

INVITED REVIEW

Molecular genetics of premalignant oral lesions

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Oral squamous cell carcinoma (OSCC) is characterized by cellular and subcellular alterations that are associated with a progression towards dedifferentiation and growth. There are several histologically distinct lesions of the oral cavity which have malignant potential. These are leukoplakia, erythroplakia, lichen planus, and submucous fibrosis. These are characterized by a spectrum of chromosomal, genetic, and molecular alterations that they share with each other as well as with the malignant lesions that develop from them. In this review we summarize the investigation of the molecular genetics of each of these lesions and relate them to the alterations, which have been demonstrated in OSCC, to define their location on the continuum of changes, which lead to malignant transformation.

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Introduction

Oral Squamous cell carcinoma (OSCC) can be preceded by the appearance of lesions which have the potential either to develop into cancer, or portend the development of cancer in the oral cavity. There are several histologically distinct lesions of the oral mucosa which are characterized as having malignant potential. Among these are leukoplakia, erythroplakia, oral lichen planus (OLP), and submucous fibrosis. These lesions are found in association with and preceding OSCC. They are variable in their malignant potential as well as their genetic background.

The progression of OSCC has been described from a genetic perspective, with a distinct pattern and timing of genetic alterations along a continuum of malignant

transformation. Premalignant lesions have been shown to demonstrate many of the genetic alterations present in OSCC (Califano *et al*, 2000; Ha *et al*, 2003; Ha and Califano, 2003). The degree and amount of similarity to OSCC found in premalignant lesions is, to some degree, dependent upon presence of atypia, however, individual lesions possess molecular genetic traits in common with OSCC even in the absence of histologically defined dysplasia.

The development of OSCC is generally predicated upon the development of multiple, clonal, genetic alteration, which lends a clonal population of cells a growth advantage over others. Due to the mechanism by which oral mucosa undergoes transformation in OSCC, i.e. chronic exposure to carcinogens in the form of tobacco, betel nut, with alcohol as a cocarcinogen, there are a wide variety of molecular alterations that have been associated with carcinogenesis. In addition to dysregulation of oncogenes and tumor suppressors, cytogenetic changes, epigenetic changes, and mitochondrial mutations have been implicated in development of OSCC. These alterations are reflected in varying degrees in premalignant lesions.

Leukoplakia

Leukoplakia is defined by WHO classification as, ‘a predominantly white lesion of the oral mucosa that cannot be characterized as any other definable lesion’ (Pindborg and Wahi, 1997). It is further characterized based upon the heterogeneity of the lesion, with increasing heterogeneity associated with increased likelihood of malignant transformation (Pindborg *et al*, 1963, 1968; Gupta *et al*, 1980; Schepman *et al*, 1998).

Leukoplakia is the most commonly diagnosed premalignant lesion in the oral cavity. It is also most associated with the development of OSCC (Cawson *et al*, 1996). Studies have demonstrated a co-incidence of leukoplakia at the time of diagnosis of OSCC of up to 60% (Gupta *et al*, 1980; Bouquot *et al*, 1988; Reibel, 2003). Patients who present with oral leukoplakia have up to a 36% incidence of subsequent OSCC development if the lesion demonstrates dysplastic features (Silverman *et al*, 1984; Lumerman *et al*, 1995;

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Schepman *et al*, 1998). In the absence of dysplasia these lesions still possess a 15% incidence of cancer development (Silverman *et al*, 1984).

Cytogenetics

Early studies defining a progression model for cancers of the upper aerodigestive tract implicated loss of heterozygosity (LOH) as a mechanism by which genetic loci containing tumor suppressor genes are eliminated. Increased LOH was correlated to histopathologic progression in the upper aerodigestive tract (Califano *et al*, 1996). LOH of the chromosome arms 3p and 9p are associated with increased malignant potential in oral leukoplakia (Emilion *et al*, 1996; Mao, 1997; Zhang and Rosin, 2001). Fifty percent of leukoplakia contains allelic loss of either the 3p or 9p chromosome arms (Rosin *et al*, 2000; van der Riet, 1994). LOH at these loci alone renders a 3.8-fold increased risk of malignant transformation, while additional LOH at the 4q, 8p, 11q, 13q, and 17p loci are associated with 33-fold increased risk of malignant transformation (Rosin *et al*, 2000). Patterns of LOH in leukoplakia are reflected in the foci of early carcinomas, which are found within these lesions (Jiang *et al*, 2001).

