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 Editorial Board of *World Journal of Experimental Medicine*
 Room 903, Building D, Ocean International Center,
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Role of human papillomavirus in the pathogenesis of oral squamous cell carcinoma

Anastasios K Markopoulos

Anastasios K Markopoulos, Department of Oral Medicine/Pathology, Aristotle University, School of Dentistry, University Campus, 54124 Thessaloniki, Greece

Author contributions: Markopoulos AK solely contributed to this paper.

Correspondence to: Anastasios K Markopoulos, DDS, MS, PhD, Professor, Department of Oral Medicine/Pathology, Aristotle University, School of Dentistry, University Campus, 54124 Thessaloniki, Greece. anmark@dent.auth.gr

Telephone: +30-2310-999523 Fax: +30-2310-999532

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Abstract

Oral cancer is one of the most common cancers and it constitutes a major health problem particularly in developing countries. Oral squamous cell carcinoma (OSCC) represents the most frequent of all oral neoplasms. Several risk factors have been well characterized to be associated with OSCC with substantial evidences. While tobacco and alcohol are the primary risk factors for OSCC development, many epidemiological studies report a strong association with human papillomavirus (HPV) in a subset of OSCC. This article presents our current knowledge on the relationship between HPV and development of OSCC. HPVs are DNA viruses that specifically target the basal cells of the epithelial mucosa. Most experimental data are consistent with the hypothesis that HPV plays a causal role in oral carcinogenesis. Genotypes, such as HPV1 infect epidermal cells, whereas HPV6, 11, 16 and 18 infect epithelial cells of the oral cavity and other mucosal surfaces. Several studies have shown that there is an increased risk of head and neck cancer in the two major HPV 16 oncogenes E6 and E7 -positive patients. The presence of antibodies to HPV E6 and E7 proteins was found to be more associated with tumors of the oro-pharynx than of the oral cavity. However, HPV alone appears to be insufficient as the cause of OSCC but requires other co-

factors. Although a viral association within a subset of OSCC has been shown, the molecular and histopathological characteristics of these tumors have yet to be clearly defined.

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Key words: Human papillomavirus; Oral squamous cell carcinoma

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INTRODUCTION

Worldwide, oral cancer accounts for 2%-4% of all cancer cases. In some regions, such as Pakistan, oral cancer reaches the 10% of all cancers, and around 45% in India^[1,2]. Within the EU the highest oral cancer incidence rates for males are found in France and Hungary (6%) and the lowest rates in Greece and Cyprus^[3,4]. In 2009 over 300 000 new cases of oral and oropharyngeal cancer were diagnosed worldwide. During the same time period, over 7000 affected individuals died of these cancers^[5]. Oral cancer includes a group of neoplasms affecting any region of the oral cavity, pharyngeal regions and salivary glands. However, this term is almost synonymous with oral squamous cell carcinoma (OSCC), which represents the most frequent of all oral neoplasms. It is estimated that more of 90% of all oral neoplasms are OSCC^[6]. It is well established that a strong association exists between

genetic factors, environment and oral cancer. Several factors are involved in the pathogenesis of oral cancer, such as age, gender, ethnicity, lifestyle, genetic background, status of health and exposure to one or more oncogenic factors^[7]. Tobacco use and alcohol consumption are well-known risk factors. Micronutrient deficiencies and poor oral hygiene^[8-10] have also been associated with increased risk. However, the observation that several patients with oral cancer have not been exposed to these risk factors suggests that additional causes may promote oral carcinogenesis. Thus, other agents, such as viruses, are being investigated.

HUMAN PAPILLOMAVIRUS AND OSCC

The human papillomavirus (HPV) family consists of more than 100 genotypes, classified in accordance with the ability to infect and transform epithelial cells. HPVs are DNA viruses that specifically target the basal cells of the epithelial mucosa^[11].

Genotypes, such as HPV1 infect epidermal cells, whereas HPV6, 11, 16 and 18 infect epithelial cells of the oral cavity and other mucosal surfaces. The ability of HPV to transform epithelial cells is divided into high-risk and low-risk types. Low-risk types are associated with development of benign lesions such as warts, while infections with high-risk types may progress to malignant lesions^[12].

The HPV involvement in oral carcinogenesis was supported on the basis of the following evidences: (1) the strongly established etiological role of HPV in cervical SCC^[13,14]; (2) the epithelial tropism of HPV; (3) the similarity between oral and genital epithelia^[15]; and (4) the detection of HPV genotypes in samples of OSCC^[16-20].

The HPV involvement in oral and oropharyngeal carcinogenesis was first proposed in 1983 by Syrjänen *et al*^[6]. Her results showed that 40% of the laryngeal and oral cancers contained histological and morphological similarities with HPV-infected lesions, and 50% of the samples demonstrated HPV structural proteins by immunohistochemistry^[21].

Since then, several studies have focused on HPV detection in oral cancer but results have been conflicting^[22-24]. It was found that the prevalence of HPV detection varies broadly, depending on the population, on the location of the cancerous lesion, type of specimen, and detection method. By contrast, HPV was more frequently detected in OSCCs of the oropharynx and tonsil than at other head and neck sites^[25-27]. However, in a systematic review that was performed by Syrjänen *et al*^[28] it was suggested that a potentially important causal association between HPV (specifically HPV16) and OSCC exists. In a recent study the overall HPV prevalence was 10.5% in oral cavity carcinomas and was higher in female than in male cases. Ninety five percent of HPV-positive cases were infected by a single HPV type. HPV 16 was the most prevalent type and was found in 95.5% of HPV-positive oral cavity carcinoma cases^[29].

Furthermore, other studies have proved the existence of a synergistic effect between HPV and alcohol. The risk of head and neck cancer was statistically significantly increased in heavy alcohol users detected with the virus, compared to that of HPV-negative cancer drinkers. Therefore, it has been proposed that alcohol can biologically modify mucosal tissue, increasing its permeability to viral infection, or by influencing the immune response to HPV^[30].

It is believed that one of the major events of HPV-induced carcinogenesis is the integration of the HPV genome into a host chromosome. HPV genome integration often occurs near fragile sites of the human genome, but there are no apparent sites for integration and no evidence for insertional mutagenesis^[31].

Slightly modifying Koch's postulates, in order to establish a relationship between a causative virus and a disease, four criteria are needed: (1) viral genome to be present in tumor lesions or in tumor cells; (2) virus must be isolated from a pathologic lesion and grown in culture; (3) cultured virus should cause disease when inoculated into a healthy organism; and (4) virus must be reisolated from the inoculated host and identified as being identical to the original specific causative factor. However, the use of Koch's postulates to establish disease causation does not fully apply to these phenomena, since the etiology of cancer is multifactorial^[32]. In the contrary, other authors suggest that the incidence of HPV infection in the oral cavities of healthy population is very low and therefore other risk factors are most likely responsible to promote oral carcinogenesis^[33].

GENITAL HPV INFECTION AND RISK OF OSCC

Several studies examined the incidence of second cancers after an initial diagnosis of ano-genital cancers^[34,35] and have showed that there is an increased risk of head and neck cancer as well as other HPV-associated ano-genital cancers in the two major HPV 16 oncogenes E6 and E7 -positive patients. This association between HPV-associated anogenital cancers and head and neck cancer was further strengthened by two larger studies^[36,37].

Additionally, the presence of antibodies to HPV E6 and E7 proteins was found to be more associated with tumors of the oro-pharynx than of the oral cavity^[12].

A recent study has shown that besides the classical horizontal transmission during the sexual life, a vertical transmission occurs in approximately 20% of case HPV positive people. In these individuals, HPV-DNA is detected in amniotic fluid, foetal membranes, blood and placental trophoblastic cells, all suggesting HPV infection in utero, i.e. prenatal transmission^[38].

HPV TESTING

HPV testing is critical for the estimation of HPV prevalence in various oral diseases. HPV testing is usually based

on PCR method. General or consensus primers targeting L1 gene are most frequently used for HPV detection because they are able to identify several HPV genotypes at the same time. Sampling techniques together with widely divergent PCR methods in different studies explain most of the variability in HPV prevalence among OSCC and control samples^[29]. *In situ* hybridization and *in situ* oncogenic protein staining techniques have also increased sensitivity and specificity and are used for HPV testing. These techniques have allowed not only the detection of HPV in cytological smears or histopathological immunosections but also the determination of the topographic site of the infection^[30]. According to recent studies, HPV-positive squamous cell carcinomas have intact *p16* gene and wild type *p53* compared to HPV negative ones^[40]. Other authors have noted that a distinctive mark of the presence of HPV in oral cancer could be found in *p16* nuclear or cytoplasmic overexpression^[41,42]. However, one goal of the scientific research is to find new biological markers able to identify the set(s) of genes involved in oral carcinogenesis.

HPV SEROLOGY

The immune response to HPV infection involves both the cell-mediated and humoral responses. However, serological evidence is circumstantial since it provides only data on prior exposure to HPV. Since not all patients with HPV-associated cancers have detectable HPV antibodies, serum antibody determination may be a limited biomarker for HPV infection and carcinogenesis. Serum antibodies to HPV capsid proteins (virus-like particles) are thought to be a marker of lifetime HPV infection^[43,44]. Antibodies against HPV E6 and E7 proteins are associated with increased risk of HPV-associated cancer^[45,46] but are rather linked more with tumors from the oro-pharynx than from the oral cavity^[12].

The use of HPV viral load in oral biopsies in conjunction with serological markers may serve to identify a subset of HPV-associated oral cancers in which HPV is biologically active.

PROGNOSIS AND FAVORABLE OUTCOME

Several lines of evidence suggest that HPV-positive and HPV-negative HNSCC represent distinct subgroups with different biological, epidemiological and prognostic profiles^[7,47]. Recent data suggest that a positive HPV status represents an important prognostic factor and is associated with a favorable outcome in head and neck cancer. Many studies confirmed that HPV-positive OSCC have a better prognosis compared with those that are HPV negative^[48-51]. There is an approximate 30% absolute survival difference at 5 years (HPV-positive = 60% vs HPV-negative = 30%)^[52]. The favorable outcome for patients harboring HPV-positive cancer cannot be easily explained. It has been proposed that HPV-positive cancer

arises through a different mechanism or exhibits less genetic instability i.e., shows a lower degree of aneuploidy and a tendency to have fewer chromosomal aberrations, when compared to HPV-negative cancer^[53]. In contrast, there appears to be a subgroup of HPV-positive patients whose clinical prognosis is worse than the typical HPV-positive patient. This subgroup has higher smoking rates, higher rates of *p53* mutations and higher expression of EGFR and Bcl-xL^[27].

