

# SECTION OF INFECTIONS (INF)

**Section head**  
Dr Silvia Franceschi

THE SECTION OF INFECTIONS (INF) IS COMPRISED OF TWO GROUPS: THE INFECTIONS AND CANCER EPIDEMIOLOGY GROUP (ICE) AND THE INFECTIONS AND CANCER BIOLOGY GROUP (ICB). ICE AND ICB HAVE WORKED CLOSELY TOGETHER AND BELONGED TO THE SAME SECTION SINCE 2004.

Persistent infections with viruses, bacteria and parasites account for nearly 20% of the cancer burden worldwide, with less developed countries being the hardest hit. Infections also represent, or might represent in the future, some of the most preventable cancer causes through immunization against or early detection and treatment of the infections. The infectious agents studied include mucosal and cutaneous human papillomavirus (HPV) types; HIV, in combination with other viruses associated with cancer; *Helicobacter* species; Hepatitis B and C virus (HBV/HCV); Epstein Barr virus (EBV) and Polyomaviruses although only a few of them will be described in the present Biennial Report.

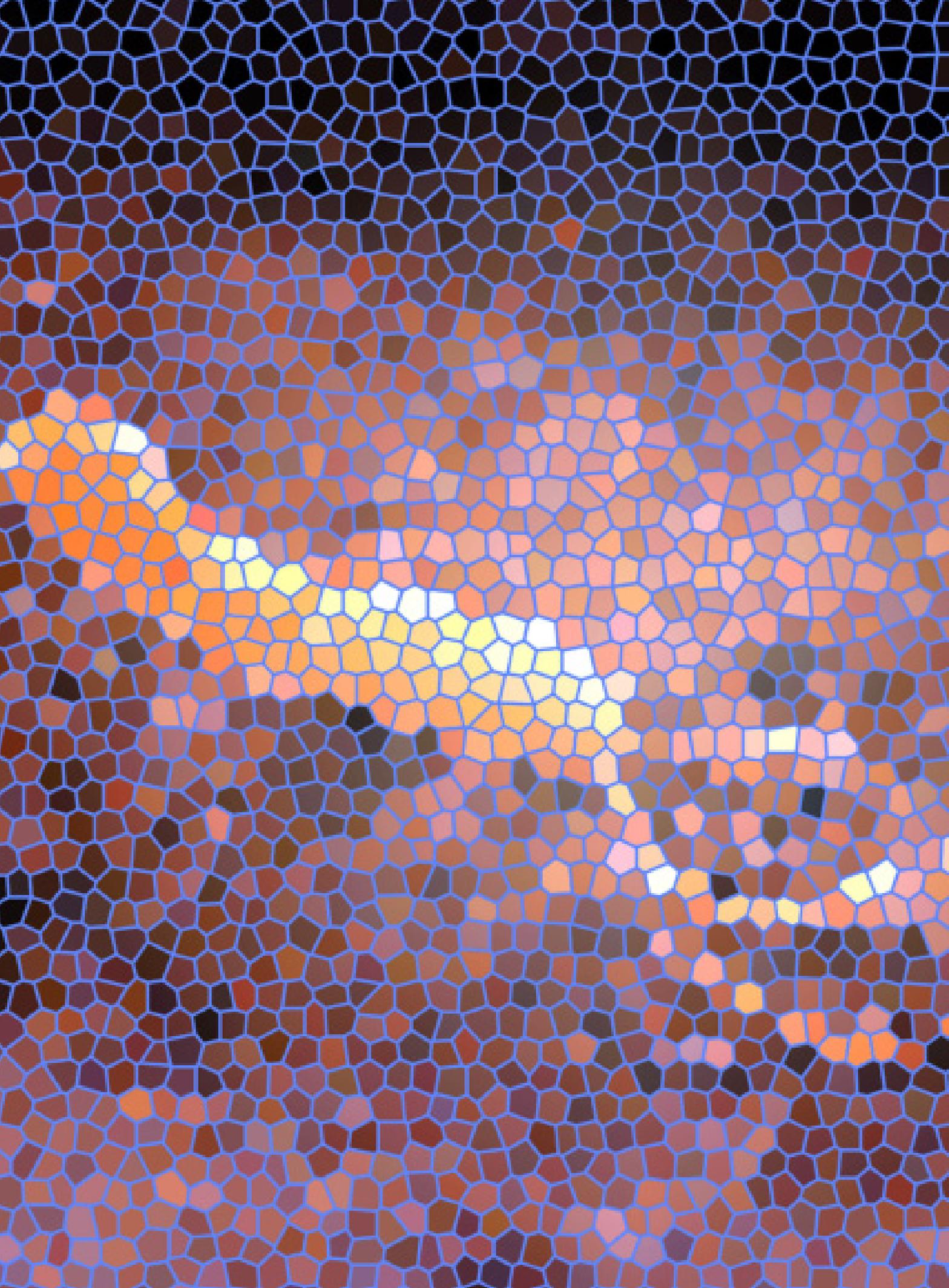
The two Groups have different emphases in relation to infectious agents. ICB, for instance, is focused on cutaneous HPV to a greater extent than ICE. Conversely, ICE is more active in the study of *Helicobacter* species and HIV. Together the two Groups have initiated new projects of HPV and cancer of the head and neck. This topic is charged

with greater methodological problems than HPV and anogenital cancer due to the more limited role of the virus (mainly in cancer of the oropharynx and among non-smokers). The fraction of cancer of the head and neck attributable to HPV has become, however, a crucial issue in respect to the decision to vaccinate adolescent boys against the virus in addition to adolescent girls.

