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Epithelial ovarian cancer: An overview

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logical cancer and the leading cause of death in the United States. In this article we review the diagnosis and current management of epithelial ovarian cancer which accounts for over 95 percent of the ovarian malignancies. We will present various theories about the potential origin of ovarian malignancies. We will discuss the genetic anomalies and syndromes that may cause ovarian cancers with emphasis on Breast cancer type 1/2 mutations. The pathology and pathogenesis of ovarian carcinoma will also be presented. Lastly, we provide a comprehensive overview of treatment strategies and staging of ovarian cancer, conclusions and future directions.

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Key words: Epithelial ovarian cancer; Breast cancer type 1; Chemotherapy

Core tip: Epithelial ovarian cancer (EOC) is one of the most common gynecological cancers. We present a number of theories on the origin of EOC including the recent hypothesis that the fallopian tube is the primary site of most serous carcinomas. We also discuss genetic anomalies that may cause ovarian cancer. The pathology of ovarian cancer by malignant transformation of the epithelium of the ovarian surface, peritoneum or fallopian tube is also presented. Finally we provide an overview of ovarian cancer treatment options, comparing various chemotherapy regimens and future predictive biomarkers and functional assays for targeted therapy for breast cancer type 1 associated EOC.

Abstract

Ovarian cancer is the second most common gynecological

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INTRODUCTION

Amongst gynecologic malignancies ovarian cancer is the second most common and the #1 cause of death^[1]. In this article we review the diagnosis and current management of epithelial ovarian cancer (EOC) which accounts for over 95 percent of the ovarian malignancies^[2]. The clinical presentation of EOC can either be acute or subacute. Acute cases present with conditions such as pleural effusion, small bowel obstruction and venous thromboembolism. Subacute cases may present with non specific symptoms such as abdominal fullness, bloating, an adnexal mass, vague pelvic or abdominal pain and gastrointestinal symptoms.

In the following review, we initially present various intriguing theories about the potential origin of ovarian malignancies. Subsequently, we discuss in depth genetic anomalies and syndromes that may cause ovarian cancers with emphasis on breast cancer type 1 (BRCA1)/2 mutations (section II). Next, the pathology and pathogenesis of ovarian carcinoma is presented (Section III). Finally, we provide a comprehensive overview of treatment strategies and staging of ovarian cancer (Section IV), conclusions (Section V) and future directions (VI).

ORIGIN

The cellular origin of EOC is not well known thus hampering the development of effective early detection methods. Sir Spencer Wells in 1872 claimed that EOCs arose from ovarian surface epithelial (OSE) cells^[3]. This hypothesis is supported by Cheng's work on *HOX* genes^[4], which shows that ectopic expression of *HOXA9*, *HOXA10* and *HOXA11* genes in mouse OSE cells followed by intraperitoneal (IP) injection into mice resulted in the establishment of cancers of serous, endometrioid and mucinous subtypes, respectively. Inclusion cysts lined by OSE were considered as precursors for EOCs in the past^[4]. However the above theory has been refuted by a number of studies^[5]. For example, a prospective study of 48230 postmenopausal women who had no family history of ovarian cancer but had annual pelvic ultrasounds was conducted in 2010. Investigators found that after a median follow-up of 6 years there was no increase in the development of EOC in women who had inclusion cysts in their initial study. Yet in another study^[6] it has been proposed that ovarian cancers arise from secondary Mullerian tract structures as they are indistinguishable from adjacent mesothelial cells lining the peritoneum.

However, in the last 5-10 years, several studies have proposed that EOCs should no longer be considered as a single disease entity. For example, high-grade serous ovarian cancers (HGSOC), which represent the most

common type of invasive EOC, are exemplified by the ubiquitous presence of TP53 mutations^[7]. In a detailed analysis of the fallopian tubes of patients who underwent prophylactic salpingo-oophorectomies, histologic studies showed that tubal lesions were present in almost 100% of cases of early serous cancers associated with familial BRCA mutations. This lends evidence to the hypothesis that fallopian tube cells may play an important role in the genesis of BRCA-associated HGSOC. Kindelberger *et al*^[8] have proposed that cancer cells are shed from the tubal epithelium and implanted on the surface of the ovary and most likely become trapped within the surface inclusion cysts to produce ovarian or primary peritoneal carcinomas.

Recently Nik *et al*^[9] hypothesized that the fallopian tube is the primary site of most serous carcinomas. Evidence supporting this hypothesis includes: (1) more than 50% of sporadic pelvic high grade serous carcinomas have serous tubal intra-epithelial cancers (STIC); (2) STICs have also been found in 10%-15% of fallopian tubes prophylactically removed from women with BRCA mutations; (3) 92% of STICs have been shown to have TP53 mutation similar to those found in concordant high grade serous carcinoma samples; (4) STIC oncogene productions such as cyclin E1, Rsf-1, and fatty acid synthase, are also overexpressed in HGSCs; and (5) STICs have been found to be present in prophylactic salpingectomy specimens in the absence of carcinoma which lends evidence against the view that STICs are formed due to metastasis from adjacent HGSCs.

GENETIC ANOMALIES AND SYNDROMES

Individuals from families with multiple cancers, cancers occurring at an early age, and two or more primary cancers in a single individual have a higher risk of hereditary ovarian cancer syndromes. A recent Cancer Genomic Atlas project analyses of mRNA expression, miRNA expression, promoter methylation, and DNA copy number in 489 high-grade serous ovarian adenocarcinomas revealed TP53 mutations in almost all tumors (65). Approximately 13% had germ line mutations in BRCA1 or BRCA2 and a small percentage had somatic mutations in NF1, RB1 and CDK12^[10]. Analysis also showed four ovarian cancer transcriptional subtypes, three miRNA subtypes, four promoter methylation subtypes and signatures associated with survival (65). Furthermore pathway analyses showed defect in homologous recombination, Notch and FOXM1 signaling was involved in the pathophysiology of serous ovarian cancer^[10].

The majority of hereditary ovarian cancers are associated with mutations in tumor suppressor genes, *BRCA1* and *BRCA2*. BRCA1 (susceptibility protein) encoded by *BRCA1* gene (located on the long arm of chromosome 17) is a nuclear-cytoplasmic shuttling protein, and many cancer-associated mutations have altered subcellular localization of BRCA1 protein^[11]. BRCA1 also plays a role in DNA repair by transcription regulation, chromatin

remodeling, homologous recombination, and cell cycle regulation. BRCA1 mutations function as either truncating or missense mutations interfering with critical regions of the gene such as the RING finger motif or BRCT region of the gene. BRCA2 (susceptibility protein) is encoded by *BRCA2* gene (located on long arm of chromosome 13), plays a crucial role in repair of double stranded DNA breaks. It has been observed that the risk of ovarian cancer is higher in women with BRCA1 mutation as compared to BRCA2 mutation^[12,13]. The cumulative risk of ovarian cancer by age 70 is estimated to be 40%-50% for BRCA1 mutation-carriers and 10%-25% for BRCA2 mutation carriers^[14]. Furthermore, BRCA1 mutations are also associated with earlier onset^[12]. In one study, the average age at diagnosis of ovarian cancer in BRCA1 and BRCA2 mutation carriers was 52 and 62 years respectively^[15].

BRCA associated cancer risks are determined by the mutation location and genetic variation of the *BRCA1* and *BRCA2* gene function. Mutations occurring within the central region of the *BRCA2* gene, called the ovarian cancer cluster region, compared to mutations in the 5' or 3' region, may be associated with a significantly higher risk of ovarian cancer in women^[16].

Research has also shown that the BRCA1 Associated Ring Domain 1 (BARD1) protein which binds to the BRCA1 protein stabilizes both proteins and targets the BRCA1 to sites where DNA strands are broken. Mutations in the *BARD1* gene may prevent the BARD1 protein from helping repair damaged DNA. Thus, BARD1 isoform expression is required for cancer cell proliferation, thereby making them cancer maintenance genes^[17]. Studies also suggest that the BARD1 protein has other functions different from its partnership with the BRCA1 protein. The BARD1 protein interacts with another protein, p53 (which is produced from the *TP53* gene) to promote controlled cell death (apoptosis) and regulate cell division. Other potential functions of the BARD1 protein are under study.

Specific genetic modifiers of cancer penetrance, sometimes called modifier genes, may influence the expression of genes like *BRCA1* or *BRCA2*. Genetic variation, particularly in the genes comprising endocrine signaling and DNA repair pathways, may modify BRCA-associated cancer risks. Another potential modifier gene in BRCA1 and BRCA2 mutation carriers is CYP1A1, which encodes an enzyme involved in the metabolism of polycyclic aromatic hydrocarbons and in the hydroxylation of estradiol^[18]. A particular allelic variant, found in 14 percent of carriers with cancer and 22 percent of unaffected carriers, reduced the risk of breast cancer by about 40 percent. Recently Qin *et al*^[19] have shown that BRCA1 inhibits the growth of ovarian cancers by regulating Ubc9 binding. With the aid of live imaging of YFP, RFP-tagged BRCA1 and BRCA1a proteins they showed enhanced cytoplasmic localization of mutant BRCA1 proteins in certain types of ovarian cancer cells. The mutant BRCA1 proteins were found to be impaired in

their capacity to inhibit growth of ES-2 ovarian cancer cells. Less commonly hereditary non polyposis colorectal cancer which is caused by mutations in mismatch repair genes, MSH2, MLH1, MSH6, PMS1, and PMS2 is also associated with ovarian cancer^[20]. Jones *et al*^[21] analyzed 42 cases of ovarian clear cell carcinoma and found that 57% of these cases had mutations in ARID1A which suggests that aberrant chromatin remodeling contributes to the pathogenesis of ovarian clear cell carcinoma.