EXPERIMENTAL EVIDENCE

Experimental evidence regarding the role of HPV in oral carcinogenesis is limited both *in vitro* and in animal experimentation. The lack of suitable experimental animal models has hindered research into HPV cancers for many years. In one of the most significant studies it has been shown that oral keratinocytes could not be transformed by HPV alone but required further mutations in other oncogenes^[54].

CONCLUSION

The vast amounts of epidemiological, molecular pathological and *in vitro* experimental data are consistent with the hypothesis that HPV does indeed have a causal role in oral carcinogenesis. However, HPV alone appears to be insufficient as the cause of OSCC but requires other co-factors. Although a viral association within a subset of OSCC has been shown, the molecular and histopathological characteristics of these tumors have yet to be clearly defined. Since HPV16 is involved in the development of some oral cancers, the implementation of a vaccine program for HPV 16 and 18 may prove to be beneficial in preventing not only cervical cancer, but possibly HPV16-positive oral cancers as well.

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Immunology of tuberculosis

Qing Zhang, Isamu Sugawara

Qing Zhang, Isamu Sugawara, Center of Tuberculosis Diagnosis and Treatment, Shanghai Pulmonary Hospital, Tongji University School of Medicine, Shanghai 200433, China

Author contributions: Zhang Q and Sugawara I equally contributed to this paper.

Correspondence to: Dr. Isamu Sugawara, MD, PhD, Professor of Medicine, Center of Tuberculosis Diagnosis and Treatment, Shanghai Pulmonary Hospital, Tongji University School of Medicine, Shanghai 200433, China. s6671112@sea.plala.or.jp
Telephone: +81-424-724853

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Abstract

Various T cells and macrophages as well as cytokines are involved in the immunopathogenesis of tuberculosis (TB). A better understanding of immunology of TB can not only lead to the discovery of new immunodiagnostic tools, accelerate and facilitate the assessment of new therapeutic methods, but also find new treatment regimens. In this highlight topic we cover the latest developments in the role of T cells, macrophages, Natural killer (NK) cells, invariant NK T (iNKT) cells and $\gamma\delta$ T cells with TB infection. Histologically, TB displays exudative inflammation, proliferative inflammation and productive inflammation depending on the time course. T cells first recognize antigen within the mycobacterially-infected lung, and then activate, differentiate, but the first T cell activation occurs in the draining lymph nodes of the lung. When protective T cells reach sufficient numbers, they can stop bacterial growth. Except for T cells, neutrophils also participate actively in defense against early-phase TB. NK cells are innate lymphocytes which are a first line of defense against mycobacterial infection. Human NK cells use the NKp46, NCRs and NKG2D receptors to lyse *Mycobacterium TB*-infected monocytes and alveolar macrophages. NK cells produce not only interferon- γ , but also interleukin (IL)-22, which is induced by IL-15 and DAP-10. iNKT cells show different phenotypes and functions. Many iNKT cells are CD4+,

few iNKT cells are CD8+, while an additional fraction of iNKT cells are negative for both CD4 and CD8. $\gamma\delta$ T cells represent an early innate defense in antimycobacterial immunity. Studies done in humans and animal models have demonstrated complex patterns of $\gamma\delta$ T cell immune responses during chronic TB. Human alveolar macrophages and monocytes can serve as antigen presentation cells for $\gamma\delta$ T cells. Furthermore, the predominance of V γ 9V δ 2 T cells in TB has been confirmed.

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Key words: Mycobacteria; Tuberculosis; Immunology; T cells; Macrophages; Dendritic cells; Invariant natural killer T cell; Neutrophils; Cytokine

Peer reviewer: Fabian Benencia, PhD, Assistant Professor of Immunology, Department of Biomedical Sciences, College of Osteopathic Medicine and BME, Russ College of Engineering and Technology, Academic Research Center, Ohio University Athens, OH 45701, United States

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INTRODUCTION

Tuberculosis (TB) is a great threat to developing countries as well as developed countries, fuelled by human immunodeficiency virus infection, drug resistance and migration of population. Various T cells are integrated in the immunopathogenesis of TB. A better understanding of this issue can not only drive the progress of new immunodiagnostic tools, accelerate and facilitate the evaluation of new therapeutic methods, but also improve new treatment tools. Here, we will update the readers on the latest developments in this field and, in particular, focus on T lymphocytes, several T cell subsets, macrophages and cytokines involved in TB immunology.

INFLAMMATORY PROCESS OF TUBERCULOSIS

Histopathologically, TB displays exudative inflammation, proliferative inflammation and productive inflammation depending on the time course. Using animal experiments and an inhalation exposure system, the pathologic condition of the infected animals was followed up for 1 year^[1]. Exudative inflammation was observed for the first ten days. Thereafter, granulomas, which corresponded to foci of proliferative inflammation, were formed. Cavity formation was not recognized in animal TB, except for rabbits. Using rabbit models, Dr. Arthur Dannenberg described the pathology of TB in more detail^[1]. There are five stages: onset, symbiosis, early stages of caseous necrosis, interplay of cell-mediated immunity and tissue damaging delayed-type hypersensitivity, and liquefaction and cavity formation. In stage 1, tubercle bacilli are usually destroyed or inhibited by the mature resident alveolar macrophages that ingest them. If bacilli are not destroyed, they grow and eventually destroy the alveolar macrophages. In stage 2, bacilli grow logarithmically within the immature nonactivated macrophages. These macrophages enter a tubercle from the bloodstream. This stage is termed symbiosis because bacilli multiply locally without apparent damage to the host, and macrophages accumulate and divide. In stage 3, the stage at which caseous necrosis first occurs, the number of viable bacilli becomes stationary because their growth is inhibited by the immune response to tuberculin-like antigens released from bacilli. Stage 4 is the stage that usually determines whether the disease becomes clinically apparent. Cell-mediated immunity plays a major role in this situation. The cytotoxic delayed-type hypersensitivity immune response kills these macrophages, causing enlargement of the caseous center and progression of the disease. If good cell-mediated immunity develops, a mantle of highly activated macrophages surrounds the caseous necrosis. In stage 5, bacilli evade host defenses. When liquefaction of the caseous center occurs, the bacilli multiply extracellularly, frequently attaining very large numbers. The high local concentration of tuberculin-like products derived from these bacilli causes a tissue-damaging delayed-type hypersensitivity response that erodes the bronchial wall, forming a cavity.

T CELL ACTIVATION AGAINST MYCOBACTERIUM TUBERCULOSIS

In human, a TB index case may infect a contact person through cough and expectoration, so the lung is the primary route of infection and often the main tissue exhibiting TB. Infectious droplet nuclei are deposited in the alveolar spaces of the contact person where *Mycobacterium tuberculosis* (*M. tuberculosis*) can be phagocytosed by alveolar macrophages, epithelial cells, dendritic cells (DC) and neutrophils^[2,3]. Alveolar macrophages and DC are then believed to transport *M. tuberculosis* to local lymph nodes where T cell activation occurs and expand. DC play important

and indispensable roles in the initiation and maintenance of protective immune responses following mycobacterial infection. The kind of immune responses initiated by DC determines the character of immune responses mounted by the host against the pathogen. The profile of cytokines and chemokines secreted by the result of infection of DC by mycobacteria further plays an important role in defining the course of mycobacterial infection. Activation of the phagocytic host cell is much required to limit growth of *M. tuberculosis*; as in the absence of activation, disease outcome is extremely poor. Effective phagocyte activation requires a specific cellular response, as infected hosts lacking specific components of the acquired response have a poor outcome^[4]. While acquired cellular protection is expressed rapidly following systemic challenge with *M. tuberculosis*, it is less rapid in the lung. Slow expression of protection in the lung allows mycobacteria to grow and modulate the infection site. Until recently it has not been clear whether the slow response to aerosol delivery of bacteria resulted from limited availability of antigen or inhibition of antigen-presentation by *M. tuberculosis*. Several studies show that the first T cell activation occurs in the draining lymph node (DLN) of the lung 8-10 d following initial challenge. The activation of T cells correlated temporally with the arrival of bacteria and availability of antigen in the DLN, however conditions for T cell activation were unique to the DLN as the presence of antigen-producing bacteria in the lung and spleen did not result in initial activation of T cells^[5,6]. While delivery of lipopolysaccharide (LPS) to the *M. tuberculosis*-infected lung failed to accelerate T cell priming^[5], increasing the bacterial dose did accelerate the response modestly suggesting that both antigen burden and refractory cells serve to slow the response. Thus, protective memory cells will not become activated until they recognize antigen, i.e., more than 8 d post infection. Once T cells become activated they differentiate into effector T cells that migrate to the lung. By day 14 of infection, when activated T cells first arrive in the lung, bacteria are within alveolar macrophages, myeloid DC and neutrophils^[4]. T cells can recognize antigen within the mycobacterially-infected lung but the antigen presentation is not optimal. It takes time for the protective T cells to reach sufficient numbers to stop bacterial growth. T cells can be divided into two subsets, Th1 and Th2, on the basis of the cytokines they produce. In tuberculosis, Th1 plays a major role in defense against tuberculosis. Th1 cells suppress Th2 cells. CD4 + T cells have unambiguously been identified as the most important lymphocyte subset for mediating protection. CD4 T lymphocytes differentiate in the peripheral tissues to adopt a variety of fates such as the Th-1 cells, which produce interferon (IFN)- γ to down-regulate Th2 responses and Th-2 cells, which produce interleukin (IL)-4. CD8 T lymphocytes produce predominantly IFN- γ . Though CD4 response is greater than the CD8 response, the latter can provide protection in the absence of CD4 help^[7]. During active TB there is a local pulmonary immune response characterized by α/β T cells and strongly enhanced *M. tuberculosis* antigen-specific Th1 responses, with large amounts of locally secreted IFN- γ ^[8].

