Genetic analysis of Ras genes in epidermal development and tumorigenesis

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Proliferation and differentiation of epidermal keratinocytes are tightly controlled to ensure proper development and homeostasis of the epidermis. The Ras family of small GTPases has emerged as a central node in the coordination of cell proliferation in the epidermis. Recent genetic evidence from mouse models has revealed that the intensity of Ras signaling modulates the proliferative capacity of epidermal keratinocytes. Interfering with Ras signaling either by combined elimination of the 3 *Ras* **genes from the basal layer of the epidermis or by overexpression of dominant-negative Ras isoforms caused epidermal thinning due to hypoproliferation of keratinocytes. In contrast, overexpression of oncogenic Ras mutants in different epidermal cell layers led to hyperproliferative phenotypes including the development of papillomas and squamous cell carcinomas. Here, we discuss the value of loss- and gain-of-function studies in mouse models to assess the role of Ras signaling in the control of epidermal proliferation.**

Introduction

Tight regulation of cell proliferation is critical for tissue homeostasis in embryonic as well as in postnatal life. Unbalanced proliferation could result either in tissue atrophy in the case of insufficient proliferation, or in tumor development in case of unscheduled growth. The skin epidermis is a tissue characterized by a high rate of cellular turnover that requires strict control of cell proliferation.¹ The stratified epidermis is the outermost structure of the skin and protects organisms against water

loss and prevents inclusion of toxic agents as well as microorganisms. This protection is achieved by the formation of a nonpermeable barrier consisting of a large, intercalated network of keratinocytes.^{2,3} The epidermis consists of various layers of keratinocytes characterized by differential proliferative capacities as well as varying degrees of differentiation.²⁻⁴ The basal layer (*stratum basale*) is highly proliferative and constantly gives rise to new basal cells as well as more differentiated suprabasal cells (*stratum spinosum*) through balanced symmetric and asymmetric cells divisions, respectively. Whereas basal keratinocytes are characterized by expression of keratins 5 and 14, suprabasal cells display a shift toward expression of keratins 1 and 10, thereby forming a more robust keratin network accompanied by an increase in cell-cell junctions.¹ As these cells further differentiate to form the granular layer (*stratum granulosum*), the process of stratification continuously proceeds to generate layers of dead, enucleated cells forming the corneal envelope (*stratum corneum*).^{2,4} Cells of the granular and corneal layers gradually reduce expression of keratins 1 and 10 and start to produce other proteins such as involucrin, loricrin, or filaggrin, thereby further contributing to establish a non-permeable barrier.²⁻⁵

Although the structural and morphological traits of epidermal development have been well characterized, the molecular pathways controlling these processes are only beginning to emerge.6 Accumulating evidence obtained from mouse models suggests that the Ras family of small GTPases plays a fundamental role in these processes. In mammals, Ras proteins are

encoded by three independent loci, *H-Ras*, *N-Ras* and *K-Ras*. 7,8 Genetic studies have indicated that *H-Ras* and *N-Ras*, either individually or in combination, are dispensable for mouse development and tissue homeostasis. In contrast, *K-Ras* is an essential gene and mice lacking this locus die between 12 and 14 d of gestation due to anemia and liver defects.⁸⁻¹¹ However, expression of *H-Ras* from the *K-Ras* locus rescues these defects and supports embryonic development and adult homeostasis. Thus, suggesting that Ras isoforms perform redundant functions and that their unique properties are largely due to tissue distribution and/or expression levels.¹² In this article we will discuss the role of Ras signaling in epidermal biology and tumorigenesis based on evidence derived from genetic studies in mouse models.

Ras Signaling in Epidermal Development and Homeostasis

In vivo genetic analyses of the role of Ras signaling in epidermal biology has been challenging due to the high redundancy of the different Ras isoforms. Dajee et al. addressed this issue by expressing a dominant-negative *H-Ras*^{S17N} mutant that presumably blocks signaling from all Ras isoforms under control of the keratin 14 promoter in mice.¹³ This study demonstrated that interfering with Ras signaling in the highly proliferative basal layer caused epidermal thinning and hyperkeratosis. Interestingly, the authors also observed a striking increase in more differentiated suprabsal cells. Likewise, overexpression of *H-Ras*^{S17N} in cultured keratinocytes diminished their proliferative capacity, thus suggesting a relevant role for Ras signaling in the maintenance of keratinocyte proliferation.