PATHOLOGY

Epithelial cancer of the ovary is thought to derive from malignant transformation of the epithelium of the ovarian surface, peritoneum, or fallopian tube. The exact molecular transformation events causing EOC are not known. Baylin *et al*^[22] have shown that epigenetic phenomenon may also play a role. Mutations of the oncogenes HER2, C-myc, K-ras, Akt, and the tumor suppressor gene p53 have been observed^[23-25]. The molecular pathways underlying cancer progression are also not well understood. Most research to date have shown that factors associated with reproduction and ovulation have the largest impact^[26,27]. Some studies have shown that somatic mutations in *BRCA1*, *BRCA2* and other genes can also lead to cancer progression.

Some of the theories for the pathogenesis of EOC include: (1) repeated ovulation with trauma^[28,29]; (2) increased estrogen concentrations as a result of excess gonadotropin secretion^[30]; (3) high androgen concentrations^[30]; and (4) stromal hyperactivity^[31].

Histopathology

The classification of EOC is usually based on the origin of the tumor^[32]: (1) About 75% of EOCs are of the serous type. They simulate the lining of the fallopian tube. This histologic variant is often associated with concentric rings of calcification known as psammoma bodies. While there is no established grading scheme for serous ovarian cancer, recent work has suggested a two-tiered system-low-grade and high-grade^[33,34]. The work of Meinhold-Heerlein *et al*^[35] has shown that low-grade serous carcinomas and serous tumors of low malignant potential involve similar genes and pathways that are distinct from high-grade serous carcinomas. These findings have led some to hypothesize that low-grade carcinomas represent the natural progression of an undetected serous ovarian tumor of low malignant potential; (2) Mucinous tumors usually resemble intestinal or endocervical epithelium. Mucinous tumors are usually large with a median diameter of 18 to 20 cm and tend to remain confined to the ovaries^[36]. Furthermore, primary ovarian mucinous tumors can be difficult to distinguish from metastatic mucinous tumors from the colon/rectum, appendix, cervix or pancreas; (3) Endometrioid tumors are hypothesized to sometimes arise from the foci of endometriosis. They are associated with slightly better survival when compared to serous adenocarcinoma, regardless of disease stage^[37],

(4) Clear cell carcinomas can also sometimes arise from endometriosis. They derive their name as their histologic features include “clear cells”. Prognosis is poor due to an increased risk of venous thromboembolism and decreased response to platinum-and-taxane based chemotherapy regimens^[38]; and (5) Brenner tumors, also known as transitional cell tumors because histologically, they resemble transitional epithelium of the bladder. Majority of Brenner tumors are benign. Histologically, there are nests of transitional-type epithelial cells with longitudinal nuclear grooves lying in abundant fibrous stroma.

TREATMENT

There are basically three forms of treatment of ovarian cancer: (1) Surgery; (2) Chemotherapy; and (3) Radiation (rarely used). Surgery is considered the mainstay of treatment for ovarian cancer. Treatment is mainly based on the histologic subtype and the stage at diagnosis, which is determined surgically by a tumor reductive procedure including hysterectomy, removal of ovaries, removal of the omentum, and any other sites of disease feasible to remove. The goal of surgery is to reduce the tumor burden to no visible disease, though an “optimal” status is assigned if no residual lesions are larger than 1 cm. However, other studies^[39] designate the status of maximal cytoreduction for tumors less than 3 cm. The following table lists the different stages of EOC: stage I : Cancer is confined to one or both of the ovaries; stage II : Either one or both the ovaries are involved and the cancer has spread to uterus and/or fallopian tubes or other sites in the pelvis; stage III : Either one or both the ovaries are involved and the cancer has spread to lymph nodes and/or sites outside the pelvis but is still within the abdominal cavity; and stage IV: Either one or both the ovaries are involved with distant metastasis.

Stages I and II

For stage I epithelial cancers, surgery alone is adequate. Here surgery is used for both staging and therapeutic purposes. Surgery includes hysterectomy, bilateral salpingo-oophorectomy, and omentectomy. Samples of the under surface of the diaphragm, peritoneal washings, pelvic/para-aortic lymph node samples are also examined for completeness. In high-grade ovarian cancer, adjuvant chemotherapy has led to better overall survival rates. Large clinical trials such as EORTC-ACTION and MRC-ICON1 involved patients with stage I and II ovarian cancer who were randomly assigned to adjuvant chemotherapy or observation^[40,41]. In EORTC-ACTION, at least 4 cycles of carboplatin/cisplatin based chemotherapy were administered whereas in MRC-ICON1 patients received 6 cycles of single agent carboplatin or cisplatin or platinum-based chemotherapy. Data from both studies showed significant improvement in recurrence-free survival and overall survival (5 year survival figures were 82% with chemotherapy and 74% with observation with a 95% confidence-interval in the difference of 2%-12%).

Stages III and IV

In the case of stages III and IV cancers, surgery includes total abdominal hysterectomy, bilateral salpingo-oophorectomy, omentectomy and debulking of any grossly visible tumor. Cytoreduction is an independent prognostic variable for survival^[39,42]. In patients with optimal cytoreduction the median survival was 39 mo as opposed to 17 mo if the surgery was suboptimal^[43].

Treatment options for patients with optimally cytoreduced stage III disease include conventional intravenous and/or IP chemotherapy. The use of IP cisplatin has shown better progression free survival (PFS) and overall survival^[44]. One of the recent studies gynecologic oncology group (GOG)-0172 showed a higher median survival rate of 66 mo for patients receiving chemotherapy *via* the IP route as opposed to 50 mo in patients who received intra-venous cisplatin and paclitaxel ($P = 0.03$)^[44]. Another study concluded that IP cisplatin works better on small tumors (< 1 cm) that are platinum responsive^[45].

Therapeutic strategies for patients with sub-optimally cytoreduced stage III and IV disease include intravenous and/or IP chemotherapy plus additional cytoreductive surgery in some circumstances. The benefits of cytoreductive surgery have not been well established in advanced disease states. While one study performed by the EORTC showed better survival rates in patients who had debulking surgery after 4 cycles of cyclophosphamide and cisplatin^[46]. Another study, GOG-0162, in patients who received paclitaxel and cisplatin with interval cytoreductive surgery did not show any survival benefit^[47]. GOG 182-ICON5^[48] compared the effectiveness of various combination chemotherapy regimens as first line therapy for patients with stage III/IV EOC who have undergone either optimal or sub-optimal cytoreductive surgery. The study shows that combining either carboplatin or paclitaxel with one of the follow new cytotoxic agents-gemcitabine, poly-ethylene glycol liposomal doxorubicin and topotecan gave favorable results.

A combination of carboplatin and a taxane (paclitaxel or docetaxel) is the standard chemotherapeutic agent for ovarian cancer with clinical response rates > 60% and median time to recurrence usually > 1 year. The combination of carboplatin and paclitaxel regimen is the standard worldwide and is sometimes used as induction chemotherapy, if patients are poor surgical candidates, or the surgeon feels that the primary surgery is not likely to be optimal. The SCOTROC trial^[49] compared the use of either docetaxel or paclitaxel in combination with carboplatin as first line chemotherapy and found similar PFS in both cases therefore offering an alternative to paclitaxel.

Recently there have been a number of studies investigating the role of bevacizumab in first-line therapy for ovarian cancer following surgical cytoreduction. Bevacizumab is a humanized-monoclonal antibody against vascular endothelial growth factor (angiogenesis inhibitor). Two trials GOG-0218 and ICON7 have shown improvement in PFS when bevacizumab was added to initial chemotherapy and continued every three weeks for

16 and 12 additional cycles respectively^[50,51]. However, overall survival has not been demonstrated, and therefore has not been adopted outside of recurrent disease or the clinical trial setting.

Eskander *et al.*^[52] have recently proposed a new strategy for combining maximal cytoreductive surgery with intra-operative hyperthermic intraperitoneal chemotherapy (HIPEC) for treatment of advanced stage EOC resulting in promising oncologic outcomes. Currently phase III clinical trials are ongoing to test the efficacy of combining cytoreductive surgery with HIPEC.

Recurrent or persistent ovarian epithelial cancer

Recurrent cancer has a wide range of presentations. Patients may present with abdominal distention or pain or symptoms related to sites where the cancer cells have spread to. The most common follow-up procedures include bimanual pelvic examination, serial measurement of CA125, laparotomy and repeating imaging studies. Platinum sensitive cancers (recurrence more than 6 mo since completion of primary therapy) are usually re-treated with a combination of carboplatin and a taxane. The OCEANS trial^[53] was conducted to test the efficacy and safety of bevacizumab with gemcitabine and carboplatin (GC) compared with GC alone (*i.e.*, bevacizumab replaced by a placebo) in platinum sensitive recurrent ovarian cancers. Results show a significant improvement in PFS when bevacizumab was used in combination with GC. Platinum resistant disease can be treated with one of several agents that typically provide response rates in the range of 10%-20%. These include bevacizumab, topotecan, gemcitabine, liposomal doxorubicin, and others. The AURELIA trial^[54] was one of the first randomized phase III trials to demonstrate the benefit of combining bevacizumab with standard chemotherapy regimen resulting in increased PFS (6.7 mo *vs* 3.4 mo) in patients with platinum resistant ovarian cancer.

The NOVEL trial^[55] proposed the idea of a “dose-dense” therapy for treating primary ovarian cancer. It is based on the hypothesis that a shortening of the time interval between the administrations of cytotoxic agents is able to achieve better cell kill. They compared the standard 3-wk paclitaxel and carboplatin combination *vs* dose-dense weekly paclitaxel and 3-wk carboplatin for advanced EOC and found that the PFS was significantly better in the former (28 mo *vs* 17.2 mo).