ALVEOLAR MACROPHAGES IN TUBERCULOSIS DEVELOPMENT

When tubercle bacilli reach alveoli, they are phagocytosed by resident alveolar macrophages. Though tubercle bacilli are killed by alveolar macrophages, tubercle bacilli can also kill macrophages through apoptosis. What is the fate of tubercle bacilli once they enter the phagosomes of macrophages? Alveolar macrophages of aerily infected guinea pigs were collected by bronchoalveolar lavage. At 12 d after infection, one out of about 10 000 alveolar macrophages of various sizes contained many tubercle bacilli^[9]. This indicates that certain alveolar macrophages permit *M. tuberculosis* to replicate in the phagosomes, although most of tubercle bacilli are killed by activated alveolar macrophages. It will be of great interest to examine the survival mechanism of *M. tuberculosis* at the single-cell level, but we still do not know why macrophages targeted by tubercle bacilli cannot kill the bacilli.

IFN- γ knockout mice were infected with avirulent H37Ra or BCG Pasteur, multinucleated giant cells were recognized in the granulomatous lesions. The lesions also contained tubercle bacilli and consisted of multinucleated cell clusters, being immunopositive with anti-Mac-3 antibody. The multinucleated giant cells were transformed alveolar macrophages. We subsequently infected various cytokine-knockout mice with *M. TB*, but no Langhans' multinucleated giant cells were recognized in the granulomas. Therefore, it seems that formation of multinucleated giant cells requires optimal combinations and concentrations of various cytokines, and the level of IFN- γ , at least, has to be significantly low.

CYTOKINES IN PROTECTION AGAINST TB

IFN- γ and tumor necrosis factor (TNF) have long been implicated as regulators of T cell responses in mycobacterial disease^[10]. The technique of gene targeting (knockout) has swept through biomedical research. IFN- γ , TNF- α , interferon response factor (IRF)-1, nuclear factor (NF)-IL6, NF- κ B p50, signal transducer and activator of transcription (STAT)1 and STAT4 knockout mice succumbed to *M. tuberculosis* infection over time. There appears to be a cytokine and transcription factor hierarchy in experimental tuberculosis. The results indicate that these molecules play major roles in defense against the disease, IFN- γ and TNF- α being the leading players in this respect^[11].

Figure 1 shows the cytokine hierarchy associated with important molecules in experimental tuberculosis. The transcription factors such as NF- κ B, STAT1, STAT4, IRF-1 and NF-IL6 are important molecules in defense against tuberculosis. The molecules [toll-like receptor (TLR)2, TLR6 and MyD-88] are less important in defense against tuberculosis in our hands^[11].

ROLE OF NEUTROPHILS

The role of neutrophils in the development of tuberculosis remained unknown for a long time. We utilized

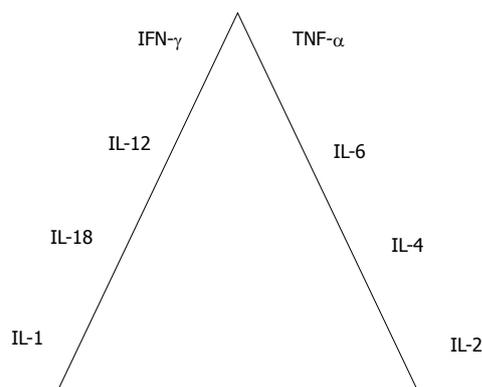


Figure 1 Cytokine hierarchy in immunology of tuberculosis. IFN: Interferon; IL: Interleukin; TNF: Tumor necrosis factor.

LPS-induced transient neutrophilia in the lungs^[9]. LPS (50 μ g/mL) was administered intratracheally to male Fischer rats, which were then infected with *M. tuberculosis* via an airborne route. Intratracheal injection of LPS significantly blocked the development of pulmonary granulomas and significantly reduced the number of pulmonary colony-forming units (CFU). Treatment with amphotericin B (an LPS inhibitor) or neutralizing anti-rat neutrophil antibody reversed the development of pulmonary lesions. LPS-induced transient neutrophilia prevented early mycobacterial infection. The timing of LPS administration was important. When given intratracheally at least 10 d after aerial infection, LPS did not prevent the development of tuberculosis. Neutrophils obtained by bronchoalveolar lavage killed *M. tuberculosis* bacilli. These results indicate clearly that neutrophils participate actively in defense against early-phase tuberculosis.

ROLE OF NATURAL KILLER CELLS

Natural killer (NK) cells are innate lymphocytes which are a first line of defense against infection. NK cells can kill autologous infected cells without prior sensitization, and are believed to play a pivotal role in innate immunity to microbial pathogens. In mouse model, NK cells are activated and produce IFN- γ during the early response to pulmonary tuberculosis^[9] and NK cell-produced IFN- γ regulates the anti-mycobacterial resistance mediated by neutrophils^[12]. However animal models do not give a clear answer to whether NK cells is important in *M. tuberculosis* infection *in vivo*. Depletion of NK cells had no effect on bacterial replication in the lung of immunocompetent mice^[13], suggesting that NK cells may be redundant in the presence of intact adaptive immunity. Surprisingly, IFN- γ knockout mice, which are impaired in their ability to clear mycobacteria, cleared them as effectively as wild-type mice when NK cells were depleted, suggesting that NK cells can inhibit protective immunity^[14].

Human NK cells use the NKp46, the natural cytotoxicity receptors (NCRs) and NKG2D receptors to lyse *M. tuberculosis*-infected monocytes and alveolar macrophages^[15], through damage of infected cells and secretion of cytokines, such as IFN- γ ^[16]. Inhibitory receptors of NK

cells include killer immunoglobulin-like receptors (KIRs) and the NKG2A: CD94 dimer and NK cell activation can also be triggered by loss of inhibitory ligands from the cell surface. In addition, NK cells can also be activated by cytokines, including type I interferons, IL-12 and IL-18. NK cells are a potent and early source of cytokines, particularly IFN- γ , but they can also produce Th2-associated cytokines, such as IL-5 and IL-13, and the regulatory cytokine IL-10^[17]. NK cell NKp46 expression and cytotoxicity are reduced in freshly isolated peripheral blood mononuclear cells (PBMCs) from tuberculosis patients, which may be attributable to suppression by monocytes and IL-10. Recent studies have found that NK cells produce IL-22^[18], which was induced by IL-15 and DAP-10, an adaptor protein that is known to be involved in NK cell activation, in response to *M. tuberculosis*. Rohan Dhiman *et al*^[19] also found that IL-22 can restrict growth of *M. tuberculosis* in macrophages by enhancing phagolysosomal fusion^[19]. Nonetheless to fully understand the importance of NK cells in *M. TB* infection it may be necessary to differentiate their contributions at different stages of disease.

ROLE OF NKT CELLS

Certain T subsets, such as NKT cells and $\gamma\delta$ T cells, have features of innate immune cells including a partially activated phenotype, a rapid response following detection of infected cells, and the modulation of other cell types. Together with NK cells, these cell subsets are functionally defined as innate lymphocytes. CD1d-restricted invariant NKT (iNKT) cells are a conserved subset of T cells that express an invariant T cell receptor (TCR) α chain (V α 24-J α 18 in humans, and V α 14-J α 18 in mice) paired with TCR β chains encoded by one or a few V β gene segments (V β 11 in humans, and predominantly V β 2, 7 and 8 in mice). These cells show different phenotypes and functions^[20]. Many iNKT cells are CD4+, and they have been mainly associated with the induction of Th2 cytokines such as IL-4, IL-5, IL-13. This subset is believed to play a prominent role in suppression of autoimmune or chronic inflammatory diseases, and in promoting allergic conditions such as asthma. Few iNKT cells are CD8+, and most of those express only the CD8 α subunit, which means that they likely express only CD8 $\alpha\alpha$ homodimers. An additional fraction of iNKT cells are negative for both CD4 and CD8 (DN T cells). They have been found to produce predominantly IFN- γ and other Th1-associated cytokines. Studies of human iNKT cells have shown that they have the ability to kill *M. tuberculosis* organisms within infected macrophages, possibly through their production of the peptide granzysin^[21]. Im *et al*^[22] found that the percentages of iNKT cells among total circulating T cells in TB patients were not significantly different compared to those in healthy controls. However, TB patients showed a selective reduction of the proinflammatory CD4-CD8- (DN) iNKT cells with a proportionate increase in the CD4+ iNKT cells. The mouse model of tuberculosis has been used by Sada-Ovalle *et al*^[23] to find that iNKT cells have a direct bactericidal effect on *M. tuberculosis*, and pro-

tect mice against aerosol *M. tuberculosis* infection^[23]. Their activation requires CD1d expression by infected macrophages as well as IL-12 and IL-18. In addition, pharmacological activation of iNKT cells with the synthetic ligand aGalCer often enhances host resistance to infection. iNKT cell use several mechanisms to modify host immunity. These include induction of DC maturation, secondary activation of effector cells (NK cells) or recruitment of inflammatory cells to the site of infection^[24,25]. Thus, by being an early producer of IFN- γ and suppressing intracellular bacterial growth, iNKT cells function as an important part of the early immune response against *M. tuberculosis* that affect both the innate and the adaptive arms of the immune response.

ROLE OF $\gamma\delta$ T CELLS

Antigen-specific $\gamma\delta$ T cells represent an early innate defense that may play a role in antimycobacterial immunity. Studies done in humans and animal models have demonstrated complex patterns of $\gamma\delta$ T cell immune responses during early mycobacterial infections and chronic TB. Like $\alpha\beta$ T lymphocytes, $\gamma\delta$ T cells carry antigen TCR that vary in the physical properties of their ligand-binding sites. $\gamma\delta$ T cells are frequently activated by a variety of pathogens including *M. tuberculosis*^[26]. Mice lacking $\gamma\delta$ T cells succumb more rapidly than control mice following intravenous challenge with virulent *M. tuberculosis*; however, such a difference has not been observed following infection by the aerosol route. $\gamma\delta$ T cells constitute a whole system of functionally specialized subsets that have been implicated in the innate responses against tumors and pathogens, the regulation of immune responses, cell recruitment and activation, and tissue repair^[27]. Human alveolar macrophages and monocytes can serve as antigen presentation cells (APCs) for $\gamma\delta$ T cells. Furthermore, the predominance of V γ 9V δ 2 T cells in TB disease has been confirmed^[28]. When MTB-activated CD4+ and $\gamma\delta$ T cells from healthy tuberculin-positive donors were analyzed for cytokine production in response to *M. tuberculosis* -infected monocytes, both groups secreted large amounts of IFN- γ ^[29]. Previous studies have also demonstrated an increased proliferative activity of V γ 9V δ 2 T cells from patients with TB^[30], but reduced production of IFN- γ , compared with that of healthy tuberculin-positive donors^[31]. Additionally, Dieli *et al*^[32] reported that decrease of V γ 9V δ 2 T cell effector functions involves not only IFN- γ production but also expression of granzysin^[32].

