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## Keratins in health and cancer: more than mere epithelial cell markers

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### Abstract

Keratins are the intermediate filament (IF)-forming proteins of epithelial cells. Since their initial characterization almost 30 years ago, the total number of mammalian keratins has increased to 54, including 28 type I and 26 type II keratins. Keratins are obligate heteropolymers and, similarly to other IFs, they contain a dimeric central  $\alpha$ -helical rod domain that is flanked by non-helical head and tail domains. The 10-nm keratin filaments participate in the formation of a proteinaceous structural framework within the cellular cytoplasm and, as such, serve an important role in epithelial cell protection from mechanical and non-mechanical stressors, a property extensively substantiated by the discovery of human keratin mutations predisposing to tissue-specific injury and by studies in keratin knockout and transgenic mice. More recently, keratins have also been recognized as regulators of other cellular properties and functions, including apico-basal polarization, motility, cell size, protein synthesis and membrane traffic and signaling. In cancer, keratins are extensively used as diagnostic tumor markers, as epithelial malignancies largely maintain the specific keratin patterns associated with their respective cells of origin, and, in many occasions, full-length or cleaved keratin expression (or lack there of) in tumors and/or peripheral blood carries prognostic significance for cancer patients. Quite intriguingly, several studies have provided evidence for active keratin involvement in cancer cell invasion and metastasis, as well as in treatment responsiveness, and have set the foundation for further exploration of the role of keratins as multifunctional regulators of epithelial tumorigenesis.

### Keywords

keratins; cancer; invasion; diagnosis; prognosis; drug resistance

### Introduction

The cytoskeleton is a proteinaceous structural framework within the cellular cytoplasm (Fuchs and Cleveland, 1998). Eukaryotic cells contain three main kinds of cytoskeletal filaments, namely microfilaments, intermediate filaments (IFs) and microtubules. Microfilaments are composed of 6-nm intertwined actin chains and are responsible for resisting tension and maintaining cellular shape, forming cytoplasmic protuberances and participating in cell–cell and cell–matrix interactions (Pollard and Cooper, 2009). The 10 nm

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#### Conflict of interest

The author declares no conflict of interest

in diameter IFs are more stable than actin filaments, organize the internal three-dimensional cellular structure and, similarly to microfilaments, also function in cell shape maintenance by bearing tension (Herrmann *et al.*, 2009). Finally, the microtubules are 23 nm in diameter hollow cylinders, most commonly comprising of 13 protofilaments, which in turn are polymers of alpha- and beta-tubulin, and play key roles in intracellular transport and the formation of the mitotic spindle (Glotzer, 2009).

In contrast to actin filaments and microtubules, IFs are encoded by a large family of genes expressed in a tissue- and differentiation state-specific manner and are classified into discrete categories based on their rod domain amino-acid sequence. Types 1 and 2 IFs are found primarily in epithelial cells and include the acidic and basic keratins, respectively; type 3 IFs include vimentin, desmin and glial fibrillary acidic protein; type 4 IFs assemble into neurofilaments; and type 5 IFs are the nuclear lamins (Herrmann *et al.*, 2007). All IFs have a dimeric central rod domain, which is a coiled coil of two parallel  $\alpha$ -helices flanked by head and tail domains of variable lengths. Antiparallel molecular dimers (referred to as tetramers) polymerize in a staggered manner to make apolar protofilaments (3 nm in diameter), which in turn associate to protofibrils (4–5 nm in diameter), and then to the 10-nm IFs (Steinert *et al.*, 1993), which are among the most chemically stable cellular structures, resisting high temperature, high salt and detergent solubilization.

In this review, we will focus on keratins, the IFs of epithelial cells and will review their functional role in the normal epithelium and their emergent significance in the pathophysiology and treatment of epithelial malignancies.

## Keratins in health

### Epithelial cell IFs

Keratins are the IF-forming proteins of epithelial cells and account for the majority of *IF* genes in the human genome. Two-dimensional isoelectric focusing and sodium dodecyl sulfate–polyacrylamide gel electrophoresis were initially used to profile the keratins of normal human epithelial tissues, cell cultures and tumors (Moll *et al.*, 1982), and resulted in the first comprehensive keratin catalog, which included 19 members and separated them into type I (or acidic, K9–K19) and type II (or basic to neutral, K1–8) keratins, and the recognition that keratin filaments form by heterotypic pairing of type I and type II proteins at equimolar amounts (Quinlan *et al.*, 1984). Additional keratins were subsequently identified (Moll *et al.*, 1990; Takahashi *et al.*, 1995), including a large number of hair follicle-specific keratins (Winter *et al.*, 1998). Given the completion of the human genome sequence, a consensus nomenclature for mammalian keratin genes and proteins is now in place (Schweizer *et al.*, 2006) and includes 28 type I (20 epithelial and 11 hair) keratins and 26 type II (20 epithelial and six hair) keratins. Similarly to other IFs, keratins contain a central  $\alpha$ -helical domain of about 310 amino acids, which is composed of subdomains 1A, 1B, 2A and 2B connected by linkers L1, L12 and L2 (Figure 1). The non-helical head and tail domains consist of subdomains V1 and H1 and H2 and V2, respectively (Herrmann *et al.*, 2007).