Dissecting the role of individual Ras isoforms by gene knockout studies is a difficult task due to the high redundancy among Ras GTPases. Mice deficient for *H-Ras* and *N-Ras* did not show any abnormalities in the skin, suggesting that *K-Ras* expression is sufficient for epidermal development and to maintain tissue homeostasis.¹¹ Moreover, ubiquitous deletion of *K-Ras* in adult mice did not induce significant defects in the skin (our unpublished observations).^{14,15} Thus, it seems

reasonable to assume that any of the Ras isoforms might be able to sustain cell proliferation in the epidermis. To determine whether Ras signaling is required for epidermal development, we eliminated all three Ras isoforms from the epidermis by generating a compound strain deficient for *H-Ras* and *N-Ras* loci that harbored conditional *K-Ras* alleles. In these mice, specific ablation of *K-Ras* from the epidermis was achieved by breeding this strain to mice expressing a Cre recombinase under the control of the keratin 5 promoter.¹⁶ In this model, Cre expression was turned on during embryonic development in the basal layer of the epidermis, thus leading to complete ablation of K-Ras protein expression by midgestation. Elimination of all 3 *Ras* loci from the epidermis was not compatible with postnatal life, indicating that Ras proteins provide essential functions in epidermal homeostasis. Indeed, combined deficiency of *H-Ras*, *N-Ras* and *K-Ras* was associated with epidermal thinning and a dramatic decrease in proliferation of epidermal keratinocytes.¹⁷

Removal of all Ras isoforms from keratinocytes in vitro also caused cell cycle arrest. Interestingly, cell cycle arrest, both in vitro and in vivo, was accompanied by downregulation of c-Myc and ΔNp63, 2 well-known regulators of proliferation recognized to play vital roles in epidermal homeostasis and development.^{18,19} The regulation of c-Myc by Ras signaling has been studied in great detail, and therefore, it was not surprising that c-Myc was absent in cells lacking Ras molecules.20 ΔNp63 on the other hand is the most abundant isoform (> 99%) expressed from the *p63* locus in keratinocytes as well as in other epithelial cell types.²¹ Mice lacking *p63* display severe defects in epidermal morphogenesis which are partially rescued by overexpression of $\Delta Np63$, thus indicating that $\Delta Np63$ is critical for keratinocyte proliferation.²² Given the similarities between the phenotypes observed in keratinocytes lacking ΔNp63 and the three Ras isoforms, it seems reasonable to propose that Ras signaling might directly regulate expression of ΔNp63.

In the absence of Ras signaling, we also observed a striking increase in the expression of the cell cycle regulators $p21^{\text{Cip1}}$ and p15INK4b in the basal layer of the epidermis.

Similar results were obtained in cultured keratinocytes.17 Both proteins are known to act as inhibitors of cyclin-dependent kinase complexes involved in cell cycle progression. Early work has established p21Cip1 as a mediator of cell cycle arrest and induction of differentiation in keratinocytes.^{23,24} Accordingly, p21^{Cip1} levels were undetectable in the highly proliferative basal layer of the epidermis and were subsequently induced upon asymmetric cell division in the suprabasal layer.17 In contrast, we detected strong $p21^{\text{Cip1}}$ expression in the basal layer of the epidermis in the absence of Ras expression. Interestingly, both c-Myc and ΔNp63 have previously been implicated as negative regulators of $p21^{\text{Cip1}}$, thus suggesting that the absence of c-Myc and/or ΔNp63 may contribute to p21Cip1 induction and subsequently, to cell cycle arrest.^{25,26} Similarly, p15^{INK4b}, which displayed an expression pattern similar to that of p21^{Cip1} in cells of the basal layer was subject to repression by c -Myc.²⁷ These observations suggest that Ras signaling is critical for keratinocyte proliferation, possibly through positive stimulation of c-Myc and ΔNp63 expression which, in turn, prevent the accumulation of the cell cycle inhibitors p21^{Cip1} and p15^{INK4b} (**Fig. 1**).

Previous genetic studies have indicated that Ras proteins mediate proliferative signaling through the Raf/Mek/Erk pathway.28,29 In vitro data from cultured keratinocytes lacking Ras expression also confirmed these observations.¹⁷ Ectopic expression of a constitutively active Erk2 kinase allowed keratinocytes to proliferate in the absence of Ras signaling. Furthermore, constitutive Erk signaling rescued c-Myc/ΔNp63 expression leading to inhibition of p21^{Cip1}/p15^{INK4b}. Likewise, genetic elimination of both *Mek* isoforms, which are crucial for Erk activation, caused hypoproliferation of keratinocytes in vivo, thus indicating that the linear Ras-Raf-Mek-Erk cascade plays a fundamental role in controlling keratinocyte proliferation.30

Although blocking Ras signaling by overexpression of dominant-negative Ras caused an increase in differentiated suprabasal cells, genetic elimination of the three *Ras* loci from the epidermis resulted in delayed appearance of differentiation markers.13,17 Disruption of both *Mek*