CONCLUSION

Among gynecologic malignancies ovarian cancer is the most lethal. The cellular origin of EOC is not well known. Early theories hypothesized that EOC arises from OSE cells, while more recent ones have proposed that it should no longer be considered as a single disease entity but rather a diverse group of tumors with specific morphologic and genetic characteristics.

Histological differences in the ovarian cancers define a number of subtypes of EOC. Subtypes are named

based on the tissue that they closely resemble and include serous, mucinous, endometrioid, clear cell, and transitional cell. Ovarian cancer is also classified as benign, borderline or malignant depending on the degree of epithelial proliferation and stromal invasion.

Treatment of EOC is based on the combination of surgery and chemotherapy. Over the past three decades, optimal surgical cytoreduction, followed by platinum-based chemotherapy has become the standard treatment for advanced ovarian cancer.

FUTURE DIRECTIONS

A recent national institute of health study discovered genomic similarities between basal-like subtype of breast cancer (triple negative breast cancer) and serous ovarian cancer^[56]. Computational analyses show that both these cancers are susceptible to agents inhibiting blood vessel growth and chemotherapeutic drugs targeting DNA repair. However, more work is needed in this direction to determine how these findings may be used functionally and clinically.

Another area that has received attention recently is the impact of oxidative stress and BRCA1 mutations in ovarian cancer. Oxidative stress induces DNA damage (as evidenced by increased 8-hydroxydeoxyguanosine) correlates with poor outcomes in ovarian cancer^[57]. Martinez-Outschoorn *et al.*^[58] found that UWB1.289 cells, which contain mutant BRCA1, produce large amounts of hydrogen peroxide leading to oxidative stress and catabolic processes in adjacent stromal fibroblasts *via* stromal NF- κ B activation. Catabolism in stromal fibroblasts was also accompanied by the up regulation of MCT4 and decreased Cav-1 expression which signify tumor microenvironment. Furthermore, the study also showed the effect of UWB1.289 could be negated by using the antioxidant N-acetyl-cysteine or by *BRCA1* gene replacement. This suggests that new trials are needed for cancer prevention using antioxidants in hereditary BRCA1 mutations.

Another recent breakthrough in the treatment of recurrent ovarian cancer is in the use of vaccines derived from lysate-pulsed dendritic cells. Kandalaf *et al.*^[59] reported a study encompassing dendritic cell based autologous whole tumor vaccination and anti-angiogenesis therapy. They took the tumor lysate from patients with recurrent ovarian cancer. The patients were initially treated with intravenous bevacizumab and oral metronomic cyclophosphamide. This was followed by bevacizumab and the vaccination of dendritic cells with autologous tumor lysate, lymphodepletion and administration of a large number of vaccine primed T-cells. The study found that cellular immunotherapy may be used for treatment of recurrent ovarian cancer. However the study included only six subjects and the therapy was found to work for four of them. Thus more work is required in this direction to ascertain the benefits of such vaccines.

Some studies such as those by Bryant *et al.*^[60] and Farmer *et al.*^[61] have shown that BRCA-deficient cells are

especially sensitive to chemical inhibitors of poly (ADP-ribose) polymerase (PARP), which plays a critical role in single stranded DNA break repair. The most studied PARP inhibitor Olaparib has shown good results^[62] in initial studies in BRCA1 mutated and sporadic ovarian cancer but further studies are needed.

There are no clear indications for ovarian cancer screening. Testing is recommended for women at high risk such as those with a significant family history, but consultation with a genetic counselor is recommended to discuss limitations and alternatives to genetic testing. Potential screening tests include the blood test for CA-125 marker and transvaginal ultrasound. However these tests are neither sensitive nor specific for ovarian cancer. They may be abnormal in benign conditions such as endometriosis, menstruation, pregnancy, and cancers of fallopian tube, breast or the GI tract. Early results from the United Kingdom Collaborative Trial of Ovarian Cancer Screening showed that combining annual CA-125 tests with ultrasound imaging was useful for detecting ovarian cancers at an earlier stage^[63]. The full results of the trial are expected in 2015. Lastly the key to developing targeted therapies for EOC will depend on understanding the biological pathways and targets involved in the development of these cancers. Our results (unpublished work) suggest Ubc9 to be expressed at elevated levels in several ovarian cancers and BRCA1-mutant serous epithelial ovarian cancer cells^[19]. We have developed BRCA1 function-based cellular assays (Patent number United States 8372580) where loss of Ubc9 binding by BRCA1 mutants can not only predict the risk for developing Triple Negative Breast Cancers and EOC, but it may lead to the development of targeted therapies for these cancers.

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Neurological and behavioral manifestations of cerebral malaria: An update

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Abstract

Neglected tropical diseases are a group of tropical diseases endemic in poor countries even though medical treatment and cures are available. They are considered a global health problem due to the severity of the physiological changes they induce in their hosts. Malaria is a disease caused by *Plasmodium* sp. that in its cerebral form may lead to acute or long-term neurological deficits, even with effective antimalarial therapy, causing vascular obstruction, reduced cerebral blood flow and many other changes. However, *Plasmodium falciparum* infection can also develop into a cerebral malaria (CM) disease that can produce neurological damage. This review will discuss the mechanisms involved in the

neuropathology caused by CM, focusing on alterations in cognitive, behavior and neurological functions in human and experimental models.

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Key words: Malaria; Cerebral malaria; Neuropathology; *Plasmodium* sp; *Plasmodium falciparum*

Core tip: This review attempts to compile the limited current knowledge on the behavioral and cognitive effects of cerebral malaria (CM) and the possible pathological mechanisms related to neurobehavioral manifestations. CM induces acute/chronic neurological damage, affecting several Central Nervous System regions responsible for behavioral, neurological and cognitive functions which may result in motor deficits, epilepsy, blindness, speech/hearing and memory/attention disorders, hyperactivity, anxiety-like behavior, neuropsychiatric manifestations of post malaria neurological syndrome, both in humans and animal models. The action mechanisms involved in the alterations are not yet clearly defined; however proinflammatory mediators have been described with consequent axonal damage and demyelination.

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INTRODUCTION

Malaria, leishmaniasis and tuberculosis together with other neglected tropical diseases (NTDs) cause 32% of

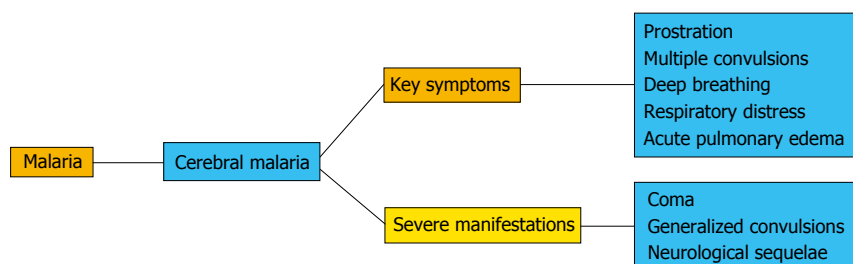


Figure 1 Clinical manifestations of cerebral malaria.

the burden of ill health in Africa and seriously impact on health outcomes in many regions of the world. NTDs share common features such as high endemicity in rural and impoverished urban areas of low-income countries. Some NTDs are disfiguring and stigmatizing, being considered poverty-promoting conditions, particularly in Africa, Asia, and the tropical regions of the Americas^[1,2].

Among various NTDs, malaria is one of the most life-threatening diseases, provided that the currently recommended interventions are not adequately implemented^[2]. In 2011, the World Health Organization (WHO) estimated that 3.3 billion people were at risk of malaria. More than 274 million clinical cases and 1.1 million deaths occurred between 2001 and 2010 worldwide, with approximately 80% of cases and 90% of deaths estimated to occur in the African Region, mostly in children under five years of age and in pregnant women^[2,3]. Kiszewski *et al.*^[4] estimated that Global resource requirements for malaria control totaling USD 38-45 billion will be spent from 2006 to 2015 for the diagnosis and treatment of malaria, mainly in countries and populations at risk of epidemic, such as sub-Saharan Africa.

Human malaria is caused by five species of obligate intraerythrocytic protozoa of the genus *Plasmodium*: *P. falciparum*, *P. vivax*, *P. ovale*, *P. malariae* and *P. knowlesi*^[2], and is transmitted by the bite of a female anopheles mosquito. At least three-dozen different species of *Anopheles* mosquitoes can transmit malaria worldwide^[5]. However, infections can also occur through exposure to infected blood products (transfusion malaria) and *via* congenital transmission^[6].

Of these, *P. falciparum* is the organism primarily responsible for severe malaria, although *P. vivax*^[3] and *P. Knowlesi*^[7,8] can also cause severe disease. According to WHO's criteria^[9], severe malaria is defined by clinical or laboratory evidence of vital organ dysfunction and/or high parasite burden; this high parasitemia can be a risk factor for death from *P. falciparum* malaria^[9].

Overall, clinical features of severe malaria include cerebral malaria (CM) with impaired consciousness (including coma), prostration, multiple convulsions, deep breathing and respiratory distress (metabolic acidosis), acute pulmonary edema and acute respiratory distress syndrome, circulatory collapse or shock and acute kidney injury^[9,10]. However, severe malaria is a complex multi-system disorder that can mimic many other diseases that are also common in malaria-endemic countries, such as central nervous system (CNS) infections, sepsis, severe pneumonia and typhoid fever^[9].

In this review, we described neurocognitive and behavioral outcomes of CM in humans and animals so as to facilitate further understanding of the disease's pathogenesis in the CNS.

