstrating the pleomorphic character of the tumour. H&E, original magnification of x2.5. (B) Pleomorphic adenoma of a 10-week-old P1-MCre- $Igf2^{p-/m}$ mouse, showing the presence of tubular structures (epithelial cells) (*) as well as spindle, myoepithelial cells (down arrow). H&E, original magnification of x20. (C) Pleomorphic adenoma of a 12-week-old P1-MCre- $Igf2^{p-/m}$ mouse, showing sebaceous/squamous metaplasia (arrowhead) and mitotic figures (right arrow). H&E, original magnification of x40. (D) Pleomorphic adenoma of a 22-week-old P1-MCre- $Igf2^{p-/m}$ mouse, showing sebaceous/squamous metaplasia (arrowhead) and mitotic figures (right arrow). H&E, original magnification of x40. (D) Pleomorphic adenoma of a 22-week-old P1-MCre- $Igf2^{p-/m}$ mouse, showing malignant characteristics such as the presence of a necrotic region (N). H&E, original magnification of x5.



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Figure 3. The accumulation of β -catenin and active- β -catenin in pleomorphic adenomas of the salivary glands of 9- and 12-week-old *P1-MCre-Igf2*^{p+/m+} mice and 30- and 37-week-old *P1-MCre-Igf2*^{p-/m-} mice as compared to the levels in salivary glands of littermate *MMTV-Cre* mice was demonstrated by Western blot analysis, using different antibodies as described in Materials and methods. An anti-actin antibody was used to visualize equal loading.

mice is illustrated in Fig. 2A. The tumours are composed of regions that contain mainly tubular structures (epithelial cells) and other regions that contain mainly spindle cells (myoepithelial cells) (Fig. 2B). Some of the tumours show sebaceous/squamous differentiation (Fig. 2C). In older tumours malignant features such as numerous mitotic figures (Fig. 2C) and necrotic regions (Fig. 2D) were observed. The same characteristics were found in pleomorphic adenomas of *P1-MCre-Igf2*^{p+/m+} mice (23).

Expression upregulation of PLAG1 target genes in P1-MCre-Igf2^{p-/m-} mice. P1-MCre-Igf2^{p-/m-} mice still develop salivary gland tumours, although after a latency period that is about twice as long as in P1-MCre-Igf2^{p+/m+} mice. Therefore, it is reasonable to conclude that also other molecular pathways, besides Igf signalling, are involved in PLAG1-induced tumourigenesis. Previously, several other genes, such as H19, Dlk1, Gtl2, Igfbp2 and Igfpb3 have been found to be upregulated in PLAG1-induced tumours. In this study, their expression levels were investigated in P1-MCre-Igf2^{p-/m-} mice and compared to those in P1-MCre-Igf2^{p-/m+} mice (Table I). In this way, we wanted to see whether or not the expression of these genes is dependent on Igf2 expression, and presumably Igf2 signalling. As might be expected, no expression of Igf2 was observed when Igf2 was inactivated in P1-MCre mice and the expression of Igf2 was significantly decreased (P=0.02) in P1-MCre- $Igf2^{p-m}$ mice.

The expression levels of all the other genes investigated were not significantly different in $P1-MCre-Igf2^{p-/m-}$ mice as compared to littermate P1-MCre-Igf2^{p+/m+} mice and are as such independent of Igf2 expression. The H19 gene of the imprinted gene cluster Igf2/H19 is still significantly upregulated when both *Igf2* alleles are knocked out in P1-MCre mice. Similarly, the genes from the imprinted gene cluster Dlk1/Gtl2 and the Igfbp2 and Igfbp3 genes are also significantly upregulated under those conditions. Zhao and co-workers reported about the involvement of Wnt signalling in PLAG1-induced pleomorphic salivary gland adenomas in non-inducible MMTV-PLAG1 transgenic mice (24). Therefore, we decided to investigate whether we could confirm this also in P1-MCre-Igf2^{p-/m-} mice. Several genes involved in Wnt signalling, such as Wnt6, cyclin D1 and ß-catenin, were found to be upregulated in P1-MCre-Igf2^{p-/m-} and P1-MCre-Igf2^{p+/m+} mice. This upregulation was low and not significant for B-catenin in *P1-MCre-Igf2*^{p-/m-} mice.

Wnt signalling in pleomorphic adenomas of P1-MCre-Igf $2^{p+/m+}$ and P1-MCre-Igf2^{p-/m-} mice. To further substantiate Wnt signalling in PLAG1-induced pleomorphic adenomas of the salivary glands of P1-MCre-Igf2^{p+/m+} and P1-MCre-Igf2^{p-/m-} mice, Western blot analysis was performed. In absence of Wnt, GSK-3 is constitutively active and is believed to promote degradation of B-catenin by N-terminal phosphorylation, ubiquitination, and proteasomal targeting subsequently. Upon Wnt signalling, the activity of GSK-3 is inhibited. As a consequence, ß-catenin can no longer be phosphorylated and accumulates to form nuclear complexes with TCF/LEF transcriptional co-activators (36). In order to demonstrate the presence of active Wnt in PLAG1-induced pleomorphic adenomas of the salivary glands of $P1-MCre-Igf2^{p+/m+}$ and P1-MCre-Igf2^{p-/m-} mice, Western blot analysis was performed on pleomorphic adenomas of these mice and on control salivary glands of MMTV-Cre littermate mice. Accumulation of β-catenin in pleomorphic adenomas of P1-MCre-Igf2^{p+/m+} and *P1-MCre-Igf2^{p-/m-}* mice was clearly demonstrated (Fig. 3). Furthermore, the presence of active-ß-catenin was demonstrated in those pleomorphic adenomas, using a monoclonal antibody that specifically recognizes the non-phosphorylated residues Ser-37 and Thr-41 of B-catenin (36). Western blot analysis for actin was performed to demonstrate equal loading. These data all point towards the presence of active Wnt in the PLAG1-induced pleomorphic adenomas, independent of Igf2 expression.