Keratins are expressed in all types of epithelial cells (simple, stratified, keratinized and cornified) (Moll *et al.*, 1982; Bragulla and Homberger, 2009). K8 and its obligate partner K18 constitute the primary keratin pair in many simple epithelial cells, such as hepatocytes, pancreatic acinar and islet cells, and proximal tubular kidney epithelial cells, and are also found in pseudostratified (for example, respiratory) and complex (for example, glandular) epithelia (Figure 2) and the urothelium; K7 and K19 are expressed in other simple epithelial cells, such as duct-lining cells, intestinal cells and mesothelial cells, in pseudostratified epithelia and the urothelium; K20 is expressed in gastrointestinal epithelia, the urothelium

and in Merkel (neuroendocrine) cells of the skin; K5 and K14 form the main keratin pair in keratinocytes of stratified squamous epithelia, and are also expressed in basal and myoepithelial cells of complex and glandular epithelial tissues; K6 and K16 have been identified in the epidermis, nail epithelia and non-keratinizing stratified squamous epithelia, but are also expressed in ductal luminal cells and in secretory cells of human eccrine sweat glands; K17 is a basal/myoepithelial cell keratin that is characteristically induced after skin injury; K1/K10, K15, K9 and K2 are all expressed in keratinocytes; K3 and K12 are the keratins of corneal epithelium; K4 and K13 are characteristic of mucosal stratified squamous epithelial cells; and K25–K28 and K71–K75 are hair-follicle-specific keratins, whereas K31–K40 and K81–K86 are keratins of the hair fiber (Moll *et al.*, 2008).

### Protectors of epithelial cell integrity and much more, and so on

Keratins serve an important role in epithelial cell protection from mechanical and non-mechanical stressors (Coulombe and Omary, 2002), a function that has been particularly well characterized in the skin, cornea and liver by both the discovery of human keratin mutations predisposing to tissue-specific injury (Omary *et al.*, 2009) and the development of keratin knockout (KO) and transgenic mouse models (Vijayaraj *et al.*, 2007). For example, mutations in keratins K5 or K14, which are expressed in the basal cells of stratified epithelial, lead to physical trauma-induced fragility and lysis of these cells resulting in intraepithelial blisters and epidermolysis bullosa simplex (Bonifas *et al.*, 1991; Coulombe *et al.*, 1991; Lane *et al.*, 1992); mutations in the cornea-specific keratins K3 or K12 result in the fragility of the anterior corneal epithelium and intraepithelial microcyst formation (Meesmann's corneal dystrophy) (Irvine *et al.*, 1997); K8 (Ku *et al.*, 2001) or K18 (Ku *et al.*, 1997) mutations are found as a predisposition to chronic (Omary *et al.*, 2009) and acute (Strnad *et al.*, 2010) liver disease. Similarly, K5-null mice survive for only a few hours after birth and exhibit extensive skin blistering (Peters *et al.*, 2001), whereas K14-null mice show a similar, but less severe, phenotype and die within 3–4 days (Lloyd *et al.*, 1995); K12 KO mice show corneal erosions (Kao *et al.*, 1996); K8 deficiency results in liver hemorrhage and embryonic lethality in C57BL/6 mice (Baribault *et al.*, 1993) together with mechanical fragility and susceptibility to hepatocyte injury during liver perfusion (Loranger *et al.*, 1997), but causes colorectal hyperplasia and inflammation, rectal prolapse and mild liver injury in the FVB strain (Baribault *et al.*, 1994; Habtezion *et al.*, 2005), whereas K18 KO mice exhibit late-onset, subclinical liver pathology (Magin *et al.*, 1998), suggesting different K8 and K18 roles in inflammatory bowel and liver diseases, although K8 mutations do not appear to be associated with human inflammatory bowel disease (Buning *et al.*, 2004; Ku *et al.*, 2007). Transgenic mouse models have yielded complementary results, further underscoring the functional significance of keratins in epithelial health preservation. Mice overexpressing human K18 bearing an Arg89-to-Cys mutation (corresponding to a highly conserved and mutation 'hot-spot' arginine residue in human skin disorders) show liver and pancreatic keratin filament disruption, hepatocyte fragility, chronic hepatitis (Ku *et al.*, 1995) and increased susceptibility to a variety of stresses, including hepatotoxic drugs, partial hepatectomy, collagenase liver perfusion and Fas-mediated apoptosis (Ku *et al.*, 1999, 2003b; Zatloukal *et al.*, 2000). Overexpression of the human liver disease-associated K8 Gly61-to-Cys variant results in stress-induced liver injury and apoptosis, and a similar phenotype is observed in transgenic mice overexpressing mutant K8 Ser73-to-Ala (Ku and Omary, 2006).

In addition to their widely accepted role as protectors of epithelial cell integrity under a variety of stressful conditions, keratins have been more recently recognized as important regulators of diverse cellular functions, such as apico-basal polarization (Oriolo *et al.*, 2007), cell size determination and protein translation control (Kim *et al.*, 2006; Vijayaraj *et*

*al.*, 2009), organelle positioning and membrane protein targeting (Styers *et al.*, 2005; Toivola *et al.*, 2005).