CONCLUSION

$\gamma\delta$ T cells appear to combine properties of both adaptive and innate immunities. The identification of unusual compounds that are recognized by human $\gamma\delta$ T cells but not by $\alpha\beta$ T cells has recently stimulated great interest in the development of $\gamma\delta$ T cell-based therapies.

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Yosuke Kakisaka, MD, Series Editor

Abdominal migraine reviewed from both central and peripheral aspects

Yosuke Kakisaka, Mitsugu Uematsu, Zhong I Wang, Kazuhiro Haginoya

Yosuke Kakisaka, Mitsugu Uematsu, Kazuhiro Haginoya, Department of Pediatrics, Tohoku University School of Medicine, Sendai, Miyagi 980-8574, Japan

Yosuke Kakisaka, Zhong I Wang, Neurological Institute, The Cleveland Clinic, Cleveland, OH 44195, United States

Author contributions: Kakisaka Y, Uematsu M, Wang ZI and Haginoya K all contributed to the substantial contributions to this manuscript, drafting the article or revising it critically for important intellectual content, and final approval of the version to be published.

Correspondence to: Yosuke Kakisaka, MD, Department of Pediatrics, Tohoku University School of Medicine, 1-1 Seiryomachi, Aobaku, Sendai, Miyagi 980-8574, Japan. kakisuke@mui.biglobe.ne.jp

Telephone: +81-22-7177287 Fax: +81-22-7177290

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experimental approach to clarify the mechanism of this peculiar disease.

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Key words: Migraine equivalent; Abdominal migraine; Central hypersensitivity; Visceral hypersensitivity; Sumatriptan**Peer reviewer:** Feng Tao, MD, PhD, Assistant Professor, Department of Anesthesiology and Critical Care Medicine, Johns Hopkins University School of Medicine, 720 Rutland Ave. / Ross 355, Baltimore, MD 21025, United StatesKakisaka Y, Uematsu M, Wang ZI, Haginoya K. Abdominal migraine reviewed from both central and peripheral aspects. *World J Exp Med* 2012; 2(4): 75-77 Available from: URL: <http://www.wjgnet.com/2220-315X/full/v2/i4/75.htm> DOI: <http://dx.doi.org/10.5493/wjem.v2.i4.75>

Abstract

Despite the 2%-5% prevalence of abdominal migraine (AM) during childhood, the precise mechanism remains unknown. In this review, we present recent studies on AM and speculate its mechanism from both peripheral and central nervous system aspects. Although the main symptoms of AM exist at the peripheral level, previous studies have reported possible dysfunction of central nervous system, including photophobia, phonophobia and abnormal visual evoked responses. Recently, a case has been reported with AM combined with "Alice in Wonderland" syndrome with visual and/or bodily distortions, which serves as another piece of evidence of central dysfunction. Another case reported an AM patient having peculiar stereotypical ecchymosis in the legs and buttocks associated with pain attack, which implied possible involvement of peripheral nervous system. Although further investigations and accumulation of AM cases are still needed, we believe that the schema hypothesized here is helpful to plan further

INTRODUCTION

It was in 1921 when abdominal migraine (AM) was first described^[1]. Thanks to efforts by previous investigators^[2], AM is now regarded as the abdominal equivalent to migraine and has been classified not only in the International Classification of Headache Disorders^[3], but also in the Rome III criteria for functional gastrointestinal disorders^[4]. To date, the mechanism of AM still remains unknown. In this review, we will present recent studies on AM and speculate its mechanism from both peripheral and central nervous system aspects, to add new knowledge to our understanding of this disease.

CENTRAL SYMPTOMS ACCOMPANYING ABDOMINAL PAIN IN AM

Although the main symptom of AM exists at the pe-

peripheral level, as the word “abdominal” indicates in the disease name, previous studies have reported possible dysfunction of central nervous system, including photophobia, phonophobia and abnormal visual evoked response^[5,6]. The percentage of visual disturbance and phonophobia in AM were reported to be about 20% and 10%, respectively^[5,7]. As expected, these percentages were markedly lower than that of migraine, for which 77% were reported to have photophobia, and 69% had phonophobia^[5]. Mortimer and Good showed similar response pattern in visual evoked potential in cases with migraine and AM, e.g., higher amplitude of fast wave activity than healthy controls and the presence of paroxysmal sharp wave activity^[6]. The existence of central nervous system symptoms in both AM and migraine indicates that AM is not only a peripheral disorder, but may also carry certain CNS process similar to migraine.

Patients with AM were reported to have central nervous system hypersensitivity. Recently, Hamed reported a case with AM coexisting with Alice in Wonderland syndrome (AWS)^[8]. The symptoms are characterized with perceptual abnormalities, distortion of body image, and alternation in subjective time sense, as Alice has in the story written by Lewis Carroll^[9]. AWS can also be observed in patients with migraine^[10]. The 20-year-old patient, as presented in the case from Hamed, had abdominal colic pain, which fits to diagnostic criteria of AM. This patient had a strong family history of migraine. Hamed stated that, despite normal brain magnetic resonance imaging and electroencephalography, medical examinations including transcranial magnetic stimulation and evoked potentials revealed enhanced cortical excitability in multiple brain lesions^[8].

PERIPHERAL SYMPTOM ACCOMPANYING TO ABDOMINAL PAIN IN AM

AM belongs to the category of functional gastrointestinal disorders, which are thought to be related to background visceral hypersensitivity^[4]. Recently, we reported a peculiar phenomenon seen in a patient diagnosed with AM who had ecchymosis in the legs and buttocks associated with abdominal pain^[11]. No currently known hypothesis could clearly explain the peculiar phenomenon. It is known that a subset of patients with migraine have similar ecchymosis in areas covered with trigeminal nerve, where the main site for migraine headache would be^[12,13]. Wesselmann and Lai showed that, in their rat model, insult to a pelvic organ resulted in extravasation in the skin region innervated by the affected nerves^[14]. In the process of investigating the mechanism of referred pain from visceral organ, they developed a rat model for pain caused by uterine inflammation. Experimental visceral inflammation in their rats pretreated with Evans blue dye resulted in dye extravasation in the skin over the abdomen, groin, lower back, thighs, perineal area and proximal tail. They speculated that the neuronal pathway account-

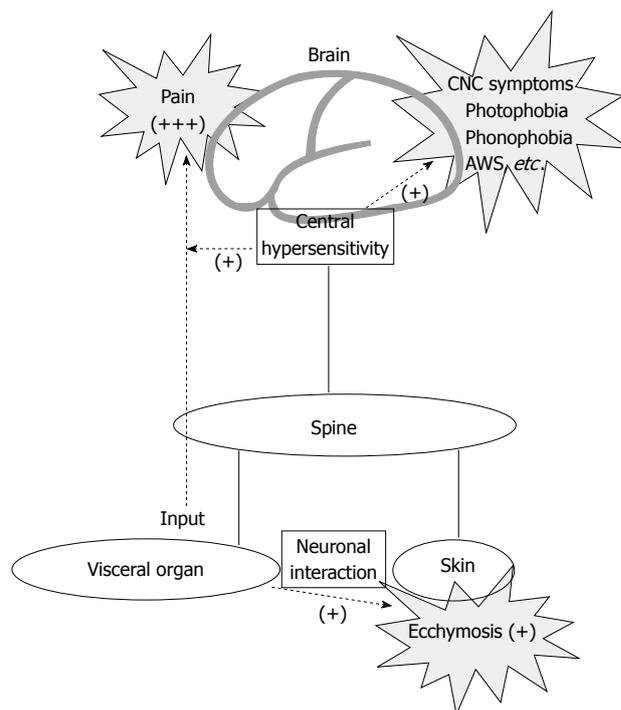


Figure 1 The central and peripheral network for symptoms relating to abdominal migraine is shown. CNS: Central nervous system; AWS: Alice wonderland syndrome.

ing for the phenomenon may include dichotomizing afferent fibers, afferent-afferent interactions *via* a spinal cord pathway, or a sympathetic reflex^[14]. When viewed in terms of human anatomy, the ecchymosis of legs and buttock can be accounted with neuronal input of visceral pain to sacral segment of spinal cord^[15]. Based on these reports, we hypothesize the following mechanism to explain the peculiar skin phenomenon in our case^[16]. First, under predisposing visceral hypersensitivity associated with AM, the visceral nerves responsible for abdominal nociception, especially those innervated by the sacral levels of spinal cord, are activated. This change then results in the occurrence of ecchymosis in the legs and buttock.

POSSIBLE MECHANISM OF TRIPTAN TO TREAT AM-RELATED PAIN

Triptan (serotonergic agonists) has been to treat acute symptom of AM^[7,11,16]. This agent has been generally thought to act on several regions, e.g., 5-HT_{1B} receptors on the meningeal vasculature, and 5-HT_{1D} receptors on trigeminal nerve terminals projecting to the dural vasculature and to the brain stem trigeminal nuclei^[17]. Jeong *et al*^[18] reported that, using their Sprague-Dawley rat model, sumatriptan brought pain relief by inhibiting GABAergic and glutamatergic synaptic transmission within the midbrain periaqueductal grey matter (PAG), a center of pain control, *via* a 5-hydroxytryptamine (5-HT) 1B and 5-HT_{1D} receptor mediated decrease in neurotransmitter release^[18]. Their result supported the central sensitization mechanism of

AM pain relief. It is important to note that, central effect of sumatriptan may not be the only way to pain relief from a report of Vera-Portocarrero's group^[19]. They evaluated in two models the effects of systemic/rostral ventromedial medulla (RVM) sumatriptan administration on visceral pain, and the role of RVM, a center of pain modulation, in the process of pain relief by sumatriptan. They developed a rat model for experimental pancreatitis by intravenous injection of dibutyltin dichloride, and another rat model for irritable bowel syndrome by intracolonic instillation of sodium butyrate. They observed the effects of systemic/RVM administration of 5-HT_{1B}/D antagonists on systemic/RVM sumatriptan action. Systemic sumatriptan elicited a dose- and time-related blockade to pain in both models that was blocked by systemic administration of either 5-HT_{1B} or 5-HT_{1D} antagonists, but not by RVM administration of these agents. Sumatriptan administered into the RVM similarly produced dose and time-related blockade of referred hypersensitivity in both models. The pain was blocked by RVM administration of the 5-HT_{1B} antagonists but not the 5-HT_{1D} antagonists. Based on the results, the authors speculated that sumatriptan suppresses either inflammatory or noninflammatory visceral pain, most likely through peripheral 5-HT_{1B}/D receptors. They also mentioned that actions at 5-HT_{1B} receptors within the RVM offer an additional potential site of action for the modulation of visceral pain by triptans.