With respect to areas of research, some are exclusive to ICB (e.g. transformation mechanisms) or ICE (worldwide distribution and trends of, as well as fraction of cancer attributable to, carcinogenic infections). New collaborations on other relevant aspects (the role of innate and acquired immunity, the impact of different HPV types and variants) have been initiated thanks to the increasing availability of tests suitable for large-scale application at ICB. Another great asset of INF is the complementary expertise on methodological issues. For example, ICB has expertise in relation to biological protocol issues while ICE is able to provide statistical advice.

Additional collaborations are ongoing with other Sections, notably the Sections of Early Detection and Prevention (EDP), Nutrition and Metabolism (NME), Genetics (GEN), Environment (ENV), Molecular Pathology (MPA) and Cancer Information (CIN).

The over 130 peer-reviewed articles published or accepted for publication by INF in 2010–2011 provide good evidence of the high productivity and the breadth of topics and international collaborations on by INF.



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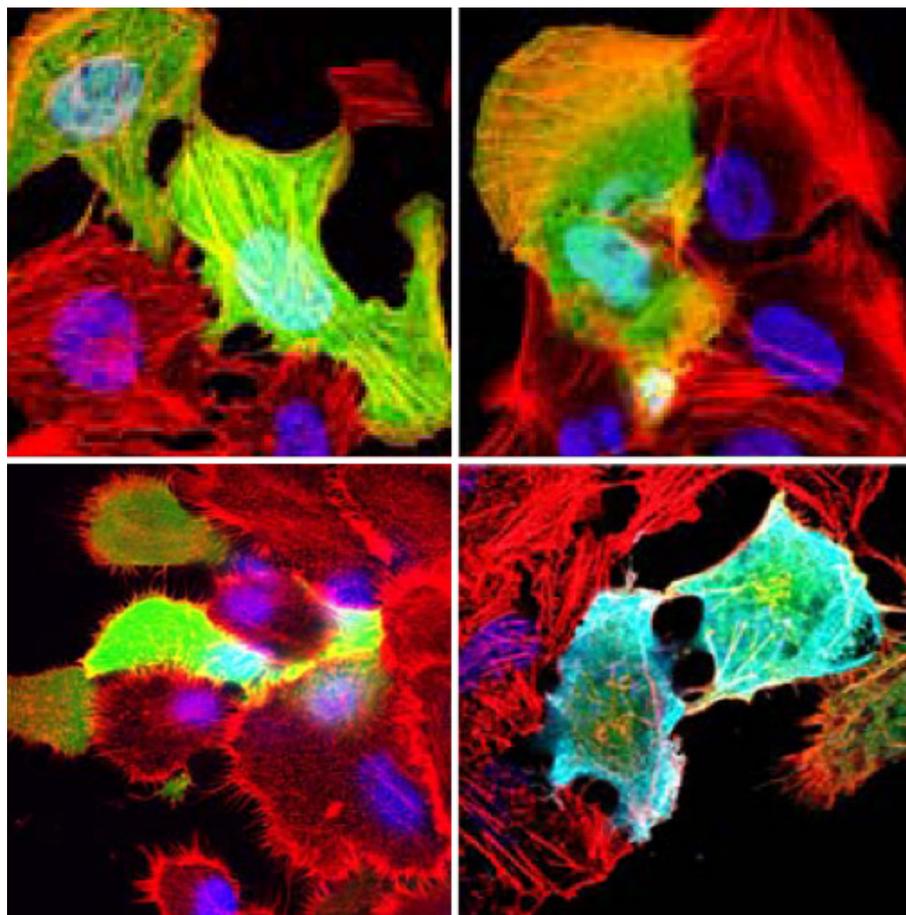
It is well established that infections are the cause of approximately 20% of human cancers worldwide (Parkin, 2006). However, new findings indicate that additional infectious agents are involved in human carcinogenesis. A human polyomavirus, Merkel Cell polyomavirus (MCPyV), has been recently discovered and is associated with a rare tumour, Merkel cell sarcoma (Feng et al., 2008). In addition, certain HPV types that infect the skin and belong to genus  $\beta$  of the HPV phylogenetic tree (Bernard et al., 2010) are suspected to be involved, together with ultraviolet radiation, in the development of non-melanoma skin cancer (NMSC) (Pfister et al., 2003).

The main goal of ICB is to establish a causal role of specific infectious agents in human cancer. Two complementary strategies are currently followed: (1) the characterization of the biological properties of proteins from potential oncogenic viruses using *in vitro* and *in vivo* model systems; and (2) the development of laboratory assays for the detection of infections in human specimens, which can be used in epidemiological studies.