Insertion or deletion of basepairs at microsatellites, termed microsatellite instability (MSI), is another cytogenetic feature shared between premalignant lesions and OSCC. The MSI is present in 55% of leukoplakic lesions (Partridge *et al*, 1998). There is a trend towards increasing MSI prevalence associated with histologic progression of premalignant lesions (Ha *et al*, 2002a). The underlying mechanisms for these findings are unclear given the absence of mismatch repair defects.

The presence of chromosomal aneuploidy in leukoplakia at loci containing putative oncogenes has been extremely controversial because of the high-profile retraction of several prominent studies (Sudbo *et al*, 2004; Curfman *et al*, 2006). Notwithstanding, these several studies have demonstrated the presence of aneuploidy in leukoplakia, although not with the prognostic value furthered in the discredited work. Studies have convincingly demonstrated a trend of increasing polysomy at several loci in the progression of upper aerodigestive tract tumors (Hittelman *et al*, 1993, 1996). Chromosome *in situ* hybridization has been used to detect replication of chromosomes in oral leukoplakia. These studies indicate that majority of leukoplakia lesions contain an abnormal number of chromosomes 7 and 17 (Lee *et al*, 1993) and lesions with a >3% proportion of cells with trisomy 9 had a significantly higher likelihood of progression to cancer (Lee *et al*, 2000).

Telomeres are tandem arrays of repeated TTAGGG hexamers found at the end of human chromosomes, which prevent degradation and fusion. Telomere length shortens with aging and progressive replication. The telomerase protein elongates telomeres in germline and fetal cells. Its expression is limited in somatic cells. Several studies have demonstrated that up to 75% of oral leukoplakia demonstrate telomerase activity (Mutirangura *et al*, 1996; Kannan *et al*, 1997; Chang *et al*, 1999; Miyoshi *et al*, 1999; Liao *et al*, 2000;

Fujimoto *et al*, 2001). Several of these studies demonstrated a correlation of telomerase activity with degree of atypia and dysplastic changes (Mutirangura *et al*, 1996; Miyoshi *et al*, 1999). Telomerase mRNA expression levels have also been shown to correlate with advancing grade of dysplasia (Luzar *et al*, 2004), implying that transcriptional upregulation is responsible for increased activity in leukoplakia and OSCC progression.

p53 mutation

Mutation of p53 is one of the most common genetic events in tumorigenesis. It is frequently mutated and present in its inactivated form in OSCC (Nylander *et al*, 2000). Mutant p53 demonstrates a longer half life than wild type, and its mutant form is often detectable by molecular biology techniques (Reibel, 2003). p53 protein expression has been detected by immunohistochemistry (IHC) in 90% of oral leukoplakia, while it is absent in normal oral mucosa (Lippman *et al*, 1995). However, it is unclear whether this expression represents mutant p53 or stabilized wild type protein. Several studies have demonstrated that p53 detection by IHC alone or with other markers appears to be associated with greater risk for malignant progression (Nishioka *et al*, 1993; Kaur *et al*, 1994; Girod *et al*, 1995; Huang *et al*, 1997b; Ries *et al*, 1998; Scheifele *et al*, 2002; Kovesi and Szende, 2003). Meta-analysis concluded that 47% of premalignant lesions had p53 expression (Warnakulasuriya *et al*, 1998), but conclusion as to the role of this finding in carcinogenesis is unclear because of the inability to distinguish between functional p53 isoforms. Parabasal detection of expression of p53 by IHC has been shown to have a stronger correlation with progression to cancer in several studies (Lippman *et al*, 1995; Cruz *et al*, 1998, 2002a,b), lending credence to the potential application of p53 detection in IHC for stratification of risk of malignant transformation in oral leukoplakia.