Discussion

IGF signalling has been reported to be involved in many different human tumour types (31-35). Furthermore, the oncogenic capacity of *IGF-II* has been demonstrated in mouse models [reviewed by Werner and co-workers (37)]. For example, ectopic expression of *IGF-II* in the mammary

glands leads to the development of mammary gland tumours after a long latency period (38,39). In contrast, MMTV-IGF-II transgenic mice do not develop overt mammary and salivary gland tumours. Nevertheless, they do develop focal areas of epithelial hyperplasia in mammary glands as well as sporadic tumours in other organs, such as in the lungs. Overexpression of a constitutively active IGF-IR whose expression was driven by the MMTV-promoter resulted in rapid appearance of mammary and salivary gland tumours, further pointing towards a contributing role of IGF signalling in tumourigenesis. For those reasons, we decided to investigate the impact of Igf expression on PLAG1-induced tumourigenesis in the salivary glands, via inactivation of *Igf2* in P1-MCre mice. The results clearly demonstrated an effect of Igf2 expression on PLAG1induced tumourigenesis. If Igf2 is disrupted in P1-MCre mice, the appearance of macroscopically visible salivary gland tumours was delayed significantly. The latency period for tumour appearance about doubled. This observation suggests that Igf2 signalling in these PLAG1-induced tumours is similarly important as in the human salivary gland pleomorphic adenomas with PLAG1 activation.

Given the above-suggested importance of Igf signalling in PLAG1-induced tumourigenesis, neutralization of Igf2 or other downstream components of this signalling pathway could be an effective therapeutic strategy in combination with other therapies to treat those tumours. Pharmacological antagonism of IGF ligands has been accomplished by neutralizing monoclonal antibodies (40-42). Most therapies target the IGF-IR (43). Several monoclonal antibodies, directed against IGF-IR (44,45) and several small molecule inhibitors have been created (46,47). Other therapies target factors even more downstream in the IGF-IR signalling pathway, such as mTOR signalling. mTOR inhibitors have shown promising clinical efficacy in subsets of cancers, with low toxicity profiles (48). In previous studies (22), we have shown that Igf-1r- NIH3T3 cells cannot be transformed in vitro by PLAG1. Therefore, the PLAG1 transgenic mouse model could constitute a tool to validate anti-cancer therapies that target Igf-1r in vivo in mice. Since the same molecular pathway also plays an important role in different human cancers, the generated data might have an impact relevant to many human cancers in case the data from the various mouse model systems that can be generated can be translated accordingly.

Since tumour development was not fully abrogated by inactivation of Igf2, it is likely that additional signalling pathways contribute to PLAG1-induced tumourigenesis as well. Zhao and co-workers (24), previously demonstrated that Wnt signalling is involved in the formation of pleomorphic adenomas of the salivary glands in MMTV-PLAG1 transgenic mice. Immunohistochemical staining demonstrated that expression of *B*-catenin was highly upregulated with overexpression of the PLAG1 transgene in tumour and normal transgenic salivary gland tissue. They suggest that PLAG1 activates the transcription of mouse ß-catenin in MMTV-PLAG1 transgenic mice. They demonstrated by luciferase experiments that PLAG1 can activate the mouse but not the human ß-catenin promoter. As such, a direct upregulation of B-catenin in MMTV-PLAG1 transgenic mice is a plausible explanation for the possible involvement of Wnt signalling in PLAG1-induced pleomorphic adenomas in mice but not in humans. Nevertheless, also in human salivary gland pleomorphic adenomas WNT signalling seems to be implicated (49). One mechanism leading to the activation of the WNT signalling pathway in human pleomorphic adenomas is expected to be the downregulation of the WNT inhibitory factor 1 (*WIF1*).

In our studies, we provide evidence for the possible involvement of Wnt signalling in PLAG1-induced pleomorphic adenomas of the salivary glands in P1-MCre- $Igf2^{p+/m+}$ as well as *P1-MCre-Igf2^{p-/m-}* mice. In contrast to Zhao and coworkers, we propose another mechanism involving Wnt-signalling in PLAG1-induced pleomorphic adenomas in mice. We establish that Wnt6 is significantly upregulated in PLAG1-induced pleomorphic adenomas as compared to normal salivary gland tissue of MMTV-Cre transgenic mice. As such, Wnt6 may bind to the frizzled receptor and activate Wnt signalling directly and not necessarily via upregulation of ß-catenin itself. In contrast to the mechanism proposed by Zhao and co-workers, this mechanism might also be involved in human pleomorphic adenomas. Nevertheless, this hypothesis still needs to be confirmed in human pleomorphic adenomas of the salivary glands, which overexpress PLAG1.

In conclusion, we clearly demonstrate that Igf signalling is involved in PLAG1-induced pleomorphic adenomas of the salivary glands in mice. Inactivation of Igf2 in P1-MCre mice leads to a delay in tumour development. Furthermore, we also demonstrated that Wnt signalling might be involved in those tumours in P1-MCre mice as well as in P1-MCre mice in which Igf2 is disrupted.

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