The rationale of our functional studies is based on the fact that viruses directly associated with human cancers have developed several mechanisms to efficiently evade the immune surveillance and to promote cellular transformation. Therefore, studies in the Group aim to characterize the ability of viruses to de-regulate cellular pathways involved in the immune response and cellular transformation to predict their oncogenic potential.

Regarding the development of novel diagnostic tools for infections, we have generated new detection assays with high-throughput, sensitivity and specificity for approximately 80 different viruses. The development of these novel detection assays allowed us to initiate and complete several epidemiological studies.

Future plans of the Group include: extension of the functional studies to emerging oncogenic viruses (e.g. human Merkel cell polyomavirus and related viruses); developing novel detection assays for additional infectious agents;



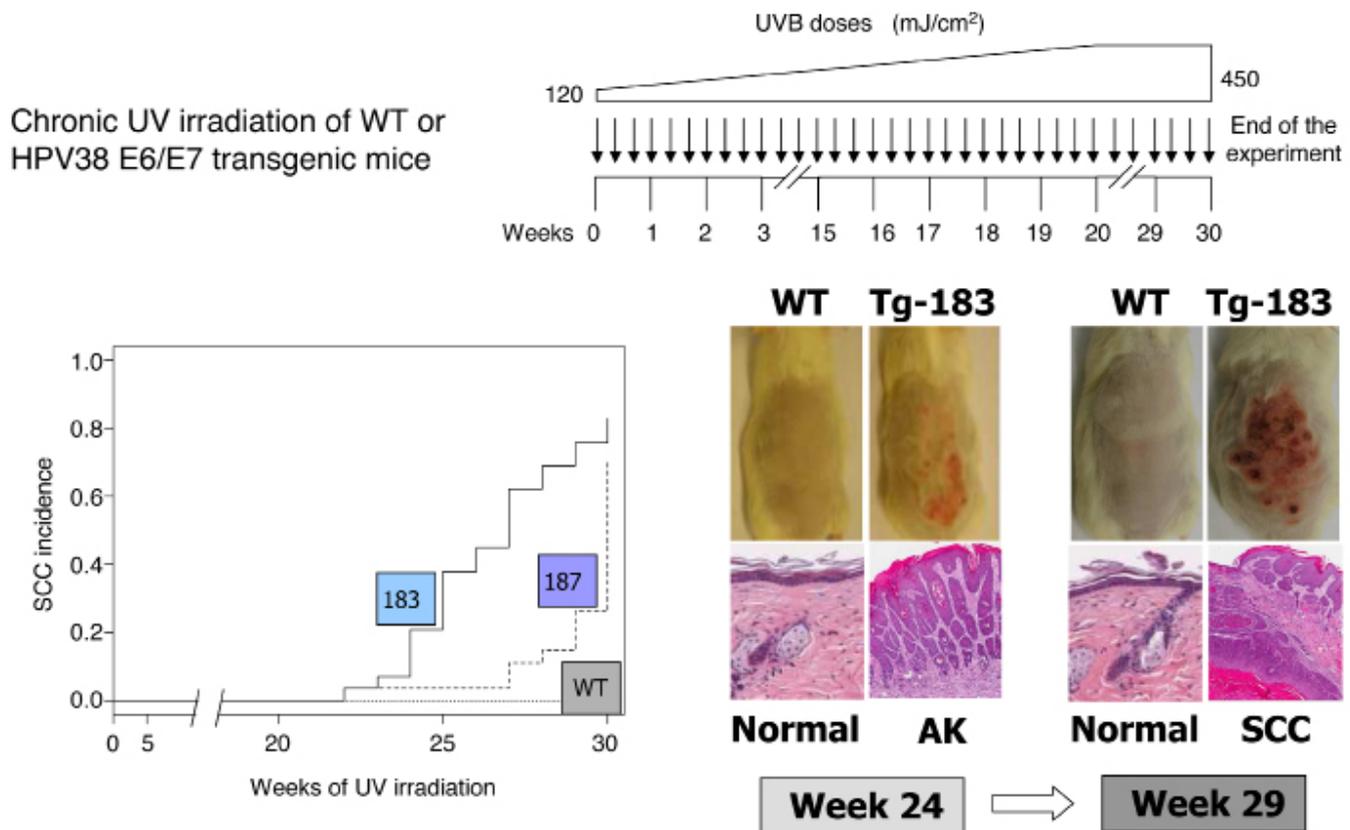
**Figure 1. Primary human keratinocytes expressing E7 oncoprotein from cutaneous HPV38 with an altered cytoskeleton**

and expanding the epidemiological studies in collaboration with groups from IARC and other institutes, including from low-resource countries.