CONCLUSION

We hypothesize a comprehensive central and peripheral interaction schema to explain the symptoms of AM. As shown in Figure 1, visceral organ produced pain and increased cortical excitability, which in turn induce central symptoms such as photophobia, phonophobia, and AWS; with intricate interactions from the central and peripheral nervous system, effects such as ecchymosis are shown on the peripheral level. Although further investigations and accumulation of AM cases are still needed, we believe that, the schema hypothesized here is helpful to plan further experimental approach to clarify the mechanism of this peculiar disease.

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Potential roles of longan flower and seed extracts for anti-cancer

Chih-Cheng Lin, Yuan-Chiang Chung, Chih-Ping Hsu

Chih-Cheng Lin, Department of Biotechnology, Yuanpei University, Hsinchu City 30015, Taiwan, China

Yuan-Chiang Chung, Department of Surgery, Cheng-Ching General Hospital, Taichung City 40764, Taiwan, China

Chih-Ping Hsu, Department of Medical Laboratory Science and Biotechnology, Yuanpei University, Hsinchu City 30015, Taiwan, China

Author contributions: Lin CC and Chung YC contributed equally to this article; Lin CC and Hsu CP substantially contributed to conception and design, acquisition of data, analysis and interpretation of data; Lin CC and Chung YC drafted the article and revised it critically for important intellectual content; Chung YC and Hsu CP contributed to final approval of the version to be published.

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Correspondence to: Chih-Ping Hsu, PhD, Department of Medical Laboratory Science and Biotechnology, Yuanpei University, No. 306 Yuanpei Street, Hsinchu City 30015, Taiwan, China. hsucp@mail.ypu.edu.tw

Telephone: +886-3-6108166 **Fax:** +886-3-6102312

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Abstract

Polyphenol-rich plants are known to possess benefits to human health. Recent studies have revealed that many Traditional Chinese Medicines (TCMs) are rich sources of polyphenols and exhibit antioxidant and anti-inflammatory activities, and these TCMs have been shown experimentally to overcome some chronic diseases, including cancer. Longan flowers and seeds, two TCMs traditionally used for relieving pain and urinary diseases, have been revealed in our recent reports and other studies to possess rich amounts of polyphenolic species and exhibit strong anti-oxidant activity, and these could be applied for the treatment of diabetes and cancer. Herein, we review the recent findings regarding the benefits of these two TCMs in the treatment of human

cancer and the possible cellular and molecular mechanisms of both substances.

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Key words: Longan flower; Longan seed; Cancer; Oncoprotein; Tumor suppressor; Traditional Chinese Medicine

Peer reviewer: Ramireddy Bommireddy, PhD, Assistant Professor, Bio5 Institute, MRB Rm 323, 1656 E Mabel St, Tucson, AZ 85724-5217, United States

Lin CC, Chung YC, Hsu CP. Potential roles of longan flower and seed extracts for anti-cancer. *World J Exp Med* 2012; 2(4): 78-85 Available from: URL: <http://www.wjgnet.com/2220-315X/full/v2/i4/78.htm> DOI: <http://dx.doi.org/10.5493/wjem.v2.i4.78>

INTRODUCTION

Cancer has become the most common disease threatening public health, which has led to interventions for the prevention and treatment of this disease. Based on the fact that cancer exhibits a slow, stepwise development, and requires several years to become a life-threatening disease, it is regarded largely as a preventable disease^[1-3]. Although improvements in medical techniques have been made in recent years, some types of cancer are still difficult to cure, even following advanced treatment. The challenge mainly arises owing to the recurrence, chemoresistance and distal metastasis of progressing cancer, which have become the important focuses of novel detection methods and treatment strategies^[4]. Epidemiological studies show a correlation between increasing consumption of phenolic compounds and a reduced risk of cancer^[5-8]. Plants are the primary source of polyphenols, and some have been regarded as forming part of a healthy diet for many years, such as tea, soybean, pome-

granate, and pine nuts^[9]. Traditional Chinese Medicine (TCM) has been developed in China for more than two thousand years. TCMs comprise various forms of herbal medicine and complementary therapy such as acupuncture, massage (Tui na), exercise (qigong), and dietary therapy. The pharmacopoeia of TCM, named the Compendium of Materia Medica, records hundreds of medicinal substances such as plants, minerals and animal products, and their health beneficial action in the body. Different parts of plants, such as the leaves, roots, stems, flowers, and seeds, are used. Several clinically-used chemotherapeutic drugs are derived from TCMs, such as camptothecin, isolated from the “happy tree” (*Camptotheca acuminata*); etoposide, semi-synthesized from a compound of *Podophyllum emodi* var. *chinense*; vincristin and vinblastin, isolated from the Madagascar periwinkle (*Catharanthus roseus*); and paclitaxel, purified from *Taxus chinensis*^[10,11]. Recent studies have further revealed that some TCMs or their components exhibit anti-tumor activities towards several types of cancer, such as liver^[12], lung^[13], gastric^[14], nasopharyngeal^[15] and colorectal cancer^[16]. Non-steroidal anti-inflammatory drugs have been documented in animal and human studies to reduce the risk of colorectal cancer and adenomatous polyps and have been implicated as a cancer prevention and treatment strategy^[1,17-19]. Longan flowers and seeds have been analyzed and were found to possess rich amounts of polyphenols, including proanthocyanidin A2, (-)-epicatechin, gallic acid and ellagic acid, and exhibit strong antioxidant and inflammatory activities^[20-24]. Recently, several studies by our research group have further revealed that longan flower and seed extracts exhibit an anti-cancer activity towards colorectal, liver, lung, cervical and breast cancer. Herein, we review the recent findings regarding the benefits of these two TCMs in the treatment of human cancer and the possible cellular and molecular mechanisms of both substances.

LONGAN FLOWERS AND SEEDS IN TCM

Longan (*Dimocarpus Longan* Lour.) is a subtropical fruit grown throughout Asia, with southern China including Taiwan being the main center of commercial production. The longan fruit is a famous summer fruit and is used as a TCM as a stomachic, febrifuge, and vermifuge, and also as an antidote to poison^[24]. In agriculture, off-season induction of flowering in longan trees is a desirable economic goal and is accomplished through the application of gibberellin biosynthesis inhibitors^[25]. To increase the size and quality of the fruit, an important operation is to prune or remove flower spikes in the cluster. Longan flowers are sold in herb markets and due to their fresh and fruity aroma are mainly used to prepare an infusion that is drunk for pleasure in Taiwan. As described in a TCM pharmacopoeia named Herbal Quanzhou, drinking the water extract of longan flowers could overcome micturition, urgency and voiding dysfunction. The powder of dried longan seeds can be used for treating bleeding, dampness, hernia, lymphomegaly of the neck and armpit,

odour, scabies and eczema, as described in another TCM pharmacopoeia named Chinese Herbal Medicine. The National Herbal Compendium of China also records that longan seed powder is generally applied for stomach pain and as a styptic. The multiple medical functions of longan flowers and seeds, and especially the reduction of swelling as recorded in the TCM pharmacopoeia, imply that these two TCMs can be applied in cases of microbial infection, inflammation, and metabolic diseases. Evidence to this end has been revealed by current scientific methods during the past decade.

Anti-oxidant activity and effect on inflammation and metabolic disorders of longan flower extracts

Although multiple medicinal applications of longan flowers are recorded in TCM pharmacopoeia, the scientific evidence related to their effect on human health has been accumulating over recent years. We have demonstrated that the hot water reflux or ethanol extract of the longan flower, contained abundant proanthocyanidins and rarely anthocyanins, suppresses nitric oxide and prostaglandin E2 production in lipopolysaccharide-stimulated macrophage cell line RAW264.7 and may be the potential source of natural dietary anti-oxidants and anti-inflammatory agent^[20]. The longan flower extract (LFE), analyzed by Professor Hwang and colleagues, exhibits a strong anti-oxidant activity, which is mainly due to (-)-epicatechin and proanthocyanidin A2^[26]. Proanthocyanidin-rich substances such as grape seed extracts have been implicated as preventive agents against cardiovascular disease and cancer, which are strongly associated with chronic inflammation diseases^[9,27,28]. In another study by Professor Hwang, consumption of LFE reduced the blood pressure and oxidative markers such as plasma thiobarbituric acid and liver antioxidant enzyme activity in fructose-fed rats. Insulin action signaling, such as insulin receptor substrate-1 and glucose transporter 4, is enhanced in these rats, indicating the effect of LFE on overcoming insulin resistance^[29]. Recent study has also revealed that feeding LFE to high-caloric-diet rats results in reduction of body weight, size of epididymal fat, serum triglycerides and atherogenic index. The main mechanism is downregulation of pancreas lipase, sterol regulatory element binding protein-1c and fatty acid synthase, and upregulation of low-density lipoprotein receptor and peroxisome proliferator-activated-receptor α expression, as well as promotion of fecal triglyceride excretion^[30]. These studies indicate that LFE can not only be applied for the treatment of urinary disorders, but also has the potential for use as a preventive or treatment agent for metabolic diseases.