The p53 functions as a powerful tumor suppressor gene making its mutation or expression alteration a powerful mechanism in carcinogenesis. Loss of function mutation, LOH, and gene promoter inactivation are mechanisms by which this can potentially occur. The LOH of the p53 (17p3) locus has been demonstrated specifically by restriction length fragment polymorphism in premalignant lesions, which have a higher risk for development of malignancy (Partridge *et al*, 1998). Single strand conformational polymorphism (SSCP) is a technique which can detect mutation of a gene by detection of aberrant hybridization to a wild type template. SSCP followed by sequencing demonstrated 11 p53 mutations in a set of brushings from 34 patients with oral leukoplakia (Lopez *et al*, 2004).

Mitochondrial alteration

Mitochondrial genomic mutations occur in response to oxidative damage and stress at a higher rate than the nuclear genome. Mitochondrial alteration has been demonstrated in a range of human tumors, including head and neck cancer (Sanchez-Cespedes *et al*, 2001), but the mechanism by which these mutations contribute

to carcinogenesis has not been demonstrated. It has been postulated to occur because of mitochondrial dysfunction in apoptosis or through reactive oxygen species generation, which perpetuates oxidative DNA damage (Gottlieb and Tomlinson, 2005). Mitochondrial microsatellite analysis of oral leukoplakia demonstrated alteration of the polycytosine tract of the diversity loop, the prevalence of which correlated to an increasing degree of atypia in lesions of leukoplakia (Ha *et al*, 2002b).

Increase in mitochondrial DNA copy number has been postulated to be a mechanism by which cells compensate for dysfunction caused by oxidative DNA damage. Increase in mitochondrial gene copy number has been shown to be present in leukoplakia in a ratio proportionate to the degree of histopathologic severity (Kim *et al*, 2004).

Epigenetic changes

Promoter hypermethylation is a well described mechanism by which tumor suppressor genes are transcriptionally inactivated in OSCC (Ha and Califano, 2006). Aberrant methylation of CpG-rich regions of the promoters prevent gene transcription by altering the structure of histone complexes. Several studies have addressed the occurrence of promoter hypermethylation in leukoplakia. The only study in the literature specifically addressing leukoplakia tissue methylation found RAR- β 2 to be hypermethylated in 53% of lesions (Youssef *et al*, 2004). Oral rinses from patients with leukoplakia demonstrated 44% incidence of methylation of p16 and 56% incidence of methylation of O⁶-methylguanine-DNA-methyltransferase (MGMT) (Lopez *et al*, 2003), two genes which have are methylated in OSCC. Studies are limited by the relatively large amount of DNA required to do methylation analysis. With advancements in the technical aspects of performing methylation analysis assays, further genes will undoubtedly be investigated leading to a more complete picture of the occurrence of methylation in leukoplakia and its role in early carcinogenesis.

Erythroplakia

Oral erythroplakia is a premalignant lesion of the oral mucosa that typically presents as a discrete, velvety red macule or plaque, <1.5 cm in diameter, on the floor of the mouth, the soft palate or the buccal mucosa (Reichart and Philipsen, 2005), 'which cannot be characterized clinically or pathologically as any other recognizable condition' (Kramer *et al*, 1978). Oral erythroplakia is most frequently diagnosed between the ages of 40 and 70 (Kumar *et al*, 2005). For reasons of a paucity of literature specifically devoted to oral erythroplakia, a definitive value for its prevalence is not readily available, however, data range from 0.02% to 0.83% (Shafer and Waldron, 1975; Lay *et al*, 1982; Zain *et al*, 1997; Hashibe *et al*, 2000). Chewing tobacco, alcohol intake, and chutta smoking are strong risk factors for the development of oral erythroplakia (Daftary and Shah, 1992; Hashibe *et al*, 2000). Reported values for the rate of malignant transformation to oral

squamous-cell carcinoma range from 14.3% to 50.0% (Reichart and Philipsen, 2005). Additional evidence of the prognostic significance of oral erythroplakia is that previous studies have found 85–90% of asymptomatic oral squamous-cell carcinomas to be initially reported as erythroplakia (Mashberg and Meyers, 1976; Regezi and Sciubba, 1993).