#### ROLE OF $\beta$ CUTANEOUS HPV TYPES IN SKIN CARCINOGENESIS

Epidemiological and biological data have shown that solar exposure and impairment of the immune system are key risk factors for the development of NMSC, which is the most common cancer in fair-skinned adult populations (Pisani et al., 2002). The link with immune status strongly supports the role of an infectious agent in NMSC etiology. Several findings suggest that  $\beta$  HPV types are the most likely infectious agents involved in this disease (Berkhout et al., 2000; de Jong-Tieben et al., 1995; Harwood et al., 2000; Andersson et al., 2008; Waterboer et al., 2008; Casabonne et al., 2007; Karagas et al., 2006; Bavinck et al., 2010); however, their direct role is still under debate. To further evaluate the role of  $\beta$  HPV types in skin carcinogenesis, we have performed several studies to

characterize the biological properties of their main oncoproteins, E6 and E7. Several experimental models have been used, ranging from primary keratinocytes to transgenic mice. In particular, we have focused on HPV38 E6 and E7 that were previously shown to induce immortalization of primary human keratinocytes, the natural host of the virus (Caldeira et al., 2003; Gabet et al., 2008). Recently our studies have demonstrated that HPV38 E6 and E7 have the ability to target several cellular pathways involved in cellular proliferation and apoptosis (Hussain et al., 2011; Yue et al., 2011; Accardi et al., 2011). The data show that HPV38, similar to several oncogenic viruses, activates the NF- $\kappa$ B pathway, increasing the resistance of human keratinocytes to tumour necrosis factor  $\alpha$  (TNF- $\alpha$ )- and UVB radiation-mediated apoptosis. Accordingly, inhibition of NF- $\kappa$ B signalling resulted in the downregulation of NF- $\kappa$ B-regulated antiapoptotic genes, including cIAP1, cIAP2 and XIAP genes and apoptosis (Hussain et al., 2011).



**Figure 2.** HPV38 cooperates with UV in the development of actinic keratosis-like lesions and squamous cell carcinoma in mice

In an additional study, we have demonstrated that HPV38 E7 induces actin stress fibre disruption and that this phenomenon correlates with its ability to downregulate Rho activity. The downregulation of Rho activity by HPV38 E7 is mediated through the activation of the CK2-MEK-extracellular signal-regulated kinase (ERK) pathway, promoting cellular proliferation. In addition, HPV38 E7 is able to induce actin fibre disruption by binding directly to eukaryotic elongation factor 1A (eEF1A) and abolishing its effects on actin fibre formation (Figure 1) (Yue *et al.*, 2011).

Findings in an animal experimental model provided additional evidence for the oncogenic potential of HPV38. We have observed that expression of HPV38 E6 and E7 in the mouse skin strongly synergizes with UV irradiation in promoting pre-malignant and malignant skin lesions. Indeed, chronic UV irradiation of HPV38 E6/E7 transgenic mice induced the development of actinic keratosis-like lesions, which in humans are considered to be precursors of squamous cell carcinomas (SCC), and subsequently of SCC in a significant proportion of the

animals. In contrast, wild-type animals subjected to identical treatments did not develop any type of skin lesions (Figure 2) (Viarisio *et al.*, 2011). Thus, it is clear that the oncoproteins E6 and E7 from  $\beta$  HPV38 significantly contribute to SCC development in the mouse skin, rendering keratinocytes more susceptible to UV-induced carcinogenesis.

#### IDENTIFICATION OF A NOVEL MECHANISM OF INACTIVATION OF THE p53 FUNCTIONS

Studies on the  $\beta$  HPV types also led to the characterization of a novel mechanism involved in the regulation of the intracellular levels of  $\Delta$ Np73 $\alpha$ , an antagonist of the p53/p73-regulated pathways (Accardi *et al.*, 2011). We observed that HPV 38 E6 and E7 promote the accumulation of the I $\kappa$ B kinase  $\beta$  (IKK $\beta$ ) in the nucleus, which in turn associate with and phosphorylate  $\Delta$ Np73 $\alpha$  at serine 422, leading to its stabilization and repression of several p53-regulated genes. Inhibition of IKK $\beta$  resulted in a rapid degradation of  $\Delta$ Np73 $\alpha$  and a rescue of the p53 functions. Interestingly, we have observed that IKK $\beta$  can stabilize  $\Delta$ Np73 $\alpha$

in some breast or head and neck cancer-derived cells. Thus, this event appeared to be important also in non-virus-induced carcinogenesis.

#### PREVALENCE OF HPV INFECTIONS IN HUMAN SPECIMENS FROM DIFFERENT ANATOMICAL SITES

We have developed novel assays based on Luminex technology for the detection of three different groups of HPV, namely (i) mucosal high-risk HPV types (n=19), (ii) mucosal low-risk HPV types (n=18) and (iii) beta and gamma cutaneous HPV types (n=31). Due the high sensitivity and versatility of our HPV detection assay, we were able to perform several epidemiological studies to evaluate the ability of HPV types (i) to infect a specific anatomical and/or (ii) to promote carcinogenesis (e.g. Polesel *et al.* 2011; Rollison *et al.* 2008). In addition, some of the cancer case studies aimed at determining the prevalence of specific mucosal high-risk HPV types in populations that have not yet been analyzed (Gheit *et al.* 2009; Sideri *et al.* 2009)