### Post-translational modifications and protein interactions

In response to stress, keratin expression is commonly altered (Toivola *et al.*, 2010) and keratins become post-translationally modified and structurally reorganized (Ku and Omary, 2006). In keratinocytes, stretching results in K10 suppression and K6 induction (Yano *et al.*, 2004), and wounding upregulates K6, K16 and K17 (Kim *et al.*, 2006). In the liver, K8/K18 levels increase about threefold (mRNA and protein) in response to injury, as noted in mice treated with agents that induce Mallory–Denk body formation (Zatloukal *et al.*, 2007) and in the hepatoma cell line HepG2 treated with doxorubicin (Wang *et al.*, 2009; Hammer *et al.*, 2010), and two- to fourfold (protein) in patients with primary biliary cirrhosis (Fickert *et al.*, 2003). In alveolar epithelial cells, shear stress causes structural remodeling of the keratin IF network (Felder *et al.*, 2008; Sivaramakrishnan *et al.*, 2008), whereas hypoxia results in network disassembly and K8/K18 degradation (Na *et al.*, 2010). Similarly, the keratin cytoskeleton disintegrates in mammary epithelial cells under metabolic (combined glucose and oxygen deprivation mimicking the tumor microenvironment; Nelson *et al.*, 2004) stress (Kongara *et al.*, 2010). For mechanical stress, and likely for other types of stress, keratin reorganization involves a temporal sequence of changes that is dependent on stress duration, and consequently stress severity. For example, in alveolar epithelial cells, thin keratin filaments coalesce to tonofibrils/keratin bundles after 1–4 h of shear stress; Mallory-like body formation is observed after 12–16 h of shear stress, and finally, the keratin network collapses by disassembly and ubiquitin-mediated degradation after 24–36 h of shear stress (Ridge *et al.*, 2005; Sivaramakrishnan *et al.*, 2009).

Keratin reorganization under stress is regulated by post-translational modifications and differential keratin association with scaffolding proteins (Coulombe and Omary, 2002). Among the different types of protein modification, phosphorylation is considered a major regulator, as it modulates intrinsic keratin properties, such as solubility, conformation and filament structure, and it also regulates other post-translational modifications (Omary *et al.*, 2006). Keratin phosphorylation occurs at Ser > Thr > Tyr residues within Arg-rich Ser-Arg-Ser-Xaa (Xaa denotes any amino acid) or Leu-Leu-Ser/Thr-Pro-Leu motifs, among others, located within the head and tail keratin domains. The number of phosphates per keratin molecule is keratin-, cell type- and biological context dependent. In general, phosphorylation levels are low in basal conditions, but increase several fold in mitosis (Toivola *et al.*, 2002) and under a variety of cellular stresses, including drug-induced apoptosis (Liao *et al.*, 1997; Schutte *et al.*, 2004), heat stress (Liao *et al.*, 1997), treatment with phosphatase inhibitors (Toivola *et al.*, 2002), shear stress (Ridge *et al.*, 2005) and metabolic stress (Kongara *et al.*, 2010). Three human K8 (S23, S73, S431) and two K18 (S33, S52) major *in vivo* phosphorylation sites have been characterized (Ku and Omary, 2006), and potentially involved kinases have been primarily determined by *in vitro* studies and appear to be at least partially stress dependent. For example, K8 phosphorylation at Ser73 is mediated by the two stress-activated mitogen-activated protein kinase family members p38 and c-jun-N-terminal kinase in response to the phosphatase inhibitors okadaic acid and orthovanadate (Ku *et al.*, 2002a; Woll *et al.*, 2007) and upon stimulation of the proapoptotic receptor Fas/CD95/Apo-1 (He *et al.*, 2002), respectively, and by protein kinase C $\delta$  (PKC $\delta$ ) under mechanical stress (Ridge *et al.*, 2005). Phosphorylation regulates the distribution of keratins into an ‘insoluble’ filamentous cytoskeletal pool and a ‘soluble’ cytosolic or detergent-extractable hyperphosphorylated pool (Omary *et al.*, 1998) and plays a role in keratin ubiquitination and turnover by the proteasome (Ku and Omary, 2000; Jaitovich *et al.*, 2008), and likely by autophagy (Kongara *et al.*, 2010). Phosphorylation is also important for the interaction of keratins with keratin-associated proteins, among them

the adapter/signaling 14-3-3 proteins, which are involved in keratin solubilization during mitosis by binding to phospho(Ser33)-K18 and undergoing nuclear-to-cytoplasmic redistribution (Ku *et al.*, 2002b) and in serum-dependent Akt/mTOR (mammalian target of rapamycin) pathway activation by binding to phospho (Ser44)-K17 and again relocating from the nucleus to the cytoplasm (Kim *et al.*, 2006).

## Keratins in cancer

### Diagnostic markers in epithelial tumors

Given the characteristic cell type-, differentiation- and functional status-dependent keratin expression patterns in epithelial cells, the availability of specific keratin antibodies, and the fact that epithelial tumors largely maintain the features of specific keratin expression associated with the respective cell type of origin, keratins have long and extensively been used as immunohistochemical markers in diagnostic tumor pathology (Figure 3; Table 1) (Moll *et al.*, 2008).