As has been demonstrated with other premalignant oral lesions, the p53 tumor suppressor gene is frequently mutated in oral erythroplakia. A study by Qin *et al* found 11 of 24 oral erythroplakia lesions to contain a total of 12 p53 mutations that resulted in altered p53 protein sequence. These mutations were located in exons 6 (33%), 5 (25%), 8 (25%), and 9 (17%) of the p53 gene. Six mis-sense mutations, three single-base pair deletions, and three splice-site mutations were observed. Histologic examination of these same specimens did not reveal a significant difference between histologic grade and the frequency of p53 mutations, a finding that suggests that p53 might have been mutated early in oral squamous-cell cancer development when the initial lesion presented as erythroplakia (Qin *et al*, 1999).

Because of the histologic similarities between oral erythroplakia and leukoplakia, it is reasonable to expect that oral erythroplakia lesions might also possess similar subcellular changes as leukoplakia, including LOH, aneuploidy, and MSI. Polysomy of chromosomes 7 and 17 has been implicated in oral erythroplakia (Hittelman *et al*, 1993). Partridge *et al* examined oral erythroplakia and leukoplakia lesions for LOH and allelic gain at several chromosomal loci known to be altered in oral squamous-cell carcinoma. It can be inferred from this study that oral erythroplakia lesions may have LOH or allelic gain at 9p, 3p, within the Rb gene, p53 gene, or the DCC gene (Partridge *et al*, 1998). A more recent study also shows a trend of chromosomal aberrations and aneuploidy associated with oral erythroplakia, although these data are the subjects of a recent controversy (Sudbo *et al*, 2002).

Lichen planus

Oral lichen planus is a benign lesion with a characteristic white, lacy, reticular pattern that classically presents on the buccal mucosa. Papular, atrophic or erosive lesions constitute the major subtypes of OLP, and present infrequently. Erosive lesions, in particular, may be quite painful and result in multiple complications, such as secondary infections (predominantly candida species), as well as poor nutrition and dehydration because of pain (Katta, 2000).

Histopathology generally reveals characteristic bands of infiltrating lymphocytes at the epidermal–dermal junction and damage to the basal cells of the epidermis. The epidermis usually has a saw-toothed appearance secondary to wedge-shaped hypergranulosis and irregular acanthosis (Silverman *et al*, 1991; Buser *et al*, 1997).

Even though the World Health Organization (WHO) classifies OLP as a precancerous lesion, the premalignant or malignant potential of OLP continues to be the subject of an ongoing and controversial debate in

the literature. Mainly several retrospective studies and case series have reported a significant risk of malignant transformation from OLP to OSCC. The reported overall risk of malignant transformation ranges from 0.4% to 5.6%, or 0.04% to 1.74% per annum (van der Meij *et al*, 2003). Malignant transformation is most closely associated with cases of atrophic or erosive OLP (Silverman, 2000). Critics contend that these associations are either coincidental or evidence that a dysplastic epithelial lesion was misdiagnosed as OLP, especially as it is often difficult to differentiate one from the other. A recommendation was therefore made to differentiate carefully between OLP lesions with dysplasia, called lichenoid dysplasia, and simple epithelial dysplasia (Krutchkoff and Eisenberg, 1985). However, as some prospective studies on patients with OLP indicate rather high rates of malignant transformation to OSCC (Silverman *et al*, 1985, 1991), these lesions should be considered premalignant.

A number of scientific investigations are beginning to uncover some of the molecular genetic aberrations within OLP. One of the early molecular genetic studies of OLP looked at the frequency of LOH at nine loci located on chromosomes 3p, 9p, and 17 p, that occur frequently in most oral tumors. The OLP lesions contained minimal genetic deviation, while the various dysplastic and malignant OSCC lesions had steadily increasing frequencies of LOH on multiple chromosomes (Zhang *et al*, 1997). In a further study into the potential for genetic instability on chromosomes 9 and 17 in OLP, (Kim *et al*, 2001) OLP was compared with lichenoid dysplasia lesions that progressed to OSCC using chromosome *in situ* hybridization. There was a statistically significant difference in the degree of genetic instability between OLP and lichenoid dysplasia, with an increase in partial imbalance of chromosome 9 (Kim *et al*, 2001). This could suggest that monosomy of chromosome 9 may have a critical role in the malignant transformation of OLP.