CM

CM is one of the most severe and rapidly fatal neurological complications caused by *Plasmodium* species, mainly *P. falciparum*, with around one million deaths per year in children from sub-Saharan Africa^[11,12]. The first manifestations of CM are non-specific fever, chills, irritability, agitation or psychotic behavior, vomiting and cough. In adults, complications are severe jaundice, respiratory distress syndrome, and severe intravascular hemolysis leading to hemoglobinuria and anemia, which further contributes to renal failure (Figure 1). The most severe manifestations are impaired consciousness with coma, generalized convulsions and neurological sequelae. Pregnant women are also vulnerable and develop anemia, hypoglycemia, coma and pulmonary edema. In children, the main symptoms are severe anemia, metabolic acidosis, hypoglycemia, coma and gastrointestinal symptoms^[13-15], as shown in Figure 1.

CM may result in acute or long-term neurological deficits, even with effective antimalarial therapy^[16,17]. CM is a neurological complication that occurs in approximately 1% of infections caused by *P. falciparum*^[18,19]; however, a high mortality rate follows^[14,20].

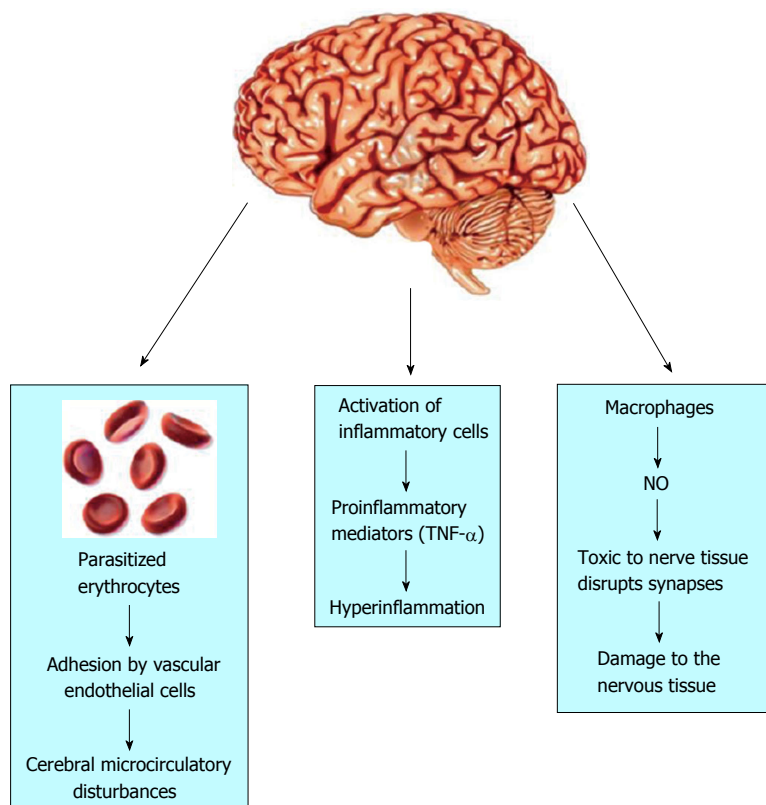
PATHOLOGICAL MECHANISMS

The pathological mechanisms that lead to neurological complications and mortality are not yet clearly defined. It is believed that in infected erythrocytes, platelets, and activated leukocytes inflammatory events occur owing to increased levels of adhesion molecules on the inflamed endothelium, leading to a reduction in microvascular blood flow, decreased delivery of nutrients to affected brain tissue and vessel walls, followed by hemorrhage and neuronal alterations^[21-23].

The blood-brain barrier (BBB) acts as a physical barrier that limits the trafficking of substances *via* transcellular transport and is responsible for regulating ion and nutrient transport into the brain, a feature that restricts the free flow of physiological molecules between the bloodstream and brain parenchyma^[18,24].

Conversely, perturbations to the BBB can lead to deregulation in any of the neurovascular components,

Figure 2 The pathological mechanisms that lead to neurological complications and mortality in patients. NO: Nitric oxide; TNF- α : Tumor necrosis factor-alpha.



which in turn can alter the brain's homeostasis leading to a multitude of neural dysfunctions and inappropriate BBB activation as observed in multiple sclerosis, Alzheimer's disease, stroke, certain depression disorders and parasitic infections, among others^[25-29]. Vascular dysfunction with subsequent BBB damage has been observed both in human CM and in animal models^[18,19,30].

The pathogenesis of CM is associated with cerebral microcirculatory disturbances resulting from the adhesion to and sequestration of parasitized erythrocytes, immune cells and platelets by vascular endothelial cells that line the small blood vessels of the brain, leading to their blockage^[30], as shown in Figure 2. In this regard, several studies provide evidence that in the erythrocytic phase the merozoites modify the surface of erythrocytes, inducing the expression of a surface protein-*Plasmodium falciparum* erythrocyte membrane protein 1-that has a strong affinity for adhesion molecules expressed on the surface of vascular endothelium, such as intracellular adhesion molecule 1, vascular cell adhesion molecule 1, and platelet endothelial cell adhesion molecule 1, among others^[31].

In sequestration, *P. falciparum*-infected erythrocytes adhere to the brain endothelium through binding to PfEMP1^[32]. There is no evidence to date of infected erythrocyte entry into brain parenchyma, suggesting that these cells remain in the vascular space where they are sequestered. This sequestration of parasitized erythrocytes leads to multiple vascular effects, including the formation of clusters of agglomerated platelets and leukocytes, increased vasoconstriction, as well as the agglutination of erythrocytes not parasitized by generating so-called rosettes, which significantly reduce cerebral blood flow in

the capillaries and cause vascular obstruction, leading to hypoxia, brain parenchymal hemorrhage^[22] and disruption of BBB integrity^[11,33].

Moreover, hyperinflammation in the brain has also been related to CM and is another mechanism responsible for the vasculopathy observed during infection (Figure 2). Some studies report that during the inflammatory response, activation of inflammatory cells may occur accompanied by an overproduction of type-1 proinflammatory mediators, especially tumor necrosis factor-alpha (TNF- α), which is produced by microglia, astrocytes, monocytes and cerebral vascular endothelium^[34]. In humans, this cytokine induces the upregulation of adhesion molecules on endothelial cell surfaces, which contributes to the increased capture of erythrocytes in the cerebral capillaries and other organs^[25,35]. Furthermore, inflammation enhances nitric oxide (NO) production by macrophages, which seems linked to the pathogenesis of the disease, considering that it is extremely toxic to nerve tissue and disrupts synapses, contributing to the damage to the nervous tissue^[36]. In addition, inflammation can lead to micro- and ring hemorrhages and necrosis of surrounding tissues and cerebral edema, resulting in significant compression of cerebral arteries that can lead to death, as well as the various symptoms of CM, such as confusion or stupor of obtundation, or deep coma with long-term neurological deficits such as cortical blindness^[25,37].

Postmortem analyses of children who died with CM revealed that the axonal and myelin damage was associated with ring hemorrhages and vascular thrombosis in the cerebral and cerebellar white matter and brainstem. Disruption of the BBB and accumulation of monocytes

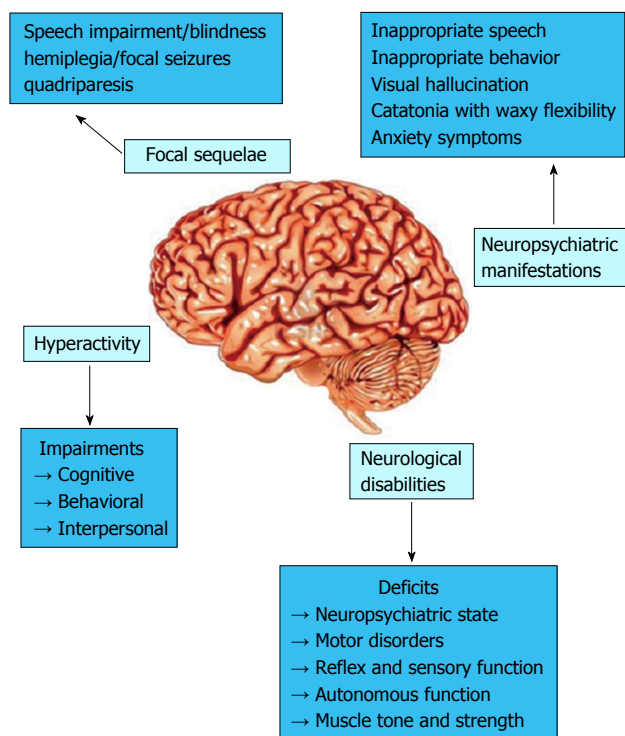


Figure 3 Neurological features of cerebral malaria.

with phagocytosed hemozoin within microvessels containing infected erythrocytes was found, suggesting a link between infected erythrocyte sequestration and intravascular/perivascular pathology in fatal pediatric CM^[38]. In animal models, the presence of apoptosis was also observed initially in endothelial cells and later in neurons and glia^[39], and may be associated with persistent cognitive impairment^[17]. These disturbances in the homeostasis of the cerebral microcirculation play an important role in the pathogenesis of CM, generating vascular obstructions, reduced cerebral blood flow and BBB disruption associated with high cerebral vasoconstriction^[24,40]. In addition, in the presence of seizures and/or fever, the metabolic demand increases with consequent risk of neural injury^[41], as shown in Figure 2.

NEUROLOGICAL FEATURES

Unfortunately, severe brain injury occurs after CM and 25% of pediatric cases result in epilepsy or long-term neurological and cognitive deficits^[42-44]. According to the time of symptom onset, CM may be classified into two patterns of neurological sequelae^[45], as shown in Figure 3. The first is immediate and characterized by coma and status epilepticus during the acute illness, resulting in focal sequelae such as hemiplegia and focal seizures, or multifocal sequelae with spastic quadriplegia, motor disorders, cognitive and behavioral impairment, blindness, speech or hearing impairment. The second pattern develops within months or years after CM, and behavioral deficits and/or epilepsy may occur.