Anti-colorectal cancer effects of LFE

Polyphenol-rich extracts have been demonstrated to exert anti-cancer effects^[31-33]. Owing to the rich amount of phenolics in LFE, our research team explored its possible role in human malignancy diseases. We selected colorectal cancer as the first subject, because it has been

the most common cancer type in Taiwan since 2007, when the dietary behavior of Taiwanese became more westernized^[34]. Recent studies have revealed that the water reflux extract of longan flowers is enriched with two major compounds, (-)-epicatechin and proanthocyanidin A2^[26], which are also found in grape seed extract as active anti-colorectal cancer agents^[35,36]. Based on these reports, we proposed that LFE could play a possible role in colorectal cancer (CRC) prevention and treatment. In our recent study^[37], we treated two CRC cell lines, SW480 and Colo 320DM, which are derived from Duke's B and Duke's C patients respectively, with LFE, and found an inhibitory effect on the proliferation of these two cell lines in a dose- and time-dependent manner. LFE treatment also affected the anchorage-independent growth of these two cell lines in soft agar, an *in vitro* assay to test the cancer cells clonogenic growth, and anoikis resistance, and was closely correlated with *in vivo* tumorigenesis^[38,39]. The uncontrolled cell division, clonogenic growth and anoikis resistance are the main malignant properties leading cancer cells to unlimited growth and tumorigenesis *in vivo*^[38-40]. The results strongly indicate that LFE is capable of influencing the malignant potential of CRC cells, which implies a role of LFE in the prevention and treatment of colorectal cancer. The mechanisms of LFE in anti-CRC growth are mainly due to cell-cycle arrest in the S phase and induction of mitochondria-mediated apoptosis. Previously, Kaur *et al.*^[36] reported that proanthocyanidin-rich grape seed extracts inhibited the proliferation of colorectal cancer cells due to their ability to cease G1-phase arrest of the cell cycle. However, LFE elevated cyclin E levels and downregulated cyclin A levels and arrested CRC cells in the DNA synthesis phase of the cell cycle. The elevation of cyclin E levels in both LFE-treated CRC cells was correlated with S-phase cell accumulation. Cyclin A is synthesized during the S phase and its functional disruption can inhibit chromosomal DNA replication^[41-43]. Together with the accumulation of cyclin E, we conclude that the effect of LFE on the cell division cycle is mainly due to hampered DNA synthesis. LFE also exhibits selected apoptosis induction in Colo 320DM rather than SW480. Induction of apoptosis is another possible mechanism by which the anti-proliferative effect of LFE on colorectal cancer cells may be exerted. In the present study, we show that LFE treatment could induce apoptosis in one of the tested CRC cells (Colo 320DM). The apoptotic cells represented DNA fragmentation, mitochondrial membrane potential loss and the activation of caspase 3. The Bcl-2 family has been demonstrated as the main mechanism of naturally-occurring phytochemicals-induced apoptosis in cancer cells^[44-47]. Bcl-2 inhibits Bax action and protects cytochrome C preservation in mitochondria, which leads to the maintenance of mitochondria membrane potential and keeping cell survive. The decrease in Bcl-2 level in LFE-treated Colo 320DM cells was correlated with apoptosis, indicating that the mechanism of apoptosis induction by LFE in this cell line is mainly due to suppression of the anti-

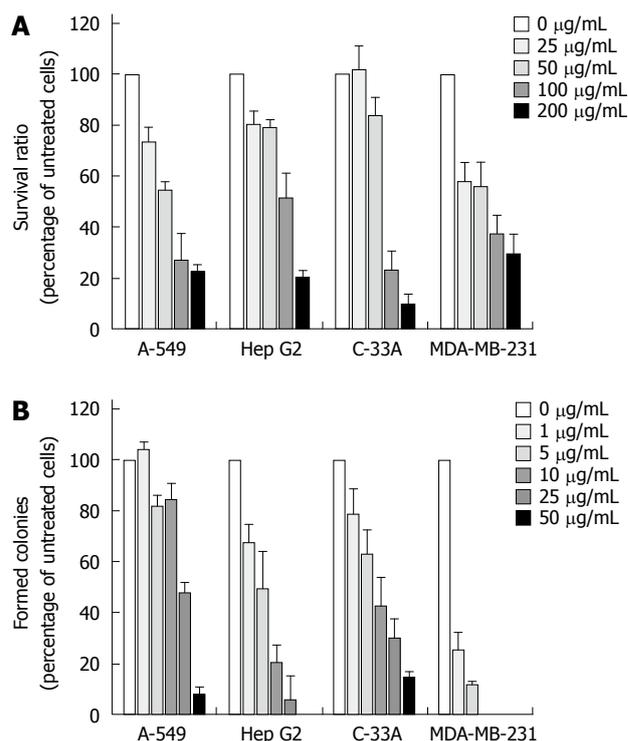


Figure 1 The inhibitory effect of longan seed extract on the growth of cancer cells. The longan seed extract (LSE)-inhibited growth assessed herein consists of cancer cell proliferation by (A) trypan blue assay and (B) colony forming activity. For the cell proliferation assay, 100 000 cancer cells as indicated were seeded in 60-mm sterile plastic dishes and treated with different concentrations of LSE. After incubation at 37 °C for 48 h, cells were detached by treatment with trypsin, and the suspended cells were stained with trypan blue. The viable cells were then counted under a phase contrast microscope. Colony formation activity was assessed by seeding 200 cells into 60-mm dishes then treating these cells with different concentrations of LSE. After incubation for 14 d, the formed colonies that contained more than 50 cells were regarded as one colony, and the numbers of colonies in the dishes were counted. The data represent the average of three independent experiments and are expressed as the mean \pm SD.

apoptotic protein Bcl-2. LFE failed to induce apoptosis in SW480 cells, which may be associated with some DNA damage repair mechanisms and tumor suppressor gene mutations such as *p53* in SW480. This is an intriguing issue worthy of further investigation.

DISCUSSION AND RESULTS

Potential role of longan seed extract in anti-CRC and other types of carcinomas

Longan seed extract (LSE) has been shown to consist of gallic acid, corilagin and ellagic acid as the main active components, resulting in anti-oxidant and tyrosinase activities^[21]. As gallic acid, ellagic acid and corilagin have been investigated in terms of their effects against different types of human cancer, we proposed that LSE, rich in these three components, could exhibit anti-cancer activity. Our recent study showed that LSE is capable of inhibiting cell proliferation and clonogenic growth in SW480, HT-29 and Colo 320DM, indicating a similar role of LSE to that of LFE in anti-CRC cells^[48]. Recently, we further tested LSE with regards to the growth inhibition

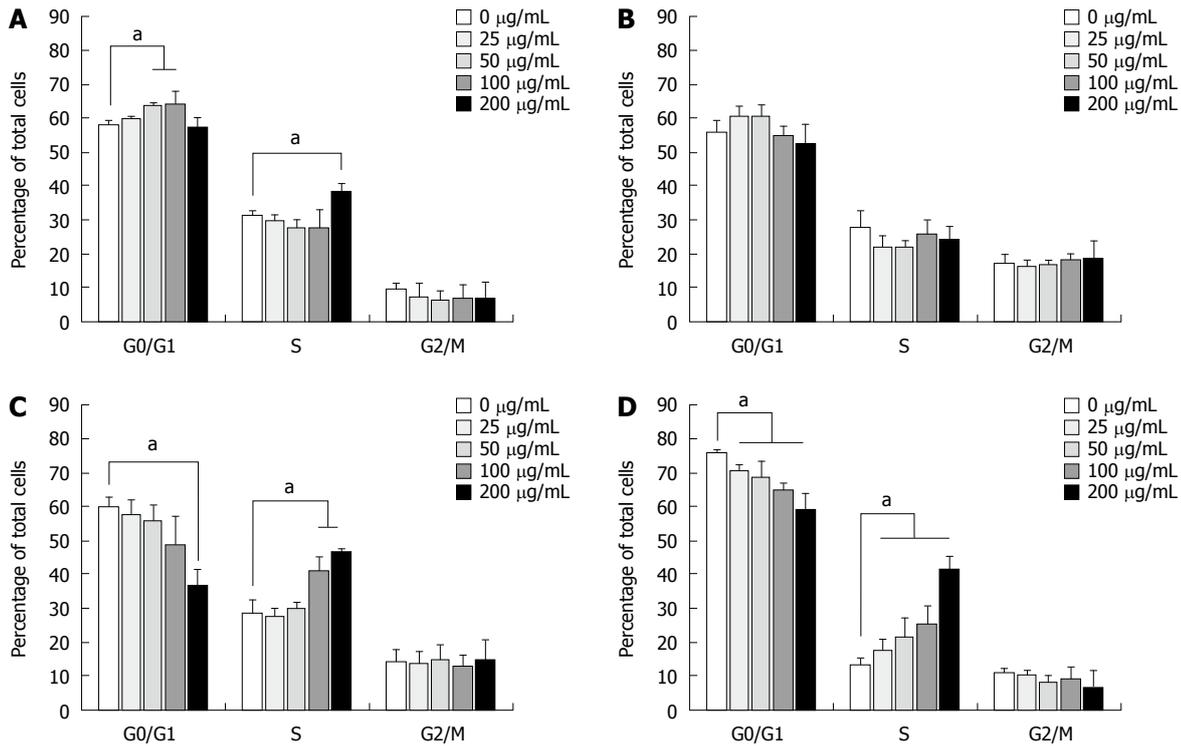


Figure 2 Cell cycle analysis of longan seed extract-treated cancer cells. About 1×10^6 cells in 10 mL medium in 100 mm plate were treated with increasing concentrations of longan seed extract as indicated, then incubated at 37 °C for 48 h. The (A) A-549, (B) Hep G2, (C) C-33A and (D) MDA-MB-231 cells harvested by trypsinization were fixed in 70% alcohol at -20 °C for 2 h and then reconstituted in phosphate-buffered saline. The cells were stained with propidium iodide solution in the dark at room temperature for 30 min. The stained cells were then analyzed using the FL-2A parameter of a flow cytometer to obtain the DNA content of the cells, and the distribution in each cell-cycle phase was determined using Modfit software. Data are expressed as a percentage of the total cells. Data represent the average of three independent experiments, and are expressed as the mean \pm SD. $^{\ast}P < 0.05$.