Perturbations of p53 and c-erbB2 protein expression are seen in OLP lesions and may promote dysregulation of apoptosis and/or tyrosine kinase signaling. Expression of the p53 tumor suppressor gene has been detected with IHC in OLP, as well as malignant and metastatic OSCC, with concurrently increasing levels of proliferating cell nuclear antigen (PCNA) expression within these lesions (Girod *et al*, 1994). The increase in the number of p53 positive biopsies significantly correlates with the degree of dysplasia and loss of differentiation in OLP. Most OLP lesions have a characteristic pattern of p53 positive nuclei confined to the basal layer of the epithelium, and in one study, remarkably, nine out of 27 (33%) of the OLP lesions contained p53 mutations when screened for mutations in exons 5 through 8 (Ogmundsdottir *et al*, 2002).

Studies looking at c-erbB2 expression in serial OLP biopsies of progressive lesions and OSCC revealed a loss of expression of the protein, suggesting that loss of c-erbB2 function could potentially indicate a neoplastic transformation and be involved in carcinogenesis (Kilpi *et al*, 1996; Parise Junior *et al*, 2004). In addition, OLP

keratinocytes harbor strong telomerase activity, which could be another indicator of their malignant potential (O'Flatharta *et al*, 2002).

Further investigation of the genetic alterations in OLP, is warranted. A more complete understanding of the genetic aberrations in this disease will help determine and better understand its malignant potential.

Submucous fibrosis

Oral submucous fibrosis (OSF) is a unique chronic disease seen almost exclusively in adult patients from south Asia, where its occurrence has a significant association with areca nut use, principally in betel quid (combined areca nut, betel leaf, tobacco, and slack lime) chewing (Sinor *et al*, 1990; Dave *et al*, 1992; Jeng *et al*, 2001). OSF is a chronic insidious disease characterized by irreversible generalized fibrosis of the oral soft tissues. The earliest clinical sign is blanching of the oral mucosal tissue, imparting a mottled, marble-like appearance. Mature lesions demonstrate palpable fibrous bands which are essential for the diagnosis. Ultimately, difficulties with mastication, speech, and swallowing develop secondary to the progressive oral fibrosis (Yusuf and Yong, 2002; Liu *et al*, 2004).

Early on, the histopathology consists mostly of chronic inflammatory cells with an eosinophilic component infiltrating the subepithelial connective tissues. Older lesions demonstrate a reduced vascularity, reduced numbers of inflammatory cells, and dense bundles and sheets of collagen deposited immediately beneath the epithelium. The diffuse hyalinization of the subepithelial stroma usually extends into the submucosal tissues, typically replacing the fatty and fibrovascular tissues (Jayanthi *et al*, 1992; Liu *et al*, 2004).

Oral submucous fibrosis has a propensity for malignant transformation, with as high as a fourth of all cases demonstrate epithelial dysplasia at the time of biopsy. The association of betel quid chewing, OSF, and oral OSCC is quite profound, especially in Taiwan and the Indian subcontinent where up to 80% of oral OSCC is associated with this habit. Epidemiologic studies have shown that the rate of malignant transformation ranges from 3% to 19% (Murti *et al*, 1985; Yusuf and Yong, 2002). The addition of tobacco to the majority of betel quid appears to increase further the risk of malignant transformation (Critchley and Unal, 2003). There is no effective treatment for OSF and the condition is irreversible once formed, hence patients should have regular, close follow up. It is prudent practice for physicians to biopsy the areas of severe disease repeatedly to monitor for malignancy (Zain *et al*, 1999).

Similarly to OLP, there are only a handful of published studies that looked at genetic aberrations in OSF, and their possible role in malignant transformation. Certain worrisome findings, such as polymorphisms of heterochromatic chromosome regions, sister-chromatid exchanges, and aberrant p53 expression and mutations may be involved in OSF carcinogenesis (Cox and Walker, 1996b).