Among gross motor deficits, hemiplegia, diplegia,

quadriplegia or quadriplegia may be observed after CM^[46]. Disorders in movement and gait can be noted, including ataxia, choreoathetosis, dystonia and poor neck control, as well as feeding difficulties^[46]. Dai *et al*^[47] demonstrated that motor coordination impairment was associated with dysregulation of Akt and GSK3 β signaling in a murine model of CM. The inhibition of the Akt pathway results in modifications in neuronal integrity, since it is a protein kinase playing a key role in the insulin signaling pathway and an important regulator of apoptosis, being consequently important for cell viability, although *via* an GSK3 β -dependent pathway. In addition, the intracranial hypertension may contribute to the motor sequelae, given that it reduces the cerebral perfusion pressure, nutrient and oxygen delivery and, where death does not occur, subsequent global ischemic injury and brainstem compression can lead to cerebral atrophy, which may result in motor and cognitive impairment^[48].

Convulsions in CM are common and inflammatory products such as quinolinic acid contribute to the neuropathology, considering that this metabolite from the kynurenine pathway is a N-methyl-D-aspartate agonist that causes neuroinflammation, convulsions, and cell death^[49-51]. Dobbie *et al*^[52] demonstrated that quinolinic acid provokes seizures in animals, possibly, altering the neurotransmission excitatory and triggering long-term deleterious effects on cognitive function and/or behavior. Sokol *et al*^[53] demonstrated irreversible neuron damage after long-term seizure activity, followed by gliosis and focal atrophy, resulting in more seizures and brain damage. The epilepsy (recurrence of seizures without apparent cause) occurs in approximately 10% of pediatric cases and may be occasioned by focal or global hypoxia or ischemia^[54,55]. The epileptogenesis mechanisms are unclear. Structural brain damage and the presence of Durck's malarial granuloma may contribute to the epileptogenesis mechanisms^[56]; however, other factors should also be considered, like genetic propensity^[57].

It has been observed that speech and language were the most common neurocognitive impairments found in Kenyan children who survived severe malaria^[58]. The authors suggested that language impairment may be part of a broad impairment that is most noted in the patterns of language, which probably contributes to deficits on verbal components of other cognitive assessments. On the other hand, Dugbartey^[59] reported that children affected by CM develop impairments in bimanual tactile discrimination, accuracy of visual scanning, visual memory, perceptual abstraction and rule learning skills, right ear auditory information processing, and dominant-hand motor speed. Other studies revealed deficits in spatial memory, mental processing, sequential processing, and attention tasks^[58,60,61]. Indeed, other kinds of memory, such as episodic memory, also seem to be affected by CM^[62].

Dai *et al*^[47,63] demonstrated that memory deficits either during or after successful treatment were associated with reduced Akt expression and dysregulation of Akt/GSK3 β signaling in a murine CM model. GSK3 β

plays a key role in the process of neurodevelopment and the transcription of brain derived neurotrophic factor, affecting long-term memory and synaptic plasticity^[64]. In this context, it has been associated with hyperphosphorylation of tau protein^[65], which is the major component in neurodegenerative disorders like Alzheimer's disease^[66]. Abnormal tau levels in the cerebral spinal fluid in CM survivors^[47,67] lead to long-term deficits in cognitive areas like memory, learning, language and psychiatric disorders^[17,42,68,69]. Specific damage in neuronal areas such as the hippocampus and sub-cortical white matter may lead to impairments in learning, memory and language function^[70-72].

Hyperactivity, impulsiveness and inattentiveness have also been observed in CM survivors^[45], similar to what occurs in attention deficit hyperactivity disorder (ADHD), which produces impairments in the cognitive, behavioral, and interpersonal domains^[73]. Dysregulated reward processing in the frontostriatal system has been proposed as a central mechanism in prevailing theoretical models of ADHD^[74,75], and altered dopamine signaling underlies a number of ADHD symptoms^[75]. Several anatomical changes in the brain are related to ADHD, including in the caudate nucleus, prefrontal cortex white matter, corpus callosum, cerebellar vermis^[76] and globus pallidus^[77], which are all areas that contain high densities of dopamine receptors. Most probably, damage occasioned by CM in the frontostriatal and cerebellar areas by a decrease in local blood flow or neuronal loss may produce impairments in dopamine signaling and consequently ADHD^[78].

Animal model parameters may reproduce some symptoms related to ADHD and stroke. In this regard, a murine study demonstrated a lower level of general activity associated with reduced response to touch escape and absent vocalization correlated with large areas of hemorrhage in animals with CM^[39]. These findings suggest an important influence of parenchymal hemorrhage distribution on the severity of neurological deficits in the late stage of the illness^[46].

An inflammatory cytokine profile has been associated with CNS dysfunction found in human and experimental CM. In the course of experimental CM induced by *Plasmodium berghei* (strain ANKA), leukocyte migration into the brain, as well as the production of TNF- α and chemokines (CCL2, CCL3, CCL5 and CXCL9) preceded neurological changes including in the neuropsychiatric state, motor behavior, autonomic function, muscle tone and strength, suggesting that the inflammatory changes may be involved in the neurological impairment^[79]. In this context, de Miranda *et al.*^[80] demonstrated an anxiety-like behavior in C57BL/6 mice infected with *P. berghei* using the elevated plus maze test. The anxiety symptoms were correlated with histopathological alterations in the brainstem, cerebrum and hippocampus and increased cerebral levels of interleukin-1 beta and TNF- α . In humans, Dugbartey *et al.*^[81] described anxiety disorders in a CM patient's recovery, suggesting that *falciparum* malaria is associated with enduring, albeit subclinical, anxiety and depressive

symptoms.

Some authors have reported correlations between neurological disabilities and glutamate levels and their contribution to the pathogenesis of these deficits, showing increased glutamate levels in cerebral spinal fluid and cerebrocortical synaptosomes from CM animals associated with alterations in neuropsychiatric state, motor behavior, reflex and sensory function, autonomic function, muscle tone and strength^[82]. Glutamate is the principal excitatory neurotransmitter in the mammalian CNS, participating in several cognitive and neurological functions under physiological conditions^[83]. Therefore, large amounts of glutamate release trigger neurotoxicity and neuronal cell death, being involved in neurodegenerative disorders^[84]. Thus, the imbalance in the neurotransmitter glutamate may be important in the establishing the pathogenesis mechanism of CM^[82].

The neuropsychiatric manifestations of post malaria neurological syndrome (PMNS) are highly variable and include an acute confusional state or acute psychosis with one or more of the following symptoms: inappropriate speech or behavior, visual hallucination, catatonia with waxy flexibility, generalized convulsion, fine postural tremor, clouding of consciousness and decreased muscle tone. It may occur within 2 mo after acute MC, with either neurologic or psychiatric symptoms^[85]. A case report on a Taiwan CM patient reported severe headache, dizziness, delirium and polyneuropathy within 2 mo after recovery^[86]; even psychotic symptoms with both visual and auditory hallucinations, aggressiveness, and inability to communicate have been related^[87,88] that can last for 12 d. The symptoms observed may not be attributed only to CM, since other factors could be responsible; however, the neurologic and psychiatric presentations were compatible with PMNS and the mechanisms are the same as those related to other neurologic CM deficits, including cerebral hypoperfusion and immunologic mechanism, which prompts psychosis in a small minority^[88].

CONCLUSION

Malaria is a parasitic disease that can affect the CNS, altering cognitive and behavioral functions. Neurological and behavioral changes described in the course of experimental or human CM are mainly a consequence of brain hyperinflammation, vascular obstruction, reduced cerebral blood flow, and disruption of the BBB associated with high levels of cerebral vasoconstriction, thrombus, ring hemorrhage, ruptured capillaries, and cerebral blood vessels filled with infected erythrocytes, with consequent axonal damage and demyelination. Additionally, neurologic alterations have been observed as motor deficits, seizures and epilepsy; neurocognitive impairment in language, speech, learning, and memory; and behavioral damage with hyperactivity, anxiety, PMNS and psychosis.

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Physics and mathematics of magnetic resonance imaging for nanomedicine: An overview

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Abstract

Magnetic resonance imaging (MRI), magnetic resonance angiography (MRA) and magnetic resonance spectroscopy (MRS) are fundamental concepts used in modern medicine to improve health care. These concepts are based on the principle of nuclear magnetic resonance (NMR). Over the years, various laboratories around the world have applied different numerical techniques based on the Bloch NMR equations to solve specific problems in physics, biology, chemistry, engineering and medicine. The ultimate goal of any physician is to obtain maximum physical, biophysical, chemical and biological information on any tissue or cell under examination. This goal can be achieved by solving the Bloch NMR flow equations analytically. In this review, we present the basic principle of NMR/MRI in a way that can be easily understood by any researcher who needs an NMR concept to solve a specific medical problems. After a very brief history of the subject, a second order, non homogeneous, time-dependent differential equation derived from the Bloch NMR equation is presented. This equation has the basic intrinsic properties of MRI, MRA and MRS that can be extracted by means of classical and quantum mechanics for possible application in nanomedicine.

reserved.

Key words: Bloch flow equations; Rotational diffusion; Molecular dynamics of biological fluids; Nuclear magnetic resonance diffusion equation; Rotational correlation time; Spherical harmonics; Molecular flow

Core tip: Magnetic resonance imaging is one of the most powerful methods for investigating structural and dynamics of biological matter. Based on quantum mechanical principles applied to Bloch nuclear magnetic resonance (NMR) flow equations, we aimed to apply the analytical solutions obtained from the Bloch NMR flow equations to nanomedicine. This may trigger research towards the design of nano devices that capable of delivering drugs directly to specifically targeted cells, with the possibility of very early diagnosis of diseases and treating them with powerful drugs at the pathological site alone, reducing any harmful side effects.