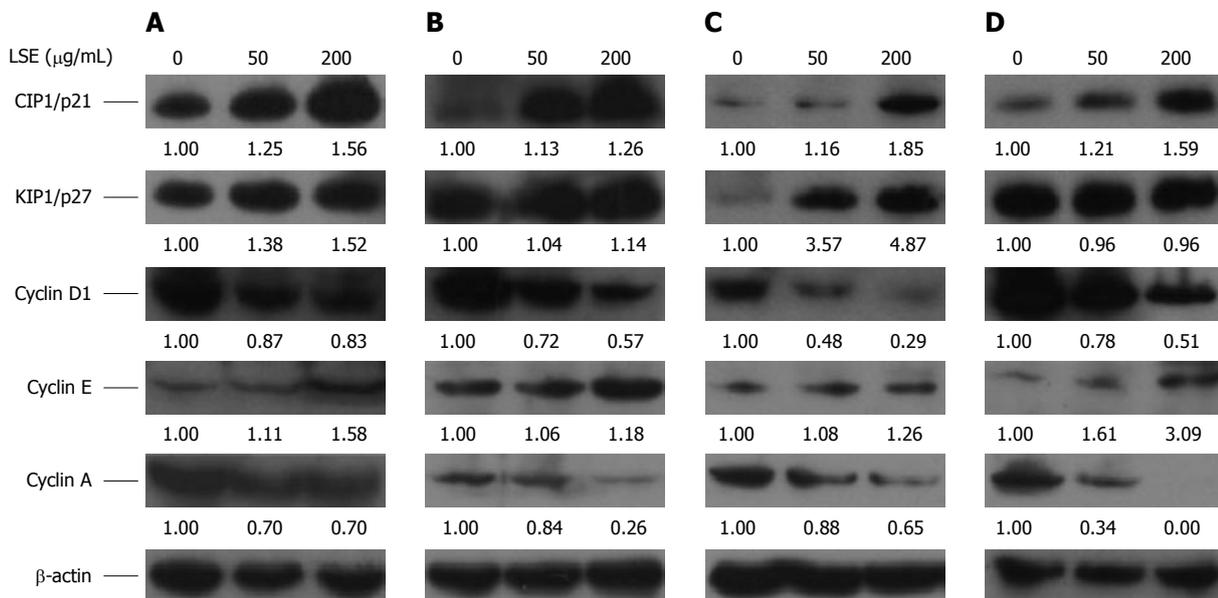


Figure 3 Immunoblots of cell cycle-controlling proteins in longan seed extract-treated cancer cells. About 50 and 200 µg/mL longan seed extract (LSE)-treated (A) A-549, (B) Hep G2, (C) C-33A and (D) MDA-MB-231 cells were incubated at 37 °C for 48 h. The harvested cells were lysed in Triton X 100-containing hypotonic buffer as per previous reports (Hsu *et al.*^[37], 2010; Chung *et al.*^[48], 2010) at 4 °C for 30 min. Cell lysates were centrifuged and the protein concentrations in the supernatants were determined using a bicinchoninic acid protein detection kit. Cell protein lysates were separated by sodium dodecyl sulfate polyacrylamide gel electrophoresis, transferred to polyvinylidene difluoride membranes and immunoblotted to show cyclin D1, cyclin E, cyclin A, CIP1/p21 and KIP1/p27, with the β-actin level used as the loading control. The images are representative results from three independent experiments. The density of each protein band was measured using ImageJ software and protein expression was normalized to β-actin, and the relative amount of each protein band was referenced to the untreated control.

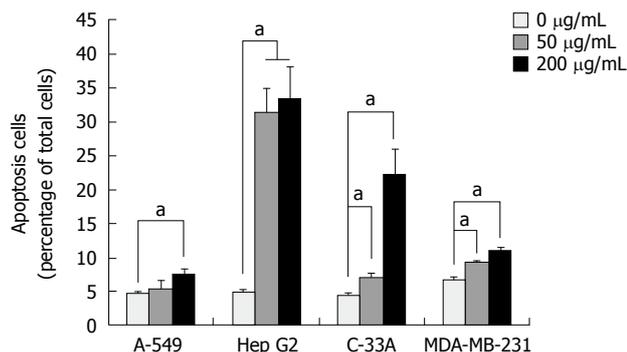


Figure 4 Detection of longan seed extract-induced apoptotic cells. Phosphatidylserine is usually distributed in the inner fleet of the plasma membrane. When cells are undergoing apoptosis, this phospholipid translocates to the outer fleet, and can be recognized by a bacteria glycoprotein named annexin V. We used annexin V conjugated with fluorescein isothiocyanate (FITC) as an apoptosis indicator and analyzed the apoptotic cells by flow cytometry. Briefly, 50 and 200 µg/mL longan seed extract-treated cells were incubated at 37 °C for 48 h. The treated cells were then suspended and stained with annexin V conjugated with FITC. Ten thousand cells were analyzed by flow cytometry using FL-1 as the parameter. Data are taken from the averages of three independent experiments and expressed as the mean \pm SD. * $P < 0.05$.

of lung adenocarcinoma cell line A549, hepatocellular carcinoma cell line Hep-G2, cervix carcinoma cell line C33A, and breast carcinoma cell line MDA-MB-231. The proliferation and colony-forming activity of these cancer cell lines were suppressed gradually by increasing LSE concentrations, and MDA-MB-231 was more sensitive to LSE than the other types of cancer cells (Figure 1). As shown in Figure 1A, the viability of MDA-MB-231 cells decreased to lower than 60% of the untreated cells following 25 µg/mL LSE treatment. A similar effect occurred in 50 µg/mL LSE-treated A549 cells and 100 µg/mL LSE-treated C33A and HepG2 cells. The colony-forming activity of these cancer cells was also suppressed. As shown in Figure 1B, the colonies of MDA-MB-231 cells were lower than 40% of the control colonies at 1 µg/mL LSE and 0% at more than 10 µg/mL LSE. Similar effects were seen in HepG2 cells at 10 and 50 µg/mL LSE, respectively. The colonies of C33A and A549 cells were lower than 40% compared to control cells at 25 µg/mL LSE, and 10%-20% compared to control cells appeared at 50 µg/mL LSE. Together, these results indicate that LSE is capable of influencing the proliferation and clonogenesis of colorectal, lung, liver, cervix and breast cancer cells.

LSE influences the expression of cell cycle-associated oncoproteins and suppressors

Our previous study demonstrated that LSE induced the cell cycle arrest of CRC cells in the DNA synthesis phase and suppressed cyclin D1 and cyclin A expression. Recently, we examined the effect of LSE on the cell-cycle progression of lung (A549), liver (HepG2), cervix (C33A) and breast cancer cells (MDA-MB-231). The S phase obviously increased in LSE-treated C33A and MDA-MB-231 cells, while the G1 phase increased in A549 cells (Figure 2). We further analyzed cell cycle-modulating

proteins including cyclin D1, cyclin E, cyclin A, CIP/p21 and KIP/p27 in LSE-treated cells, and found that LSE systemically suppressed cyclin D1 and cyclin A expression and concomitantly enhanced CIP/p21 and KIP/p27 (Figure 3). The growth inhibition effect of naturally-occurring products on human cancer cells may arise from downregulation of oncoproteins or enhancement of tumor suppressor proteins^[49-51]. Overexpression of cyclin D1 has been shown to play a pivotal role in promoting cancer cell proliferation, focus formation, tumorigenesis, drug resistance and metastasis, and has long been regarded as one of the important oncoproteins^[52-56]. Loss of expression or function of CIP1/p21 and KIP1/p27 has been implicated in the genesis or progression of many human malignancies^[57,58]. The suppression of cyclin D1 and enhancement of CIP1/p21 and KIP1/p27 expression by LSE treatment imply that the inhibitory effects of LSE on cancer cell growth may arise from the regulation of these proteins. The related cellular events are cell-cycle arrest in LSE-treated cancer cells, as these proteins are cell cycle-controlling proteins. Cyclin D1 and cyclin E are generated after mitogen stimulation in quiescent cells. These two proteins associate with CDK4/CDK6 and CDK2 and then enter the nucleus to phosphorylate/inactivate retinoblastoma protein, which leads cells to enter into the S phase^[59]. Cyclin/CDKs activity is negatively regulated by inhibitors of cyclin-dependent kinases (INKs). CIP1/p21 and KIP1/p27 belong to the Kip/Cip family of INKs, which associate with CDK4,6/cyclin D1 and CDK2/cyclin E, A complex and inactivate their kinase activity by interfering with ATP binding and the cyclin/CDK structure^[60]. Fifty µg/mL LSE-treated A549 cells exhibit decreased cyclin D1 and E and elevated CIP1/p21 and KIP1/p27, indicating the molecular mechanism of the LSE-induced G1-phase arrest. However, other cancer cells treated with the same concentration of LSE show no change or increased cyclin E and exhibit S-phase arrest (MDA-MB-231) or little change in the cell cycle (C33A, HepG2). S-phase arrest of LSE-treated cells occurs in MDA-MB-231 cells treated with more than 25 µg/mL LSE and C33A and A549 cells treated with more than 200 µg/mL LSE. Cyclin A, which is synthesized in the G1/S transition and associates with CDK2 to promote the S/G2 phase, is remarkably decreased in all LSE-treated MDA-MB-231 cells and in A549 and C33A cells treated with 200 µg/mL LSE. Our previous study indicated that elevated cyclin E and decreased cyclin A may be the key mechanism leading cancer cells to arrest in the S phase^[57]. The results further confirm the distribution of cyclin E and A in S-phase arrest of cancer cells. The results taken together indicate that LSE interferes with tumor-promoting activities and cell-cycle progression by suppression of oncoproteins such as cyclin D1 and A and enhancement of suppressors such as CIP1/p21 and KIP1/p27.