Adenocarcinomas, that is, epithelial cancers arising in glandular tissues, comprise the largest group of human epithelial malignancies and may arise in different organs. The ability to differentiate adenocarcinomas according to their tissue of origin is essential for the selection of the most appropriate treatment regimens, and simple epithelial keratins are the markers predominantly used for this purpose. Most adenocarcinomas express the simple epithelial keratins K8, K18 and K19, whereas K7 and K20 expression is variable. Keratin typing is of particular diagnostic significance in the case of colorectal adenocarcinomas, which similarly to the normal gastrointestinal epithelium are almost always K20-positive, but K7-negative (or have lower K7 expression compared with K20) (Moll *et al.*, 2008). K20 and K7 co-expression has been reported as a characteristic of more advanced colorectal cancers (Hernandez *et al.*, 2005), whereas reduced K20 levels have been detected in association with high microsatellite instability (McGregor *et al.*, 2004). Pancreatic, biliary tract, esophageal and gastric adenocarcinomas uniformly express K7 and more variably, but up to 65%, K20 (Chu *et al.*, 2000), whereas a K7<sup>+</sup>/K20<sup>-</sup> phenotype is characteristic of ovarian, endometrial and lung adenocarcinomas (Moll *et al.*, 2008). Endometrial adenocarcinomas may co-express stratified epithelial keratins, such as K5, as an indication of squamous metaplasia (Chu and Weiss, 2002a). Non-squamous, malignant salivary gland carcinomas are also K7<sup>+</sup>/K20<sup>-</sup>, with the exception of salivary duct carcinomas, which may be positive for both keratins (Nikitakis *et al.*, 2004). Furthermore, almost all thyroid tumors (follicular, papillary and medullary subtypes) and two-thirds of malignant mesothelioma cases are K7<sup>+</sup>/K20<sup>-</sup>. The latter tumors, in contrast to most adenocarcinomas, consistently express keratinocyte-type keratins, notably K5, and vimentin (Yaziji *et al.*, 2006). Appendiceal and lung carcinoids, adrenal cortical, prostatic and hepatocellular carcinomas are negative for both K7 and K20 (Chu and Weiss, 2002b).

Most breast adenocarcinomas, including both ductal and lobular subtypes, constitutively express K7, K8, K18 and K19. However, K8 exhibits a predominantly peripheral staining pattern in ductal carcinoma as compared to a ring-like, perinuclear pattern in lobular carcinoma (Lehr *et al.*, 2000). In poorly differentiated adenocarcinomas corresponding to the basal-like subtype as defined by microarray-based expression profiling of breast tumors (Sorlie *et al.*, 2001), keratins characteristic of the basal cells of stratified epithelium, such as K5/6, K14 and K17, are also expressed. More recently, phospho(Ser73)-K8 was identified as a possible biomarker for lower beclin1 expression, and thus defective autophagy status, in breast tumors (Kongara *et al.*, 2010).

Keratin expression is a particularly useful guide in the correct classification of renal cell carcinomas (RCCs) (Liu *et al.*, 2007), as clear-cell RCCs mainly express K8 and K18 with

minor K19 expression, papillary tumors strongly express K19 and K7 in addition to the basic K8/K18 pair and chromophobe RCCs typically express K7 and K8/K18, but little K19. Benign oncocytomas may histologically resemble chromophobe RCCs, but are K7 negative (Liu *et al.*, 2007). Transitional cell carcinomas generally conserve the urothelial keratin pattern showing combined expression of K8/K18, K7 and K19 together with K13 and K20 (Moll *et al.*, 1992).

Squamous cell carcinomas, independently of their site of origin, are characterized by the expression of the stratified epithelial keratins K5, K14 and K17 and the hyperproliferative keratinocyte-type keratins K6 and K16 (Moll *et al.*, 2008). K1/K10 may also be focally expressed, and K4 and K13 to a lesser extent. In poorly differentiated squamous cell carcinomas, co-expression of the simple epithelial keratins K8, K18 and K19 is often observed.

Use of keratins as diagnostic markers in tumor pathology is by far their most common application in the field of cancer. In cases remaining unclear on the basis of clinical presentation and conventional histopathology, including carcinomas that are poorly differentiated or spreading over several organs and metastases of unknown primary tumor site, keratin typing is especially valuable for correct tumor identification and subsequent selection of the most appropriate treatment plan.