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INTRODUCTION

Nuclear magnetic resonance (NMR) is a very important analytical and experimental tool for physical, chemical and structural analysis of certain organic materials. Magnetic resonance is a branch of spectroscopy that detects the quantum-mechanical transitions induced by electromagnetic (EM) radiation in a system of discrete energy levels of electrons or nuclei placed in a static magnetic field^[1,2]. NMR employs EM waves in the radio-frequency range between 900 MHz and 2 KHz. Some nuclei experience nuclear resonance, while others do not. Exhibition

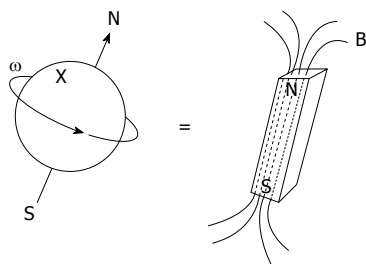


Figure 1 The charged nucleus (for example, ^1H) rotating with angular frequency $\omega = 2\pi\nu$ creates a magnetic field B and is equivalent to a small bar magnet whose axis is coincident with the spin rotation axis^[4].

of this phenomenon is dependent on whether they possess a property called “spin”^[2].

NMR is one of the most powerful methods for investigating the structure and dynamics of matter in different states of aggregation. This is due to the following features: (1) the interactions of nuclear magnetic moments are very weak compared with the thermal energy; therefore, we are dealing with para-magnetism. Moreover, the energy delivered by the radio-frequency generator are much larger compared with the strength of these inter-nuclear couplings. That leads to the possibility of manipulating these interactions in a specific way and simplifying the spectral response; (2) the radio-frequency photons have much lower energy compared with the energy of chemical bonds. Therefore, the interaction of EM radiation with matter, particularly biomolecules, is non-ionizing; and (3) the number of radio-frequency photons with a specific frequency is very large. Hence, the phase of the associated EM wave is very well defined. The high degree of coherence of radio-frequency radiation is essential to implement NMR experiments, including magnetic resonance imaging (MRI)^[3].

SPIN

Spin is a fundamental property of nature, like electrical charge or mass. Spin comes in multiples of $1/2$ and can be positive (+) or negative (-). Protons, electrons and neutrons possess spins. Individual unpaired electrons, protons and neutrons each possess a spin of $1/2$. In the deuterium atom (^2H), for example, with one unpaired electron, one unpaired proton and one unpaired neutron, the total electronic spin is equal to $1/2$ and the total nuclear spin is equal to 1. Two or more particles with spins having opposite signs can pair up to eliminate the observable manifestations of spin. An example is helium, (^4He). In NMR, it is the unpaired nuclear spins that are important. When placed in a magnetic field of strength B , a particle with a net spin can absorb a photon, of frequency ω . The frequency of ω depends on the gyromagnetic ratio γ , of the particle [as shown in equation (1)], given by the expression:

$$\omega = \gamma B \quad (1)$$

For hydrogen nuclei, the gyromagnetic ratio $\gamma = 42.58$ MHz/T^[4]. Nuclei are composed of positively charged

Table 1 Properties of nuclei most useful for biological studies^[5]

Nucleus	Spin quantum number (I)	Natural abundance (%)	Gyromagnetic ratio γ (10^{-7} rad/T sec)	Sensitivity ¹ (% vs ^1H)	Electric quadrupole moment (Q) ($\text{e} \cdot 10^{24} \text{ cm}^2$)
^1H	1/2	99.9844	26.7520	100.000	-
^2H	1/1	0.0156	4.1067	0.965	0.00277
^{13}C	1/2	1.1080	6.7265	1.590	-
^{15}N	1/2	0.3650	-2.7108	0.104	-
^{19}F	1/2	100.0000	25.167	83.300	-
^{31}P	1/2	100.0000	10.829	6.630	-

¹Relative sensitivity for equal number of nuclei at constant magnetic field strength.

protons and uncharged neutrons held together by nuclear forces^[4,5], as shown in Figure 1.

The shell model for the nucleus tells us that nucleons, just like electrons, fill orbitals. When the number of protons or neutrons equals 2, 8, 20, 28, 50, 82 and 126, the orbitals are filled, because nucleons have spin, just like electrons do, and their spins can pair up when the orbitals are being filled and cancel out. Almost every element in the periodic table has an isotope with a non-zero nuclear spin^[4,5]. NMR can only be performed on isotopes whose natural abundance is high enough to be detected; some of the nuclei that are of interest in NMR/MRI are listed in Table 1.

We have seen that $\omega = \gamma B$ and hence the energy of the radio waves needed to cause a transition between the two spin states is given by equation (2):

$$E = \eta \gamma B \quad (2)$$

When the energy of the photon matches the energy difference between the two spin states, absorption of energy occurs. In an NMR experiment, the frequency of the photon is in the radio frequency (RF) range. In NMR spectroscopy, ω is between 600 and 800 MHz for hydrogen nuclei. However, in clinical MRI, ω is typically between 15 and 80 MHz for hydrogen imaging^[6] (Table 2).

To get a better understanding of how particles with spin behave under a magnetic field, we consider a proton that has a spin property. If we imagine the spin of this proton as a magnetic moment vector, causing the proton to behave like a tiny magnet with a North and South Poles. When the proton is placed in an external magnetic field, the spin vector of the particle aligns itself with the external field, just like a magnet would. There is a low energy configuration or state where the poles are aligned N-S-N-S and a high energy state N-N-S-S.

This particle can undergo a transition between the two energy states by the absorption of a photon. A particle in the lower energy state absorbs a photon and ends up in the higher energy state. The energy of this photon must exactly match the energy difference between the two states. The energy E , of a photon is related to its frequency ω , by Planck's constant ($\eta = h/2\pi$, $h = 6.626 \times 10^{-34}$ Js).

Table 2 Nuclear Spin values and gyromagnetic ratios of some nuclei^[5]

Nuclei	Unpaired protons	Unpaired neutrons	Net spin	γ (MHz/T)
^1H	1	0	1/2	42.58
^2H	1	1	1/1	6.54
^{31}P	1	0	1/2	17.25
^{23}Na	1	2	3/2	11.27
^{14}N	1	1	1/1	3.08
^{13}C	0	1	1/2	10.71
^{19}F	1	0	1/2	40.08

$$E = \hbar\omega \quad (3)$$

In NMR and MRI, the quantity ω is called the resonance frequency or the Larmor Frequency^[6].

MRI

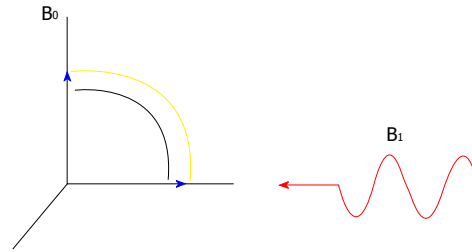
MRI is an imaging technique used primarily in medical settings to produce high quality images of the inside of the human body. MRI is based on the principles of NMR, a spectroscopic technique used by scientists to obtain microscopic chemical and physical information about molecules. The technique was called MRI rather than nuclear MRI because of the negative connotations associated with the word nuclear in the late 1970's. MRI started as a tomographic imaging technique; that is, it produced an image of the NMR signal in a thin slice through the human body. MRI has advanced from a tomographic imaging technique to a volume imaging technique. MRI is based on the absorption and emission of energy in the RF range of the EM spectrum^[3,7].

In the past, many scientists were taught that one cannot obtain an image smaller than the wavelength of the energy being used to image it. MRI gets around this limitation by producing images based on spatial variations in the phase and frequency of the RF energy being absorbed and emitted by the imaged object.

Clinical MRI uses the magnetic properties of hydrogen and its interaction with both a large external magnetic field and radio waves to produce highly detailed images of the human body. Hydrogen has a significant magnetic moment and is the most abundant nucleus in the human body. For these reasons, we use only the hydrogen proton in routine clinical imaging^[7].

To perform MRI, we first need a strong magnetic field. The field strength of the magnets used for MR is measured in units of Tesla. One (1) Tesla is equal to 10000 Gauss. The magnetic field of the earth is approximately 0.5 Gauss. Given that relationship, a 1.0 T magnet has a magnetic field approximately 20000 times stronger than that of the earth. The type of magnets used for MRI usually belongs to one of three types; permanent, resistive, and superconductive.

A permanent magnet is sometimes referred to as a vertical field magnet. These magnets are constructed of two magnets (one at each pole). The patient lies on a scanning table between these two plates^[8].

**Figure 2** A 90-degree flip of the net magnetization.

The advantages of these systems are: relatively low cost, no electricity or cryogenic liquids are needed to maintain the magnetic field, their more open design may help alleviate some patient anxiety and their nearly non-existent fringe field. It should be noted that not all vertical field magnets are permanent magnets.

Resistive magnets are constructed from a coil of wire. The more turns to the coil, and the more current in the coil, the higher the magnetic field. These types of magnets are most often designed to produce a horizontal field because of their solenoid design. As previously mentioned, some vertical field systems are based on resistive magnets. The main advantages of these types of magnets are: no liquid cryogen, the ability to “turn off” the magnetic field and their relatively small fringe field.

Superconducting magnets are the most common. They are made from coils of wire (as are resistive magnets) and thus produce a horizontal field. They use liquid helium to keep the magnet wire at 4 degrees Kelvin where there is no resistance. The current flows through the wire without having to be connected to an external power source. The main advantage of superconducting magnets is their ability to attain field strengths of up to 3 Tesla for clinical imagers and up to 10 Tesla or more for small bore spectroscopy magnets^[9].