Figure 1. Ras activity and epidermal proliferation. Genetic elimination of *H-Ras*, *N-Ras* and *K-Ras* from epidermis (Ras KO) causes a defective epidermis characterized by low levels of expression of c-Myc and Δ Np63 and high expression levels of p21^{Cip1} and p15^{INK4b} in the basal layer. In contrast, normal epidermis (wild-type Ras) expresses high levels of c-Myc and ΔNp63 in the basal but not in the suprabasal layer. An opposite pattern of expression is shown by p21^{Cip1} and p15^{INK4b} which are highly expressed in the suprabasal layer but not in the basal layer. In most scenarios, expression of endogenous oncogenic *H-Ras* and *K-Ras* mutants in the epidermis do not affect epidermal development. However, when oncogenic *Ras* mutants are expressed at unphysiologically elevated levels in transgenic mice, they efficiently induce papillomas and squamous cell carcinomas. See text for details.

isoforms displayed a phenotype similar to the one observed after *Ras* elimination.30 These observations suggest that interfering with Ras or its downstream target Mek in the epidermis results in hypoproliferation accompanied by defects in differentiation and possibly also barrier formation.³⁰ The reason for the increase in differentiated suprabasal cells observed in the epidermis expressing dominant-negative Ras is currently unknown, but might involve altered signaling capacities of Ras-independent pathways, probably affecting those driven by other members of the Ras superfamily of proteins. However, elimination of the *Ras* loci from keratinocytes in vitro did cause induction of suprabasal marker proteins, thus indicating that arrested keratinocytes in vitro do not exactly recapitulate the behavior of keratinocytes in the basal layer of the epidermis, at least after elimination of the 3 *Ras* loci. The appearance of senescence markers in vitro, but not in vivo, further supports this hypothesis.17

Taken together, these results indicate that elimination of all Ras isoforms, or

their downstream targets such as the Mek kinases, strongly interferes with the tightly regulated control of proliferation in the epidermis; thus, indicating that Ras proteins perform essential functions in epidermal development. Furthermore, these observations demonstrate that mitogenic signals cannot be effectively transmitted in their absence, thereby ultimately causing severe hypoproliferation of epidermal keratinocytes.

Ras Signaling in Epidermal Tumorigenesis: Transgenic Mice

There is ample evidence for a causative role of deregulated Ras signaling in tumor development.³¹ To date, mutations in one of the *RAS* genes have been detected in at least 16% of all human cancers, although the actual number of tumors harboring a constitutively active RAS pathway might be significantly higher, given that activating mutations were found in upstream regulators such as the EGFR, or downstream targets such as

the B-RAF and MEK kinases.32 In keratinocyte-derived skin cancer, such as squamous cell carcinoma, *RAS* mutations occur in up to 22% of cases, with *H-RAS* being the most frequently mutated locus followed by *K-RAS*. 33 Likewise, it has been observed that RAS GTPases are constitutively activated in the majority of squamous cell carcinomas in spite of carrying wild-type *RAS* alleles.33

To study the role of Ras signaling in skin cancer, researchers have been taking advantage of mouse models for many years. Initially, it was demonstrated that the chemical carcinogen 7,12-dimethylbenz(a) anthracene (DMBA) induced mutations in *H-Ras* and initiated skin tumors in combination with the inflammation promoter 12-O-tetradecanoylphorbol-13 acetate (TPA), often accompanied by amplification of the *H-Ras* locus.^{34,35} Later on, a number of transgenic strains were developed that specifically expressed *H-Ras* or *K-Ras* oncogenes in the epidermal compartment. Development of transgenic strains

constitutively expressing *H-Ras* or *K-Ras* oncogenes under control of strong promoters active in the basal layer, such as the keratin 5 or keratin 14 promoters, resulted in embryonic lethality.³³ To avoid this drawback, one group used a truncated keratin 5 promoter that displayed a patchy, restricted expression pattern, being mostly active only in hair follicles and a few cells of the interfollicular epidermis.36 However, despite its restricted expression pattern, expression of an *H-Ras* oncogene was sufficient to induce papillomas that occasionally progressed to carcinomas even in the absence of a tumor promoter.36 Other strategies such as expression of an inducible *H-Ras* oncogene fused with the ligand binding domain of the estrogen receptor from the keratin 14 promoter or a *K-Ras* oncogene under control of an inducible keratin 5 promoter also yielded hyperproliferative phenotypes ranging from benign papillomas to invasive squamous cell carcinomas even in the absence of tumor-promoting inflammatory agents.^{37,38} Likewise, infection of keratinocytes in

mice with retroviruses expressing *H-Ras* oncogenes yielded benign papillomas that occasionally even progressed to carcinomas, but only when promoted with TPA.39