### Prognostic markers in epithelial tumors

Beyond their well-established role as diagnostic markers in cancer, keratins have also been recognized as prognostic indicators in a variety of epithelial malignancies (Table 2). For example, in colorectal cancer, reduced expression of K8 and K20 has been associated with epithelial-to-mesenchymal cancer cell transition, which is generally indicative of higher tumor aggressiveness, and decreased patient survival (Knosel *et al.*, 2006). Also, persistent or higher expression of a caspase-cleaved K18 fragment at Asp396 (produced by apoptotic epithelial cells and detected by an epitope-specific antibody M30) in the serum of colon cancer patients after primary tumor resection is indicative of systemic residual tumor load and significantly correlates with recurrence risk within 3 years (Ausch *et al.*, 2009). Higher serum-cleaved K18/M30 levels before treatment are also predictive of shorter survival in lung cancer patients (Ulukaya *et al.*, 2007). More recently, the ratio of caspase cleaved (M30) to total K18 (M65), conveniently determined in the serum or plasma using commercially available enzyme-linked immunosorbent assay kits, is being explored as a biomarker for therapy efficacy monitoring in carcinoma patients (Linder *et al.*, 2010). Similarly, in patients with intrahepatic cholangiocarcinoma, a high serum K19 fragment (CYFRA21-1) concentration is associated with decreased recurrence-free and overall survival (Uenishi *et al.*, 2008). Intratumoral K20 expression and K20 positivity in the bone marrow and/or blood correlate with worse prognosis in pancreatic adenocarcinomas (Soeth *et al.*, 2005; Matros *et al.*, 2006; Schmitz-Winnenthal *et al.*, 2006). Furthermore, in gastric cancer, real-time quantitative reverse transcription–polymerase chain reaction for K20 in peritoneal lavage fluid predicts peritoneal recurrence in patients undergoing resection with curative intent (Katsuragi *et al.*, 2007); K10 and K19 positivity in hepatocellular carcinomas are significant predictors of shorter overall and disease-free survival after surgical resection (Yang *et al.*, 2008); and absence of squamous differentiation as evidenced by loss of K5/6 expression is associated with more aggressive endometrial carcinomas and reduced survival (Stefansson *et al.*, 2006). In clear-cell RCC, tumoral co-expression of K7 and K19 is associated with the lack of cytogenetic alterations, low nuclear grade and better clinical outcome (Mertz *et al.*, 2008), whereas detection of K8/18-positive circulating tumor cells correlates with positive lymph node status, presence of synchronous metastases at the time of primary tumor resection and poor overall survival in renal cell cancer (Bluemke *et al.*, 2009). Detection of disseminated keratin-positive tumor cells in the bone marrow of prostate

cancer patients before surgery is an independent risk factor for metastasis within 48 months (Weckermann *et al.*, 2009). In skin cancer, keratin expression in malignant melanoma is of particular interest, as K18 mRNA is surprisingly identified in one-third of melanoma tissue samples and is an adverse prognostic factor (Chen *et al.*, 2009).

In breast cancer, the molecularly defined basal-like subtype characterized by estrogen receptor (ER), progesterone receptor and human epidermal growth factor receptor-2 negativity, but epidermal growth factor receptor and K5/6 positivity, is associated with younger patient age, high tumor grade and poor prognosis, including shorter disease-free and overall survival (Cheang *et al.*, 2008; Yamamoto *et al.*, 2009). Expression of K17 in breast tumors is also prognostic of poor clinical outcome and this is independent of tumor size and grade in node-negative disease (van de Rijn *et al.*, 2002). Detection of K19 mRNA-positive circulating tumor cells before adjuvant chemotherapy predicts reduced disease-free and overall survival in patients with ER-negative, triple-negative and human epidermal growth factor receptor2-positive early breast tumors (Ignatiadis *et al.*, 2007), whereas the presence of K19 mRNA-positive circulating tumor cells in the blood after completion of adjuvant chemotherapy in women with early breast cancer of any subtype indicates the presence of chemotherapy-resistant residual disease and is again associated with higher risk of disease recurrence and decreased patient survival (Xenidis *et al.*, 2009). Gene expression profiling has indicated that K18 is frequently downregulated in metastatic breast cancer (Hedenfalk *et al.*, 2001; Zajchowski *et al.*, 2001), a finding associated with advanced tumor stage and grade, bone marrow micrometastasis, and shorter cancer-specific survival and overall survival (Woelfle *et al.*, 2003, 2004). Also, ubiquitin-immunoreactive degradation products of K8 and K18 are detected in breast carcinomas and may determine tumor aggressiveness (Iwaya *et al.*, 2003).

### Functional role in tumorigenesis

Given their emerging regulatory role in normal cell physiology and their frequently altered expression in cancer, the question as to whether keratins play any functional role in epithelial tumorigenesis arises. Although most keratin KO and transgenic mice do not have any apparent tumor phenotype, K8 deficiency (in the FVB background) results in colorectal hyperplasia and inflammation (Baribault *et al.*, 1994; Habtezion *et al.*, 2005), and also affects (shortens) the latency, but not the incidence or the morphological features of polyoma middle T-induced mammary adenocarcinomas (Baribault *et al.*, 1997); human K8 overexpression results in early neoplastic-like alterations in the pancreas, including loss of acinar architecture, dysplasia and increased cell proliferation (Casanova *et al.*, 1999), and correlates with the extent of spontaneous pancreatic injury (Toivola *et al.*, 2008); and finally, ectopic expression of K8 in the skin causes epidermal hyperplasia in young mice, epidermal atypia and preneoplastic changes in aging mice, and malignant progression of benign skin tumors induced by chemical skin carcinogenesis assays (Casanova *et al.*, 2004).

Several studies have provided evidence supporting an active keratin role in cancer cell invasion and metastasis. Transfection of K8 and K18 in mouse L cells, which are fibroblasts and express vimentin, results in keratin filament formation and is associated with deformability and higher migratory and invasive abilities, indicating that keratins may influence cell shape and migration through interactions with the extracellular environment (Chu *et al.*, 1993). Similarly, experimental co-expression of vimentin and K8/K18 increases invasion and migration of human melanoma (Chu *et al.*, 1996) and breast cancer (Hendrix *et al.*, 1997) cells *in vitro*.