**ROLE OF DOK1 TUMOUR SUPPRESSOR  
IN NON-VIRUS AND VIRUS-ASSOCIATED  
CANCER**

The Downstream of tyrosine kinase (DOK1) is an adaptor tyrosine kinase substrate with a tumour suppressive activity. We have previously shown that *DOK1* gene can be mutated in chronic lymphocytic leukemia (CLL). *DOK1* mutated in CLL is a nuclear protein in contrast to the wild-type *DOK1* which is cytoplasmic. In addition, a nuclear *DOK1* with a mutated nuclear exclusion site is impaired in inhibiting cell proliferation (Lee *et al.* 2004; Lee *et al.* 2007; Niu *et al.* 2006). We also found a nuclear mislocalisation of *DOK1* in HPV-immortalized keratinocytes. Thus,

the subcellular localization of *DOK1* correlates with its tumour suppressive activities. Further studies revealed that the expression of *DOK1* gene is repressed through hypermethylation of its promoter in the majority of healed and neck cancer (HNC) lines analyzed as well as primary human neoplasm including solid tumours (93% in HNC, 81% in lung cancer) and hematopoietic malignancy (64% in Burkitt's lymphoma) (Saulnier *et al.* 2011). In addition, an inverse correlation was observed between the level of *DOK1* gene methylation and its expression in tumour and adjacent non tumour tissues. Studies are ongoing to evaluate the potential role of *DOK1* as a prognostic marker in HNC and other cancer types.

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HUMAN PAPILLOMAVIRUS

The study of human papillomavirus (HPV) infection, the cause of cervical cancer and target of effective vaccines and screening tests, has been the main focus of the Infections and Cancer Epidemiology Group (ICE) in 2010–2011. The IARC HPV prevalence surveys were continued to include additional populations for whom no or very limited information on the burden of HPV or cervical cancer was available (Figure 1). Evidence on the large variability in HPV prevalence was expanded and can inform the prioritization of HPV vaccine introduction in highest-risk countries in times of financial constraint.

TIME SINCE FIRST INTERCOURSE AND THE RISK OF CERVICAL CANCER

Young age at first sexual intercourse is an important risk factor for cervical cancer (International Collaboration of Epidemiological Studies of Cervical Cancer, 2009). We envisaged, therefore, a model to elucidate the issue by interpreting the age at first sexual intercourse in terms of proxy of age at first HPV infection and, hence, duration of exposure to the virus (Plummer *et al.*, 2011). This approximation is plausible, as it is known that HPV infection is highly contagious and frequent in many world populations, and first infection with HPV often occurs in women soon after first sexual intercourse.

To reduce the confounding effect of multiple sexual partners, we investigated the relationship between risk of cervical carcinoma and time since first intercourse (TFI) using data on monogamous women only (5074 cases and 16 137 controls) from the International Collaboration of Epidemiological Studies of Cervical Cancer, 2009. Odds ratios (ORs) and 95% confidence intervals (CIs) were estimated using conditional logistic regression. In addition, we used age-specific incidence rates in unselected populations to characterize the age profile of cervical cancer incidence.

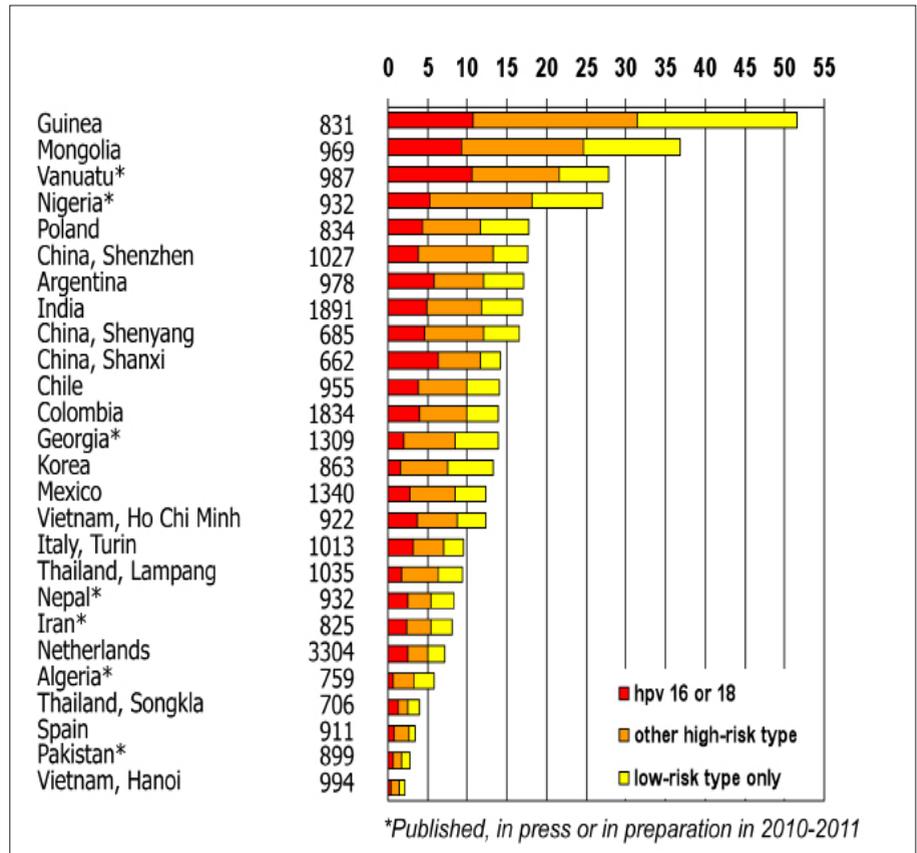


Figure 1. Prevalence (%) of cervical human papillomavirus DNA in sexually active women, IARC Prevalence Surveys, 1990–2011