LSE induced mitochondria-mediated apoptosis

Apoptosis is the essential mechanism by which unwanted

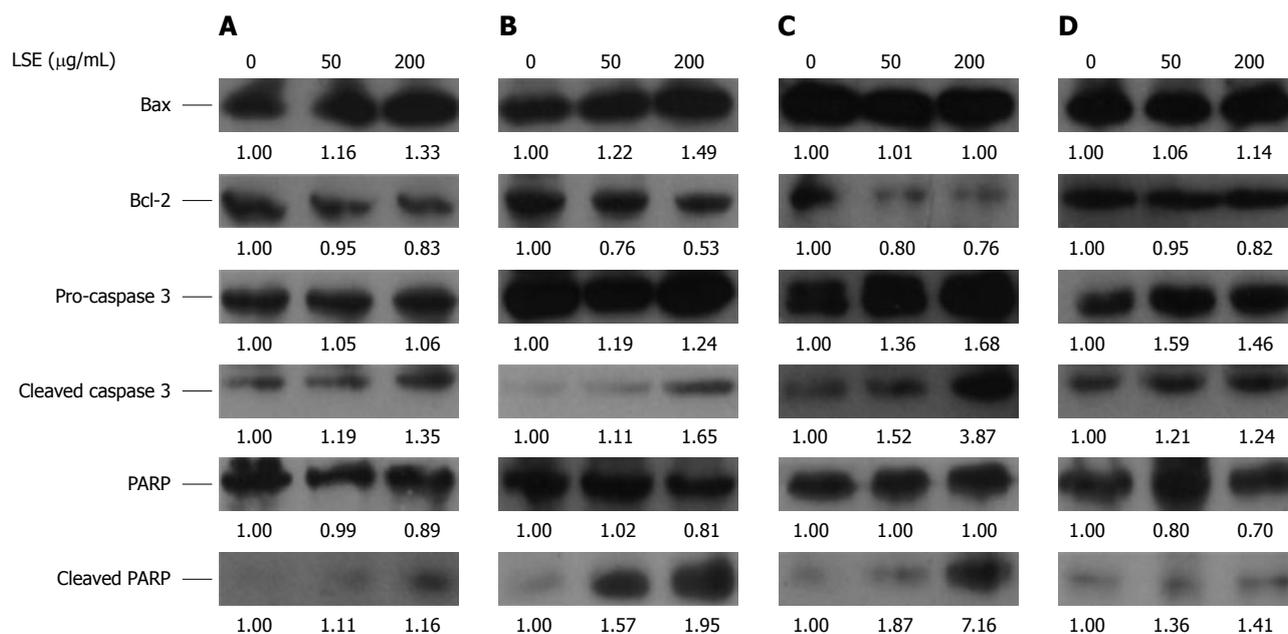


Figure 5 Immunoblots of apoptosis-associated proteins in longan seed extract-treated cancer cells. The same cell lysates from longan seed extract (LSE)-treated (A) A-549, (B) Hep G2, (C) C-33A and (D) MDA-MB-231 cells as described in Figure 3 were separated by sodium dodecyl sulfate polyacrylamide gel electrophoresis, transferred to polyvinylidene difluoride membranes and immunoblotted to show the levels of Bax, Bcl-2, pro-Caspase 3, cleaved-caspase 3, poly (ADP-ribose) polymerase-1 (PARP-1) and cleaved-PARP. The images are representative of three independent experiments.

or damaged cells are eliminated during development or maintenance of tissue homeostasis in multiple cellular organisms^[61,62]. Defective regulation of apoptosis has been closely associated with many human chronic diseases such as neural degeneration, autoimmune disease, AIDS and cancer^[63]. Inducing cancer cells into apoptosis is the main mechanism by which anti-neoplasm drugs or natural products suppress cancer cell growth^[62]. In our previous study, induction of apoptosis was found to be another possible mechanism of the antiproliferative activity of LSE on CRC cells^[48]. However, one CRC cell line appeared to be resistant to LSE-induced apoptosis. Result of present study further showed that LSE selectively induced significant apoptosis in HepG2 and C33A cells but only a slight elevation of apoptosis in A549 and MDA-MB-231 cells (Figure 4). Caspase 3 was activated by the proteolytic cleavage of upstream apoptosome and the consequent cleavage of substrates such as PARP. Many reports suggest that the activation of caspase 3 is a common event during polyphenolics-induced apoptosis of cancer cells^[35-37,64]. Our previous study showed that LSE enhances caspase 3 activity in CRC cells and induces apoptosis. Our recent results further showed that LSE induced pro-caspase 3 expression and cleavage (Figure 5). LSE-induced caspase 3 activation and apoptosis may operate through the Bcl-2 family of proteins. The Bcl-2 family members are important mediators of mitochondria-induced apoptosis in cancer cells^[61,65,66]. These proteins form multimers, which act as pores in cell membranes, controlling the flow of molecules^[67]. Bcl-2 has been associated with apoptosis inhibition, whereas expression of Bax has been associated with apoptosis induction^[68,69]. Bcl-2 inhibits apoptosis by inhibiting the

release of cytochrome c (Apaf 2) and apoptosis inducing factor (AIF) from the mitochondria to the cytoplasm, and by limiting the activation of caspase 3 by inhibiting its activator protein, Apaf 1^[70]. Recent studies indicate that the ratio of Bax:Bcl-2 proteins is the determining factor in transmitting the apoptosis signal^[46,67,71,72]. In our study, the Bcl-2 levels were decreased in LSE-treated cancer cells, especially in sensitive cells^[48]; however, the change in Bax levels in these cells are not affected, indicating that LSE-induced apoptosis is mainly due to the regulation of the level of Bcl-2.

CONCLUSION

The longan is one of the most important fruits in China, economically speaking. The flowers and seeds of the longan were regarded as waste for a long time, and failed to be utilized. However, according to TCM pharmacopoeia, longan flowers and seeds possess multiple pharmaceutical applications. Recent advanced biotechnology and pharmacology techniques allow us to gain a deeper insight into the functions of these two TCMs using scientific methods. LFE could suppress oxidation and inflammation, decrease blood pressure, triglycerides and body weight, and overcome metabolic diseases such as diabetes mellitus. We provide data to demonstrate that LFE is also capable of inducing cell-cycle arrest and apoptosis, at least in colorectal cancer cells, implying that LFE could also be applied as an anti-neoplasm agent. LSE systemically inhibits colorectal, lung, liver, cervix and breast cancer cells, indicating the utilization of LSE in cancer prevention and treatment. LSE could suppress oncoproteins such as cyclin D1, A and Bcl-2 and elevate suppressors

such as caspase 3, Bax, CIP1/p21 and KIP1/p27. This may provide a possible role of LSE as a multiple-target therapeutic agent to control abnormal growth and malignancy in cancer. The *in vivo* efficacy of both LFE and LSE in mice tumorigenesis is the next important issue for further investigation, and indeed this research is ongoing in our research team. In conclusion, recent advanced studies have validated the novel pharmaceutical functions of LFE and LSE, especially their anti-cancer functions, and have provided scientific evidence to further the application of these two TCMs in the pharmaceutical industry.

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Baohong Zhang, PhD, Assistant Professor of Biology, Department of Biology, East Carolina University, Greenville, NC 27858, United States

Editorial Office

World Journal of Experimental Medicine

Editorial Department: Room 903, Building D,
Ocean International Center,
No. 62 Dongsihuan Zhonglu,
Chaoyang District, Beijing 100025, China
E-mail: wjem@wjnet.com
http://www.wjnet.com
Telephone: +86-10-85381891
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Acknowledgments

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- 2 **Lin GZ**, Wang XZ, Wang P, Lin J, Yang FD. Immunologic effect of Jianpi Yishen decoction in treatment of Pixu-diarhoea. *Shijie Huaren Xiaobua Zazhi* 1999; **7**: 285-287

In press

- 3 **Tian D**, Araki H, Stahl E, Bergelson J, Kreitman M. Signature of balancing selection in Arabidopsis. *Proc Natl Acad Sci USA* 2006; In press

Organization as author

- 4 **Diabetes Prevention Program Research Group**. Hypertension, insulin, and proinsulin in participants with impaired glucose tolerance. *Hypertension* 2002; **40**: 679-686 [PMID: 12411462 PMID:2516377 DOI:10.1161/01.HYP.0000035706.28494.09]

Both personal authors and an organization as author

- 5 **Vallancien G**, Emberton M, Harving N, van Moorselaar RJ; Alf-One Study Group. Sexual dysfunction in 1, 274 European men suffering from lower urinary tract symptoms. *J Urol* 2003; **169**: 2257-2261 [PMID: 12771764 DOI:10.1097/01.ju.0000067940.76090.73]

No author given

- 6 21st century heart solution may have a sting in the tail. *BMJ* 2002; **325**: 184 [PMID: 12142303 DOI:10.1136/bmj.325.7357.184]

Volume with supplement

- 7 **Geraud G**, Spierings EL, Keywood C. Tolerability and safety of frovatriptan with short- and long-term use for treatment of migraine and in comparison with sumatriptan. *Headache* 2002; **42** Suppl 2: S93-99 [PMID: 12028325 DOI:10.1046/j.1526-4610.42.s2.7.x]

Issue with no volume

- 8 **Banit DM**, Kaufer H, Hartford JM. Intraoperative frozen section analysis in revision total joint arthroplasty. *Clin Orthop Relat Res* 2002; (**401**): 230-238 [PMID: 12151900 DOI:10.1097/00003086-200208000-00026]

No volume or issue

- 9 Outreach: Bringing HIV-positive individuals into care. *HRS-A Careaction* 2002; 1-6 [PMID: 12154804]

Books

Personal author(s)

- 10 **Sherlock S**, Dooley J. Diseases of the liver and biliary system. 9th ed. Oxford: Blackwell Sci Pub, 1993: 258-296

Chapter in a book (list all authors)

- 11 **Lam SK**. Academic investigator's perspectives of medical treatment for peptic ulcer. In: Swabb EA, Azabo S. Ulcer disease: investigation and basis for therapy. New York: Marcel Dekker, 1991: 431-450

Author(s) and editor(s)

- 12 **Breedlove GK**, Schorfheide AM. Adolescent pregnancy. 2nd ed. Wiczorek RR, editor. White Plains (NY): March of Dimes Education Services, 2001: 20-34

Conference proceedings

- 13 **Harnden P**, Joffe JK, Jones WG, editors. Germ cell tumours V. Proceedings of the 5th Germ cell tumours Conference; 2001 Sep 13-15; Leeds, UK. New York: Springer, 2002: 30-56

Conference paper

- 14 **Christensen S**, Oppacher F. An analysis of Koza's computational effort statistic for genetic programming. In: Foster JA, Lutton E, Miller J, Ryan C, Tettamanzi AG, editors. Genetic programming. EuroGP 2002: Proceedings of the 5th European Conference on Genetic Programming; 2002 Apr 3-5; Kinsdale, Ireland. Berlin: Springer, 2002: 182-191

Electronic journal (list all authors)

- 15 Morse SS. Factors in the emergence of infectious diseases. Emerg Infect Dis serial online, 1995-01-03, cited 1996-06-05; 1(1): 24 screens. Available from: URL: <http://www.cdc.gov/ncidod/eid/index.htm>

Patent (list all authors)

- 16 **Pagedas AC**, inventor; Ancel Surgical R&D Inc., assignee. Flexible endoscopic grasping and cutting device and positioning tool assembly. United States patent US 20020103498. 2002 Aug 1

Statistical data

Write as mean \pm SD or mean \pm SE.

Statistical expression

Express *t* test as *t* (in italics), *F* test as *F* (in italics), chi square test as χ^2 (in Greek), related coefficient as *r* (in italics), degree of freedom as ν (in Greek), sample number as *n* (in italics), and probability as *P* (in italics).

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Quantities: *t* time or temperature, *c* concentration, *A* area, *l* length, *m* mass, *V* volume.

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