One of the early genetic studies found a statistically significant increase in the size C-band heteromorphism patterns on chromosome 1 in OSF and OSCC patients when compared with healthy subjects (Dave *et al*, 1991). Another cytogenetic study found an increase in the frequency of sister-chromatid exchanges and chromosome aberrations in areca nut consumers with OSF and OSCC, further emphasizing the dangers of this habit, even without the concurrent use of smokeless tobacco (Dave *et al*, 1992).

Oral submucous fibrosis lesions also abnormally express and stain positive for p53, a finding that can once again be explained by specific clustered mutations in exon 5 of the p53 gene (Cox and Walker, 1996a; Chiba *et al*, 1998; Liao *et al*, 2001; Bathi and Prabhat, 2003). The PCNA growth fraction correlates significantly with that derived by Ki-67 labeling, but there was no correlation found between growth fraction and the extent of dysplasia. Once again p53 and PCNA expression was characteristically restricted to the basal epithelial layer, a potential common theme in premalignant lesions (Cox and Walker, 1996a). Furthermore, expression levels and mutation frequencies of p53 were progressively higher in OSCC than in OSF lesions, especially in betel quid chewers. Both groups had significantly higher expression levels and mutation frequencies when compared to normal mucosa, similar to OLP lesions (Chiba *et al*, 1998). Betel quid chewing could now be associated with chromosomal damage, as well as potential genetic mutations and aberrant protein expression.

Another tumor suppressor gene adenomatous polyposis coli (APC) could also potentially be involved in the malignant potential of OSF. Remarkably, in a small subset of patients with OSF, all the patients contained at least one mis-sense mutation, and 87% had an additional non-sense mutation that created a truncated protein and decreased expression levels of APC (Liao *et al*, 2001). Such alteration of the APC gene in OSF may imply a risk of progression to oral cancer, although additional work should be performed on a larger cohort of patients to characterize these alterations further. These are interesting results as LOH with mutation of APC has not been detected frequently in oral cancers, although several studies have described LOH in 25% of oral squamous cell cancers suggested a higher number, with 53.8% showing LOH (Largey *et al*, 1994; Huang *et al*, 1997a; Williams, 2000). Hence APC could play a role in the malignant transformation of OSF-OSCC, because of its functions in the regulation of the Wnt signaling pathway via its interaction with beta catenin (Sierra *et al*, 2006).

The growth of cancer is closely dependent on the balance between cell growth and cell death. The Bcl-2 family of proteins regulates apoptosis and bcl-2 and bax are two of its major mediators. In one report, patients with oral cancer and a variety of premalignant lesions including OSF, revealed aberrant expression of bcl-2 and bax exclusive of p53 expression. In contrast, up to 30% of OSCC demonstrated over expression of both proteins, and had a significant correlation between positive nodal status and expression of p53 and bcl-2 (Teni *et al*, 2002). Interestingly, only a few studies have

been undertaken to investigate apoptosis in OSCC, but one study by Jordan *et al* demonstrated strong Bcl-2 immunoreactivity in poorly differentiated oral cancers and upregulation of expression in dysplastic epithelium adjacent to invasive tumor, whereas in contrast bax immunoreactivity was the strongest in well-differentiated OSCC (Jordan *et al*, 1996). These results suggest that alterations of the Bcl-2 family of proteins may play a role in the in the early stages of epithelial carcinogenesis and development of OSCC, and work needs to continue to evaluate these effects in early premalignant lesions such as OSF.

Conclusions

The distinction between benign and potentially malignant oral lesions is currently based upon histologic examination of biopsy specimens from suspicious lesions. In the absence of frank carcinoma or dysplasia, our ability to quantitate the risk associated with various clinically distinct oral lesions is limited. In fact, there is a significant overlap and subtlety in the diagnosis of these various lesions. The molecular studies that have been undertaken to this point serve as the basis by which we will be eventually able to augment not only clinical assessment and classification of oral lesions, but also predict their malignant potential more accurately. Considerable work remains to be performed in determination of the genetic alterations present, and the appropriate classification and risk stratification of oral lesions.

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