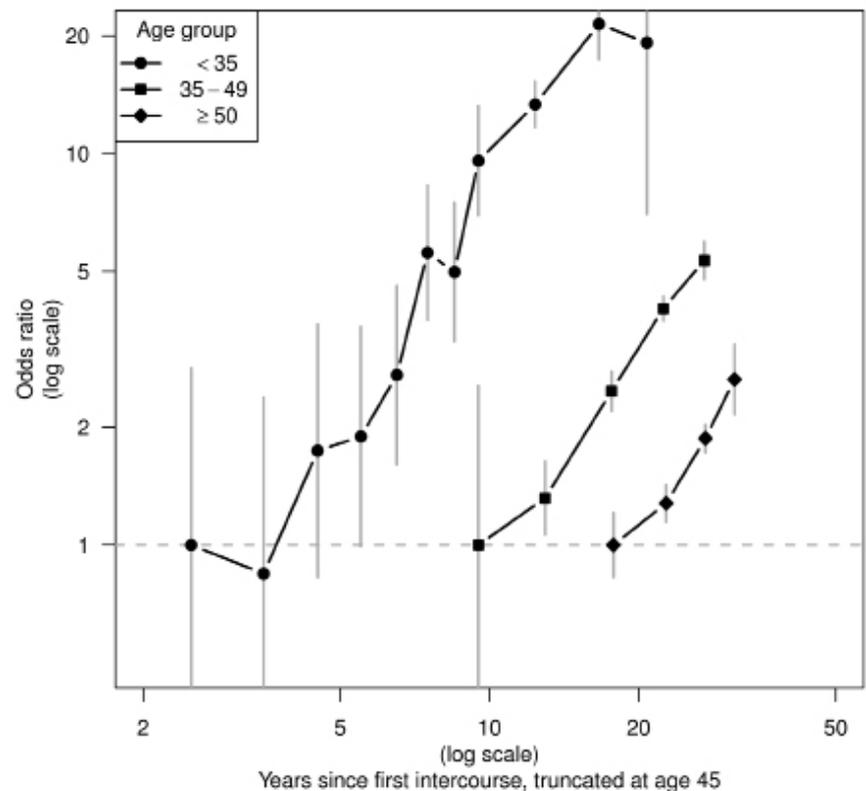


Figure 2. Odds ratios (and 95% floating confidence intervals) for cervical cancer by time since first intercourse stratified by age group (Plummer *et al.*, 2011).

There was no significant difference in slope between the three age strata ( $\chi^2 = 2.67$  with 2 degrees of freedom,  $P = 0.26$ ). The data are thus consistent with a simplified model in which the OR increases as a power of truncated TFI that is constant at all ages. The OR for invasive cervical carcinoma is approximately proportional to the square of TFI (exponent 1.95, 95% CI: 1.76–2.15) up to age 45. Age-specific incidence rates of cervical cancer in unscreened populations are consistent with this model up to age 45, but remain fairly constant at older ages.

We concluded that cervical cancer resembles other cancers caused by strong early-stage carcinogens (e.g. lung cancer and tobacco smoking), with incidence rates proportional to a power of duration of exposure. But cervical cancer also resembles cancers of the breast and other hormone-dependent epithelia, where a similar flattening of age-specific incidence rates is seen at the time menopausal changes start.

Our findings have important implications for immunization strategies against HPV. HPV vaccines have been demonstrated to be highly effective in preventing HPV infection for up to eight years (McKeage and Romanowski, 2011), but the longer term protection is currently unknown. Our model suggests that delaying first exposure to HPV by vaccination would have the same lifelong effect as delaying age at first sexual intercourse. For example, a vaccine against HPV16 and 18 that lasted 15 years would prevent almost all cancers due to these HPV types below age 40 and would reduce the risk almost 5-fold above age 45 (data not shown). Assuming that the vaccine will not be effective against other HPV types, the overall effect would be to reduce all cervical cancer incidence above age 45 by more than 2-fold (Figure 3).

Conversely, our analysis suggests little advantage of vaccinating older women in the prevention of cervical cancer. Women can be infected by carcinogenic HPV at any age (Plummer *et al.*, 2011), but the lifetime cervical cancer risk caused by a new HPV infection will fall sharply with age at infection (Rodríguez *et al.*, 2010).