CREATION OF AN MR SIGNAL

A radio wave is actually an oscillating EM field. The RF field is also referred to as the B_1 field. It is oriented perpendicular to the main magnetic field (B_0). If we apply a pulse of RF energy into the tissue at the Larmor frequency, we first find the individual spins begin to precess in phase, as will the net magnetization vector. As the RF pulse continues, some of the spins in the lower energy state absorb energy from the RF field and make a transition into the higher energy state. This has the effect of “tipping” the net magnetization toward the transverse plane. This phenomenon is illustrated in Figure 2. For the purpose of this explanation, we will assume sufficient energy is applied to produce a 90-degree flip of the net magnetization. In such an example, it is said that a 90-degree flip angle or a 90-degree pulse has been applied^[10].

Oriented perpendicular to B_0 is a receiver coil. As the magnetization (now referred to as transverse magnetization, or M_{xy}) precesses through the receiver coil, a current or signal is induced in the coil. The principle behind

this signal induction is Faraday's Law of Induction. This states that if a magnetic field is moved through a conductor, a current will be produced in the conductor. If we increase the size of the magnetic field, or increase the speed with which it moves, we will increase the size of the signal (current) induced in the conductor.

To detect the signal produced in the coil, the transmitter must be turned off. When the RF pulse is discontinued, the signal in the coil begins at given amplitude (determined by the amount of magnetization precessing in the transverse plane (Figure 2) and the precessional frequency) and fades rapidly away. This initial signal is referred to as the Free Induction Decay (FID). The signal fades as the individual spins contributing to the net magnetization lose their phase coherence, making the vector sum equal to zero. At the same time, but independently, some of the spins that had moved into the higher energy state give off their energy to their lattice and return to the lower energy state, causing the net magnetization to re-grow along the z axis. This re-growth occurs at a rate given by the tissue relaxation parameter, known as T_1 ^[9,10].

DEFINITION OF TERMS IN NMR/MRI

Spin packets

A spin packet is a group of spins experiencing the same magnetic field strength. At any instant in time, the magnetic field caused by the spins in each spin packet can be represented by a magnetization vector; \vec{M} . The vector sum of the magnetization vectors from all the spin packets is the net magnetization. Adapting the conventional NMR coordinate system, the external magnetic field and the net magnetization vector at equilibrium are both along the Z axis.

T_1 relaxation time

The time constant that describes how M_z returns to its equilibrium value is called the spin lattice relaxation time (T_1). The equation governing this behavior as a function of time t after its displacement is:

$$M_z = M_0 (1 - e^{-t/T_1}) \quad (4)$$

At equilibrium, the net magnetization vector lies along the direction of the applied magnetic field B_0 and is called the equilibrium magnetization M_0 . In this configuration, the Z component of magnetization M_z equals M_0 . M_z is referred to as the longitudinal magnetization. There is no transverse (M_x or M_y) magnetization here.

Larmor frequency

The resonant frequency of a nucleus is determined by a combination of nuclear characteristics and the strength of the magnetic field. The specific relationship between resonant frequency and the field strength is an inherent characteristic of each nuclide and is generally designated as gyromagnetic ratio γ . The resonant frequency is also known as the Larmor frequency.

T_2 relaxation time

The time constant that describes the return to equilib-

rium of the transverse magnetization, M_{xy} , is called the spin-spin relaxation time, T_2 .

$$M_{xy} = M_{xy0} e^{-t/T_2} \quad (5)$$

T_2 is always less than or equal to T_1 . The net magnetization in the XY plane goes to zero and then the longitudinal magnetization grows in until we have M_0 along Z.

Excitation

If a pulse of RF energy with a frequency corresponding to the nuclear precession rate is applied to a material, some of the energy will be absorbed by the individual nuclei. The absorption of energy by a nucleus flips its alignment away from the direction of the magnetic field. This increased energy places the nucleus in an excited state. In this excited state, the precession is now transformed into a spinning motion of the nucleus around the axis of the magnetic field^[1-14].

BRIEF HISTORY ON THE DEVELOPMENT OF NMR AND MRI

The history of the development of the concept of NMR started with Felix Bloch at Harvard, and Edward Purcell at Stanford, both of whom were awarded the Nobel Prize in 1952, discovered the magnetic resonance phenomenon independently in 1946, using different instrumentation. In the period between 1950 and 1970, NMR was developed and used for chemical and physical molecular analysis. In 1971 Raymond Damadian (an Armenian-American medical practitioner and inventor of the first MR Scanning Machine) showed that the nuclear magnetic relaxation times of tissues and tumors differed, thus motivating scientists to consider magnetic resonance for the detection of disease. In 1973 the X-ray-based computerized tomography (CT) was introduced by Hounsfield. MRI was first demonstrated on small test tube samples that same year by Paul Lauterbur. He used a technique similar to that used in CT. In 1975 Richard Ernst, a Swiss physical chemist, proposed MRI using phase and frequency encoding, and the Fourier Transform. This technique is the basis of current MRI techniques. A few years later, in 1977, Raymond Damadian demonstrated MRI called field-focusing NMR. In this same year, Peter Mansfield developed the echo-planar imaging (EPI) technique. This technique was later developed to produce images at video rates (30 ms/image). Edelstein and coworkers demonstrated imaging of the body using Ernst's technique in 1980. A single image could be acquired in approximately five minutes by this technique. By 1986, imaging time was reduced to about five seconds, without sacrificing significant image quality. In the same year, the NMR microscope was developed, which allowed approximately 10m resolution on approximately one cm samples. In 1987 EPI was used to perform real-time moving imaging of a single cardiac cycle. In this same year, Charles Dumoulin perfected magnetic resonance angiography (MRA), which allowed imaging of flowing blood without the use of contrast agents.

In 1991, Richard Ernst was rewarded for his achievements in pulsed Fourier Transform NMR and MRI with the Nobel Prize in Chemistry. In 1992 functional MRI (fMRI) was developed. This technique allows the mapping of the functions of the various regions of the human brain. Five years earlier, many clinicians thought EPI's primary application was to be in real-time cardiac imaging. The development of fMRI opened up a new application for EPI in mapping the regions of the brain responsible for thought and motor control. In 1994, researchers at the State University of New York at Stony Brook and Princeton University demonstrated the imaging of hyperpolarized ^{129}Xe gas for respiration studies.

In 2003, Paul C Lauterbur of the University of Illinois and Sir Peter Mansfield of the University of Nottingham were awarded the Nobel Prize in Medicine for their discoveries concerning MRI. MRI is clearly a young, but growing science^[1,3,5-16].

THE THEORY OF NMR

The appearance of NMR spectra, and consequently the molecular structure they are able to provide, arises from the discrete nature of the energy levels pertaining to a nuclear spin system. The energy levels are mainly a result of Zeeman interaction, $-\vec{\mu}\vec{B}_0$ between the static magnetic field of induction \vec{B}_0 and nuclear magnetic moment $\vec{\mu}$. The quantum-mechanical quantity called spin momentum, \vec{I} is related to magnetic moment by $\vec{\mu} = \gamma\eta\vec{I}$, where γ is the gyromagnetic ratio and η is the Planck's constant divided by 2π .

In the absence of the magnetic nuclear, the spin states are generated. The application of a static magnetic field \vec{B}_0 which induces a magnetic interaction, is described by Zeeman Hamiltonian $H = -\vec{\mu}\vec{B}_0$. Taking the magnetic field orientation to be along the z-direction we get:

$$H = -\gamma\eta B_0 L_z \quad (6)$$

The Eigen values E_m of this Hamiltonian can be evaluated from the Schrodinger equation

$$H|m\rangle = -\gamma\eta B_0 m|m\rangle \quad (7)$$

where $|m\rangle$ is the Eigen state corresponding to the Eigen value $E_m = -\gamma\eta B_0 m$. The magnetic quantum number is m , where $m = l, l-1, \dots, -l$. Therefore, the equidistant energy differences are for the single-quantum transitions $m = \pm 1$ given by^[1,4,5,7]

$$\Delta E = \eta\omega_0 \quad (8)$$

where the Larmor frequency is defined as^[1,4,5,7]

$$\nu_0 = \nu_L = \omega_0/2\pi$$

Another important ingredient for a magnetic resonance experiment is represented by the presence of the RF field. Only the magnetic component of the EM field, *i.e.*, $B_1(t) = B_{10} \cos(2\pi\nu t)$ interacts with the magnetic moment of the nuclei. The amplitude of the RF field is B_{10} and ν is the carrier frequency. This field is produced by an RF coil and leads to a perturbation Hamiltonian:

$$\vec{H}_p = -\gamma\eta\vec{B}_{10}\vec{I}\cos(2\pi\nu t) \quad (9)$$

From the time-dependent perturbation theory of quantum mechanics, it can be stated that a transition between two states $|\psi\rangle$ and $|\phi\rangle$ is allowed, provided that $\langle\psi|H_p|\phi\rangle \neq 0$. This takes place if $\nu \approx \nu_0$ (*i.e.*, the resonance condition) and the alternative magnetic field \vec{B}_0 is polarized perpendicular to the static magnetic field \vec{B}_{10} ^[11].

In general, NMR experiments are performed at high temperatures, employing a large number of spins. These features lead to the possibility to treat classically some aspects of the experiments. The excess of spins oriented along the static magnetic field \vec{B}_0 with respect to those oriented in the opposite direction results in a macroscopic nuclear magnetization \vec{M} , aligned along the static magnetic field, which is called the equilibrium magnetization. It can be displaced from this equilibrium by an appropriate perturbation, for instance, by an RF excitation. It is then subject to a precessional motion around \vec{B}_0 with the Larmor frequency ν_L . The EM perturbation that brings \vec{M} into a plane perpendicular to \vec{B}_0 allows the observation of the Larmor precession through an electromotive force that occurs in a coil whose axis is contained in that plane. This can be done by rotation of the magnetization using a resonant 90° RF pulse. The nuclear magnetization \vec{M} can be oriented antiparallel to \vec{B}_0 by the action of a 180° pulse. The majority of NMR experiments used pulse sequences composed of 90° and 180° RF pulses^[9-18].