Targeting Ras oncogene expression to suprabasal layers by using the keratin 1 or keratin 10 promoters for transgene expression did not per se result in tumor formation, but rather required a second stimulus such as a wound or inflammation.^{40,41} Another transgenic strain that expressed an oncogenic *H-Ras* transgene under control of the mouse ζ-globin promoter developed benign papillomas as well as malignant squamous carcinomas, but only when treated with the tumor promoter phorbol-12-myristate-13-acetate (PMA).⁴² Other, indirect strategies to activate Ras signaling, such as expression of a constitutively active form of the guanine nucleotide exchange factor SOS under control of the keratin 5 promoter, yielded severe skin hyperplasia and papilloma development.⁴³ Taken together, these studies indicate that overexpression of *H-Ras* or *K-Ras* oncogenes can be sufficient to initiate skin carcinogenesis.

Ras Signaling in Epidermal Tumorigenesis: Genetically Engineered Mice

A major limitation of the models described above is that papilloma or tumor development requires ectopic expression of a *Ras* transgene. More recently, several laboratories have generated mouse strains that harbor oncogenic mutations in their endogenous *Ras* loci. Expression of an endogenous *K-Ras*^{G12D} oncogene following activation of an inducible Cre recombinase under control of the keratin 5 promoter produced benign papillomas when promoted with TPA.⁴⁴ Moreover, combining endogenous *K-Ras* oncogene expression with expression of a mutant *p53* allele (R172H) yielded a significant increase in carcinomas after TPA promotion, thus providing evidence for a cooperation between mutated *K-Ras* and *p53* alleles in skin carcinogenesis.⁴⁴

However, expression of an endogenous *H-Ras*G12V oncogene in the germ line of mice failed to yield any skin phenotype even in homozygosity.⁴⁵ Moreover, exposure of these animals to repeated TPA treatments also failed to induce papillomas or any other type of tumor growth. However, these mutant mice developed papillomas with the same frequency as their wild-type littermates when treated with DMBA and TPA.⁴⁵ Interestingly, those papillomas that developed in heterozygous *H-Ras*G12V mice treated with DMBA and TPA harbored mutations in their wild-type allele. No mutations, other than the G12V mutation engineered in the germ line, were present in the *H-Ras* locus in homozygous *H-Ras*^{G12V} animals. Thus, indicating that DMBA must mutate other loci to initiate skin carcinogenesis in these mice. These observations also suggest that oncogenic *H-Ras* isoforms are not sufficient to initiate skin carcinogenesis when expressed at endogenous levels, although they may contribute to papilloma formation.45 A similar mouse model generated in another laboratory expressing endogenous *H-Ras*G12V in heterozygosity did develop skin papillomas after a long latency even in the absence of TPA.⁴⁶ Yet, all papillomas analyzed displayed elevated copy numbers of the mutated *H-Ras*G12V allele, thus suggesting that oncogenic *H-Ras* needs to be expressed above a certain threshold to be able to induce skin papillomas. Although a rigorous analysis of ectopic oncogenic *H-Ras* expression levels in the transgenic strains mentioned earlier is lacking, it appears likely that mutated *H-Ras* might be expressed at higher levels than its endogenous counterpart.

The contribution of Ras signaling to skin carcinogenesis has been further supported by carcinogenesis studies using H-Ras knockout mice.⁴⁷ Treatment of these mutant mice with the standard DMBA+TPA carcinogenesis protocol resulted in significantly fewer papillomas than wild-type mice. Interestingly, a high proportion of those papillomas that arose in mice lacking *H-Ras* alleles, carried mutated *K-Ras* oncogenes, suggesting that *K-Ras* can substitute for *H-Ras* in skin carcinogenesis. These observations, taken together, highlight the importance of using mouse models harboring mutations

in their endogenous loci, since they might substantially differ from transgenic strains in certain settings, possibly as a result of the lack of proper transcriptional regulation of the artificial transgenes.

Conclusions

From the work generated in various laboratories over the past years, a picture is beginning to emerge where the level of Ras activity has direct consequences on the proliferation of epidermal keratinocytes (**Fig. 1**). Whereas lack of Ras activity causes hypoproliferation and atrophy of the epidermis, increased Ras activity might lead to hyperproliferation and eventually tumor development in the skin. Yet, the molecular mechanisms as well as the downstream targets of Ras proteins that control epidermal development, homeostasis, and tumor development remain largely unknown. A large array of molecular players and signaling pathways acting in epidermal biology have been identified over the last years with the help of mouse models.35,48 Therefore, it would not be surprising if some of these regulators eventually turned out to be connected to Ras signaling pathways. Nevertheless, genetic studies using mouse models will be an adequate way to verify these signaling networks, especially with regard to the development of new strategies for the treatment of skin cancer.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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