Incubation of human pancreatic cancer cells with sphingosylphosphorylcholine, a bioactive lipid present in high-density lipoprotein particles and found at increased levels in the blood and malignant ascites from ovarian cancer patients, induces keratin reorganization to a

perinuclear, ring-like structure, which is accompanied by K8 and K18 phosphorylation at Ser431 and Ser52, respectively (Beil *et al.*, 2003). This change in the keratin network architecture results in increased cellular elasticity and enhanced cell migration, indicating that sphingosylphosphorylcholine -induced keratin remodeling may directly contribute to the metastatic potential of epithelial cancer cells (Suresh *et al.*, 2005). Cell deformability is also increased in association with keratin network alterations owing to sphingosylphosphorylcholine, likely resulting in greater cancer cell ability to invade the surrounding tissue and permeate through the stroma, and thus facilitating its escape from the primary tumor (Rolli *et al.*, 2010). Furthermore, recent work has implicated alterations in keratin phosphorylation as a contributing factor to colorectal cancer progression, as K8 is a physiological substrate of phosphatase of regenerating liver-3, which is known to promote invasiveness and the metastatic potential of colorectal cancer cells, and high phosphatase of regenerating liver-3 levels are associated with reduction or loss of phosphorylated K8 at the invasive front of human colorectal cancer specimens and in liver metastases (Mizuuchi *et al.*, 2009).

Several studies have explored the role of keratins in cancer cell invasion by investigating K8-mediated plasminogen activation to the serine protease plasmin, which is involved in extracellular matrix remodeling and, as such, in tumor progression and metastasis. Plasminogen is activated on the cell surface by the urokinase-type plasminogen activator bound to urokinase-type plasminogen activator receptor and the C-terminal domain of K8 that penetrates the cellular membrane (K8 ectoplasmic domain), as shown in hepatocellular and breast carcinoma cells (Hembrough *et al.*, 1995). Although unlikely that keratin makes it to the cell surface through the regular secretory pathway (Riopel *et al.*, 1993), a monoclonal antibody to the K8 ectoplasmic domain prevents urokinase-type plasminogen activator binding and inhibits plasmin generation, which in turn results in altered cell morphology, greater cell adhesion to fibronectin and reduced breast cancer cell invasion potential (Obermajer *et al.*, 2009), indicating that K8 together with urokinase-type plasminogen activator, plasminogen and fibronectin form a signaling platform that can modulate cell adhesion and invasiveness of breast cancer cells.

K18 may play a regulatory role in hormonally responsive breast cancer, as it can effectively associate with and sequester the *ERα* target gene and *ERα* coactivator LRP16 in the cytoplasm, thus attenuating *ERα*-mediated signaling and estrogen-stimulated cell cycle progression in breast tumor cells (Meng *et al.*, 2009). Furthermore, autophagy defects, which promote mammary tumorigenesis (Karantza-Wadsworth *et al.*, 2007), result in K8, K17 and K19 upregulation in mouse mammary tumor cells under metabolic stress *in vitro* and in allograft mouse mammary tumors *in vivo* (Kongara *et al.*, 2010), potentially implicating deregulation of keratin homeostasis in defective autophagy-associated breast cancer, a hypothesis worthy of further investigation. Defective autophagy has also been implicated in abnormal keratin accumulation in the liver, as Mallory–Denk body-like inclusion formation, which is a common finding in hepatocellular carcinomas, is directly affected by pharmacological autophagy modulation (Harada *et al.*, 2008).

Keratin 17, which is rapidly induced in wounded stratified epithelia, regulates cell size and growth by binding to the adaptor protein 14-3-3σ and stimulating the mTOR pathway, thus regulating protein synthesis (Kim *et al.*, 2006). Additional evidence that keratins may function upstream of mTOR is provided by studies in mice with ablation of all keratin genes, where embryonic lethality from severe growth retardation is associated with aberrant localization of the glucose transporters GLUT1 and GLUT3m resulting in adenosine monophosphate kinase activation and suppression of the mTORC1 downstream targets S6 kinase and 4E-BP1 (Vijayaraj *et al.*, 2009). In an apparently reciprocal relationship, AKT isoforms regulate intermediate filament expression in epithelial cancer cell lines, as



overexpression of AKT1 increases K8/K18 levels and AKT2 upregulates K18 and vimentin (Fortier *et al.*, 2010). Thus, keratins, which are often aberrantly expressed in epithelial cancers, interact in multiple ways with the AKT/mTOR pathway, which itself is frequently abnormally activated in aggressive tumors, raising the possibility that the role of AKT in epithelial tumorigenesis is at least partially keratin mediated and/or dependent.