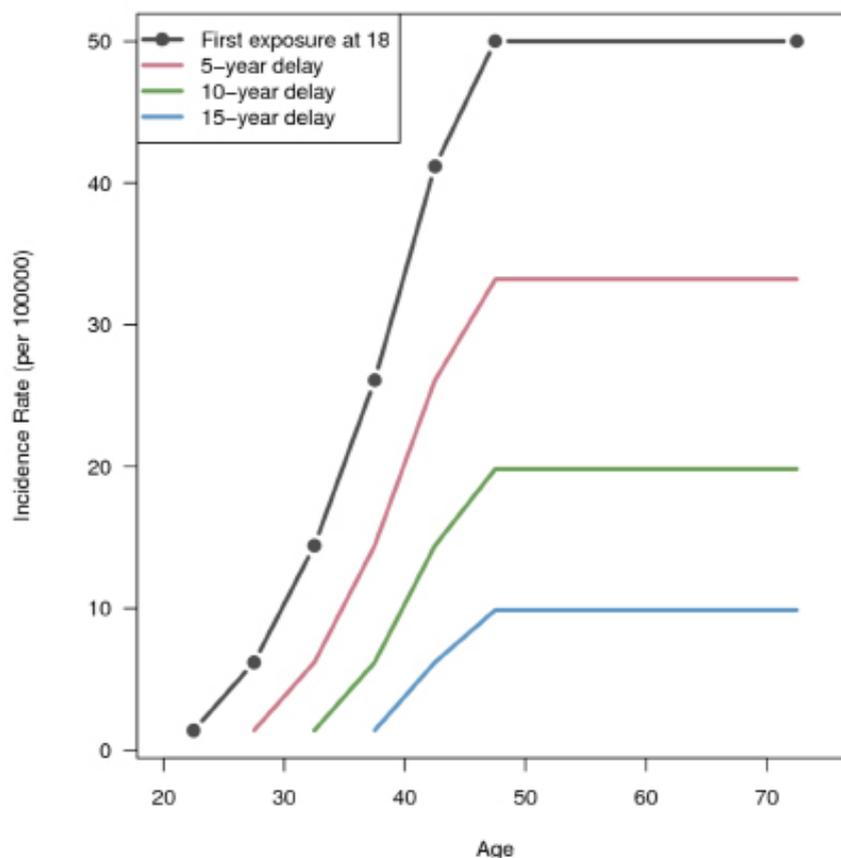


Figure 3. Predicted effect of a vaccine against HPV16 and 18 of limited duration (derived from Plummer *et al.*, 2011)

#### RANDOM CLUSTERING OF HPV INFECTIONS

To understand viral interactions and cross-reactivity of natural or vaccine-induced immunological responses, it is important to assess whether certain combinations of HPV types are more or less likely to be found together, beyond what would be expected by shared sexual transmission and common risk factors.

The ICE has promoted international collaborations that aim to assess the pattern of HPV type clustering in a range of large-scale studies that differ by type of population included (e.g. cancer-free women or men) and HPV detection methods used. These included IARC HPV Prevalence Surveys (mainly low-resource countries) (Vaccarella *et al.*, 2010); The Guanacaste Study of HPV Natural History, Costa Rica (Vaccarella *et al.*, 2011b); The New Technologies in Cervical Cancer (NTCC) screening study, Italy (Carozzi *et al.*, 2011); and The HPV in Men study (United States, Mexico, and Brazil) (Vaccarella *et al.*, 2011a).

An appropriate statistical approach based on multilevel modelling has been developed. We used multivariate logistic regression to model type-specific HPV positivity. The presence of each HPV type was considered as a separate outcome for each woman. The model allows for the inclusion of available covariates such as age, study area and lifetime number of sexual partners. Subject-level random effects represent unobservable risk factors common to all HPV types and allow better adjustment for the complexity of sexual behaviour.

In all study populations considered (see the largest study included, the NTCC, in Figure 4) (Carozzi *et al.*, 2011), high-risk HPV coinfections seemed to occur at random in the female cervix, as well as the male external genitalia. In particular, there was no evidence that HPV16 and 18 are more or less likely to be found in combination with other oncogenic types. The few significant excesses of certain pairs of HPV types that were found could be confidently attributed to artefacts of certain HPV detection methods (e.g. cross-hybridization of similar HPV types) (Vaccarella *et al.*, 2010).

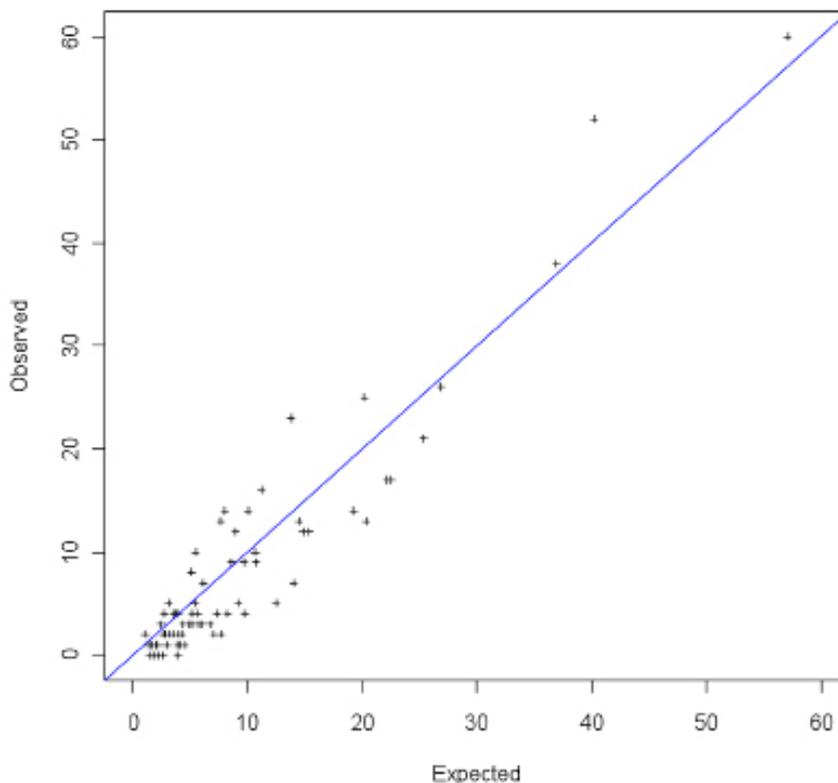
Overall, our collaborative analysis provides evidence that the removal of certain HPV types through vaccination would not result in an indirect increase or decrease in the prevalence of other untargeted types.