Keratins are also important for chaperone-mediated intracellular signaling, which may in turn play a role in epithelial tumorigenesis. Atypical PKC is an evolutionarily conserved key regulator of cellular asymmetry, which has also been identified as an oncogene causative of non-small-cell lung cancer and a predisposing factor for colon cancer, when overexpressed (Fields and Regala, 2007). Recent work showed that both filamentous keratins and heat-shock protein 70 are required for the rescue rephosphorylation of mature atypical PKC, thus regulating its subcellular distribution and maintaining its steady-state levels and activity (Mashukova *et al.*, 2009). Furthermore, given an excess of soluble heat-shock protein 70, the keratin network was expected to be a rate-limiting step in the atypical PKC rescue mechanism, a hypothesis confirmed in two different K8-overexpression animal models (Mashukova *et al.*, 2009). In both cases, cellular regions with abnormal and excessive intermediate filament accumulation also exhibited grossly mislocalized active atypical PKC signal, indicating that chaperone-assisted oncogenic kinase activity, including Akt1, may also depend on keratins and expanding on already available knowledge on the role of keratins as chaperone scaffolds (van den *et al.*, 1999; Toivola *et al.*, 2010).

Although K8 mutations have been implicated in the progression of acute and chronic (Ku *et al.*, 2001) liver disease, they have not been directly linked to hepatocellular, pancreatic (Treiber *et al.*, 2006) or any other carcinoma. To date, the only keratin and tumor type for which a specific variant or single-nucleotide polymorphism has been associated with cancer predisposition is K5 in basal cell carcinoma (Stacey *et al.*, 2009), as a genome-wide single-nucleotide polymorphism association scan for common basal cell carcinoma risk variants identified the G138E substitution in K5 as conferring susceptibility to basal cell carcinoma, but not to squamous cell carcinoma, cutaneous melanoma or fair-pigmentation traits. Given the increasing number of genome-wide association studies for different cancers, it is possible that additional keratin variants influencing specific cancer risk may be discovered in the near future.

### Role in drug responsiveness

Keratins protect epithelial cells from mechanical stress, but also provide resistance to other cellular stressors that can lead to cell death, including death receptor activation and chemotherapeutic drugs. For example, K8- and K18-null mice, which lack keratin intermediate filaments in their hepatocytes owing to keratin instability when the partner keratin is missing, and hepatocytes cultured *ex vivo* from K8-null mice are more sensitive to Fas-mediated apoptosis than their wild-type counterparts (Gilbert *et al.*, 2001). Similarly, a K18 mutation (Arg89Cys) disrupting the keratin filament network predisposes hepatocytes to Fas- but not tumor necrosis factor-mediated apoptotic injury (Ku *et al.*, 2003b). These findings clearly show that K8 and K18 mediate resistance to Fas-induced apoptosis in the liver; however, they may also be relevant to cancer therapy, as keratin levels are affected by anticancer drugs, such as mitoxantrone (MX) (Cress *et al.*, 1988) and doxorubicin (Hammer *et al.*, 2010), and proapoptotic receptor agonists may have selective antitumor activity, as activation of the extrinsic apoptotic cell death pathway by binding of the apoptosis ligand 2/ tumor necrosis factor-related apoptosis-inducing ligand to cognate death receptors results in apoptosis of different cancer cell types without significant toxicity toward normal cells (Ashkenazi, 2008; Gonzalvez and Ashkenazi, 2010).

Aberrant keratin expression has already been shown to confer a multidrug resistance phenotype, as mouse L fibroblasts are rendered resistant to MX, doxorubicin, methotrexate, melphalan and vincristine, but not to ionizing radiation, upon K8 and K18 transfection (Bauman *et al.*, 1994). Similarly, NIH 3T3 fibroblasts with ectopic K8/K18 expression exhibit resistance to MX, doxorubicin, bleomycin, mitomycin C and melphalan, but not to cisplatin (Anderson *et al.*, 1996). Furthermore, monocyte chemoattractant protein-7/MX, an MX-selected human breast cancer cell line with a multidrug resistance phenotype owing to overexpression of the breast cancer resistant protein, also exhibits elevated K8 levels, which synergize with breast cancer resistant protein in increasing drug resistance, likely acting via different mechanisms, as anti-K8 short hairpin RNA reverses MX resistance without promoting intracellular drug accumulation as breast cancer resistant protein knockdown does (Liu *et al.*, 2008b). The multidrug resistance of monocyte chemoattractant protein-7/MX cells is at least partially owing to their increased adhesion to the extracellular matrix, which is in turn mediated by K8 expression on the cell surface, indicating that alterations in the expression level and cellular localization of K8 may actively decrease response to cancer treatment (Liu *et al.*, 2008a). Whether pharmacological keratin modulation can be used as an adjunct to chemotherapy for improving therapeutic outcomes remains to be explored.

## Concluding remarks

Keratins are important protectors of epithelial structural integrity under conditions of stress, but have also been recognized as regulators of other cellular functions, including motility, signaling, growth and protein synthesis. In cancer, keratins have traditionally been used as diagnostic tools, but accumulating evidence points to their importance as prognostic markers and, more interestingly, as active regulators of epithelial tumorigenesis and treatment responsiveness. Further investigation into the multifunctional role of keratins in cancer is warranted, and will hopefully result in the emergence of improved diagnostic and prognostic markers and the identification of novel therapeutic targets, in turn leading to earlier cancer detection and the rational design of more efficacious cancer therapies.

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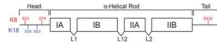
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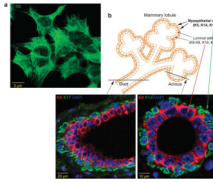
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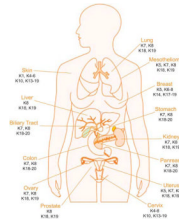
**Figure 1.**

Keratin structure. Keratins form obligate heteropolymers (between one type I and one type II keratin) and share a common structure consisting of a central coiled-coil  $\alpha$ -helical rod domain that is flanked by non-helical head and tail domains. The  $\alpha$ -helical rod domain is subdivided into four subdomains (coils IA, IB, IIA and IIB), which are connected with three linkers (L1, L12 and L2). Most post-translationally modified sites are found within the head and tail domains (conserved phosphorylation sites on human K8 and K18 are shown).



**Figure 2.**

Keratins in mammary epithelial cells *in vitro* and *in vivo*. **(a)** K8 immune staining in immortalized mouse mammary epithelial cells (Karantza-Wadsworth and White, 2008) in two-dimensional culture. **(b)** The mammary gland is a compound tubuloalveolar epithelial cell structure consisting of secretory acini grouped within lobules and draining into intralobular ducts, which in turn drain into interlobular ducts. Lobules are organized into 15–20 lobes emptying into lactiferous sinuses and from there into lactiferous ducts, which open onto the nipple. Ducts (left panel) and acini (right panel) are lined with luminal epithelial cells expressing K8/K18, K19 and K6. These are surrounded by myoepithelial cells, which are characterized by K5, K14 and K17 expression.



**Figure 3.**

Keratin expression in human cancer. Keratins are normally expressed in a cell type-, differentiation- and functional status-dependent manner, and epithelial cancers largely maintain the characteristics of keratin expression associated with their respective cell type of origin, so keratins have long been recognized as diagnostic markers in tumor pathology. Examples of keratins commonly used in the diagnosis of human epithelial malignancies are presented here.

**Table 1****Keratins as diagnostic markers in tumor pathology**

<b>Cancer site and subtype</b>	<b>Keratin expression</b>
Biliary duct	K7, K8, K18–20
Bladder, transitional cell	K5 <sup>a</sup> , K7, K8, K18, K19, K20 <sup>a</sup>
Breast	K5 <sup>a,b</sup> , K6 <sup>a,b</sup> , K7, K8, K14 <sup>a,b</sup> , K17 <sup>a,b</sup> , K18, K19
Cervix	K4–8, K10, K13–19
Colon	K7 <sup>a</sup> , K8, K18–20
Kidney, clear cell	K8, K18, K19 <sup>a</sup>
Papillary	K7, K8, K18, K19
Chromophobe	K7, K8, K18, K19 <sup>a</sup>
Liver	K7 <sup>a</sup> , K8, K18, K19 <sup>a</sup> , K20 <sup>a</sup>
Lung, adenocarcinoma	K7, K8, K18, K19
Small cell	K8, K18, K19 <sup>a</sup>
Ovary, adenocarcinoma <sup>c</sup>	K7, K8, K18, K19
Pancreas	K5 <sup>a</sup> , K7, K8, K18, K19, K20 <sup>a</sup>
Pleura (mesothelioma)	K5, K7 <sup>a</sup> , K8, K18, K19
Prostate	K8, K18, K19
Skin, squamous	K1, K4–6, K8 <sup>d</sup> , K10, K13–17, K18 <sup>d</sup> , K19 <sup>d</sup>
Merkel cell	K8, K18, K20
Stomach	K7 <sup>a</sup> , K8, K18, K19, K20 <sup>a</sup>
Uterus	K5 <sup>a</sup> , K7, K8, K18, K19

<sup>a</sup>Focal/heterogeneous staining in some, but not all, cases.

<sup>b</sup>Focal or extended staining in basal-like tumors.

<sup>c</sup>Non-mucinous.

<sup>d</sup>In poorly differentiated cases.

**Table 2**

## Keratins as prognostic markers in tumor pathology

Cancer site	Keratin expression pattern	Detection site	Prognosis
Biliary duct	High K19 fragment (CYFRA21-1)	Serum	Worse
Breast	K5/6, K17	Tumor	Worse
	K19 mRNA	CTCs <sup>a</sup>	Worse
	Reduced K18 mRNA	Tumor	Worse
Colon	Ubiquitinated K8 and K18 fragments	Tumor	Worse
	Reduced K8, K20	Tumor	Worse
Kidney	Persistent or higher K18 fragment (M30) after primary tumor resection	Serum	Worse
	K8, K18	CTCs <sup>a</sup>	Worse
Liver	K7, K19	Tumor	Better
	K10, K19	Tumor	Worse
Lung	High K18 fragment (M30)	Serum	Worse
Pancreas	K20	Tumor	Worse
	K20	Serum	Worse
Prostate	K8, K18, K19 before surgery	Bone marrow	Worse
Skin (melanoma)	K18	Tumor	Worse
Stomach	K20	Peritoneal fluid	Worse
Uterus	Loss of K5/K6	Tumor	Worse

<sup>a</sup>Circulating tumor cells.