#### DISTRIBUTION OF HPV TYPES IN CERVICAL CANCER IN WOMEN INFECTED BY HIV

Though data on the prevalence of HPV types in cervical carcinoma in women with HIV are scarce, they are essential to elucidate the influence of immunity on the carcinogenicity of different HPV types, and the potential impact of prophylactic HPV vaccines in populations with high HIV prevalence. We therefore conducted a case-case study in Kenya and South Africa (De Vuyst *et al.*, 2011). During 2007–2009, frozen tissue biopsies from women with cervical carcinoma were tested for HPV DNA using GP5+/6+-PCR assay. One hundred and six HIV-positive (mean age 40.8 years) and 129 HIV-negative women (mean age 45.7) with SCC were included. Among HIV-positive women, the mean CD4 count was 334 cells/ $\mu$ L and 48.1% were on combined antiretroviral therapy. HIV-infected women had many more multiple HPV infections (21.6% of HPV-positive carcinomas) compared to HIV-negative women (3.3%;  $P < 0.001$ ) and the proportion of multiple infections in HIV-infected women was inversely related to CD4 level.

An excess of HPV18 of borderline statistical significance was shown in HIV-positive compared to HIV-negative cases (Prevalence ratio (PR) = 1.9, 95% CI: 1.0–3.7, adjusted for study centre, age and multiplicity of infection). HPV16 and/or 18 prevalence combined, however, was similar in HIV-positive (66.7%) and HIV-negative cases (69.1%) (PR = 1.0, 95% CI: 0.9–1.2). No significant difference emerged for other HPV types.

Our data are in agreement with a few other smaller studies on the topic. They suggest that current prophylactic HPV vaccines against HPV16 and 18 may prevent similar proportions of cervical cancers in HIV-positive, as in HIV-negative, women provided vaccine-related protection continues after HIV infection.



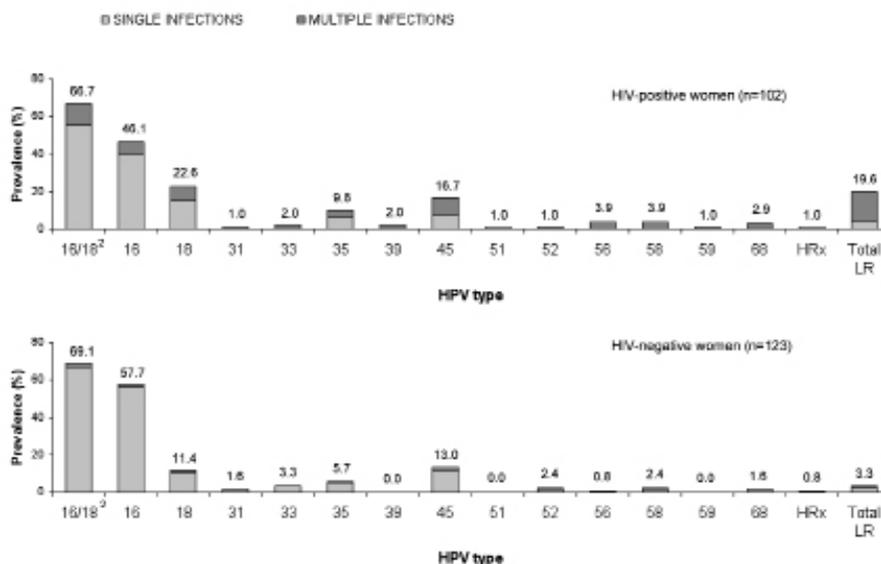
**Figure 4. Observed versus Expected occurrence for 2-way combinations of 13 high-risk human papillomavirus (HPV) types. The New Technologies in Cervical Cancer study, Italy (Carozzi *et al.*, 2011)**

Plus signs represent occurrences of HPV pairs. HPV pairs located in the upper triangle indicate positive clustering, while those located in the lower triangle represent negative clustering between the HPV types involved. None of the P-values for joint HPV infections were significant at the chosen significance level of 0.01.

**Figure 5. Prevalence of human papillomavirus (HPV) in 225 women with cervical squamous cell carcinoma by HIV status and multiplicity of HPV infection (De Vuyst *et al.*, 2011)**

10 HPV-negative women were probably false negatives and were excluded; <sup>2</sup>Either 16 or 18 as single infection or in combination with any type as multiple type infection;

HPV: human papillomavirus; HRX: uncharacterized high-risk type; LR: low-risk.



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