PULSED NMR SPECTROSCOPY

A coil of wire placed around the x-axis will provide a magnetic field along the x-axis when a direct current is passed through the coil. An alternating current will produce a magnetic field that alternates in direction. In a frame of reference rotating about the z-axis at a frequency equal to that of the alternating current, the magnetic field along the x'-axis will be constant, just as in the direct current case in the laboratory frame. This is the same as moving the coil about the rotating frame coordinate system at the Larmor Frequency. In magnetic resonance, the magnetic field created by the coil passing an alternating current at the Larmor frequency is called the B_1 magnetic field. When the alternating current through the coil is turned on and off it creates a pulsed B_1 magnetic field along the x'-axis. The spins respond to this pulse in such a way as to cause the net magnetization vector to rotate about the direction of the applied B_1 field. The rotation angle depends on the length of time τ for which the field is switched on and its magnitude, B_1 ^[2,6,7,9].

A 90° pulse is one that rotates the magnetization vector clockwise by 90° about the x'-axis and rotates the equilibrium magnetization down to the y'-axis. In the laboratory frame, the equilibrium magnetization spirals down around the z-axis to the xy-plane. One can now see why the rotating frame of reference is helpful in describing the behavior of magnetization in response to a pulsed magnetic field. A 180° pulse will rotate the magnetization vector by 180° and rotates the equilibrium magnetization

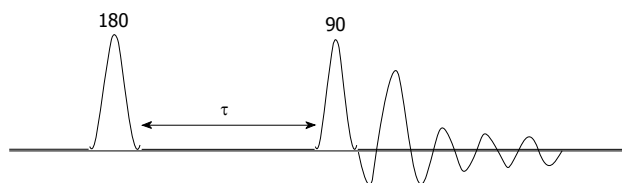


Figure 3 A series of spectra recorded with different values of τ to map out the recovery of the magnetization.

down along the z-axis.

The net magnetization at any orientation will behave according to the rotation equation. For example, a net magnetization vector along the y' -axis will end up along the y' -axis when acted upon by a 180° pulse of B_1 along the x' -axis. A net magnetization vector between x' - and y' - will end up between x' and y' after the application of 180° pulse of B_1 applied along the x' -axis^[9].

Longitudinal magnetization is aligned along the field axis B_0 (that is, the z-axis) and has a finite equilibrium value of M_{z0} . M_{z0} represents the equilibrium magnetization at the start of any NMR experiment.

Transverse magnetization is perpendicular to B_0 , precesses around the z-axis at the Larmor frequency and has an equilibrium value of zero^[13].

$$\omega = 2\pi\nu = -\gamma B_0$$

A simple 1D NMR spectrum is obtained by a 90° pulse, followed by detection of the FID and Fourier transformation of the FID. More complicated pulse sequences allow measurement of specific parameters, 2D and multi-dimensional data.

MEASUREMENT OF T_1 RELAXATION TIMES

The inversion-recovery (IR) pulse sequence can be used to measure the T_1 relaxation times of all the resonances in a spectrum. IR pulse sequence is pictorially represented in Figure 3.

Alternatively, the zero crossing point for each peak can be used to estimate the T_1 . Using the time τ_0 at which the signal I is zero:

$$\tau_0 = T_1 \ln 2 = 0.693 T_1 \quad (10)$$

This provides a very useful spot check for the value of T_1 in any sample. We must note that the relaxation delay between subsequent scans must be set to at least $5 T_1$ for experiments for good estimates of T_1 .

The saturation-recovery pulse sequence starts from perfectly equal populations of α and β spin states ($M_z = 0$, achievable by saturation). During a subsequent waiting period t , the z-magnetization reappears in an exponential recovery until it has assumed equilibrium value M_{z0} for a very long time t :

$$M_z = M_{z0} (1 - e^{-t/T_1}) \quad (11)$$

An experiment of this nature does not require long recovery delays between scans; however, saturation of the spin states is not always easy^[10].

PRACTICAL IMPORTANCE OF T_1 RELAXATION

Recovery delays

Any pulsed NMR experiment is repeated many times, and the scans added together to improve signal-to-noise (S/N) ratio. If the signals are not fully relaxed before each pulse/acquisition, then the signal in each scan will progressively decrease.

A recovery delay of about $5 \times T_1$ between subsequent scans almost completely restores M_{z0} , yielding reliable integrals. Recovery delays of about $1.4 T_1$ maximizes S/N ratio, but the integrals of slowly relaxing signals will be smaller than those of the rapidly relaxing signals.

Solvent saturation

If a signal, or a whole spectrum, is irradiated continuously with RF, then the populations N_α and N_β will equalize and no signal can be observed. This can be used for selective removal of a peak, e.g., a solvent peak from a spectrum. For example, in biological samples, H_2O would yield a huge signal without solvent suppression. A simple way of solvent suppression is presented by selective saturation by pre-irradiation = weak irradiation of the solvent signal during the recovery delay before the 90° pulse^[10,18].

Weak interactions between the small magnetic moments of nuclear spins with the environment result in slow relaxation rates and allow the design of long and complicated pulse sequences. In contrast to optical spectroscopy, nuclear spins can access only a finite number of energy levels. This allows the accurate calculation of the outcome of pulse sequences. Transverse magnetization can be destroyed by a "pulsed field gradient": an electric current is sent through a gradient coil for a few milliseconds. This results in a wide distribution of Larmor frequencies during the gradient and, hence, averaging of the transverse magnetization vectors to zero^[18].

NUCLEAR ENERGIES IN A MAGNETIC FIELD

The energy of the magnetic moment of a nuclear spin in a magnetic field is given by

$$E = -\mu B \quad (12)$$

where μ is the spin angular momentum and B is the magnetic field (in general B is a vector quantity). To conduct an NMR experiment, a sample is first placed in a static field. By convention, the direction of the static magnetic field is along the z-axis, and the magnitude of the magnetic field is given by B_0 (no longer a vector because it points only along the z-axis). In this case, the energy of a nuclear spin in an NMR magnet becomes

$$E = -\mu_z B_0 = -\gamma I_z B_0 \quad (13)$$

where γ is the gyromagnetic ratio (sometimes called the magnetogyric ratio) and I_z is the spin quantum number in the z-axis direction. The energy associated with a particu-

lar quantum number m is given as:

$$E_m = -m\hbar\gamma B_0 \quad (14)$$

NMR transition energies are very small. These small energies translate into low sensitivity. When samples are placed into a magnetic field, a small excess of nuclei fall into the α state. This excess of spins in the α over the β states accounts for the entire net magnetization that is used in the NMR experiment. The ratio of the number of spins in the β state to those in the α state is given by a Boltzmann distribution:

$$N_\alpha/N_\beta = e^{\Delta E/(\hbar\gamma T)} \quad (15)$$

where ΔE is the difference of energies of the α and β states, $\hbar\gamma$ is Boltzmann constant, and T is the absolute temperature. Higher magnetic fields produce correspondingly larger differences in spin states, leading to greater sensitivity^[12,14,15].

BULK MAGNETIZATION IN AN ELECTRIC FIELD

If the bulk magnetization is along the field direction, as it is at equilibrium, then there is no torque and hence no motion. As expected, at equilibrium the system is stationary. If the system is away from equilibrium and the bulk magnetization vector is oriented other than along the z-axis, then the magnetization precesses (rotates) about the z-axis with an angular velocity given by the energy separation of the two states (γB_0). This torque will not change the length of the magnetization vector; it only varies its orientation. This orientation cannot be the only motion, since the system would never return to equilibrium. Therefore, along with the rotation, there is a relaxation of the vector to bring it back along the z-axis. Therefore the x- and y-components of the nuclear magnetization decay towards zero, and the z-component decays towards the equilibrium value (M_0)^[4,10,14].

Considering bulk magnetization M that arises from all the magnetic moments in a sample, M experiences a torque when placed in a magnetic field, according to the expression given below:

$$dJ(t)/dt = M(t) \times B(t) \quad (16)$$

where $J(t)$ is the bulk spin angular momentum. The vector quantities in equation (16) are time dependent. The time-dependence of the magnetic field comes about when we apply RF pulses along the x- or y-axis. Equation (16) is essentially identical to an equation that describes the motion of a gyroscope^[18-20]:

$$dL(t)/dt = r \times mg \quad (17)$$

where $L(t)$ is the gyroscope's angular momentum, r the radius from the fixed point of rotation, m is the mass, and g is gravity. Thus, a nuclear spin in a magnetic field will behave much like a gyroscope in a gravitational field. To make equation (16) useful, we use the relationship for the z-component of the magnetic moment:

$$\mu_z = \gamma L_z = \gamma \hbar m \quad (18)$$

Then multiply each side by γ to yield

$$dM(t)/dt = M(t) \times \gamma B(t) \quad (19)$$

Equation (19) is the basis of the Bloch equations^[18-20].

BLOCH EQUATIONS

In 1946 Felix Bloch formulated a set of equations that describe the behavior of nuclear spin in a magnetic field under the influence of RF pulses. He modified equation (19), given above, to account for the observation that nuclear spins “relax” to equilibrium values following the application of RF pulses. Bloch assumed they relax along the z-axis and in the x-y plane at different rates, but following first order kinetics. These rates are designated $1/T_1$ and $1/T_2$ for the z-axis and x-y plane, respectively. T_1 is called spin-lattice relaxation and T_2 the spin-spin relaxation. With the addition of relaxation, equation (19) becomes:

$$dM(t)/dt = M(t) \times \gamma B(t) - R [M(t) - M_0] \quad (20)$$

where R is the “relaxation matrix”. Equation (20) can best be explained by considering each of its components:

$$\begin{aligned} dM_z(t)/dt &= \gamma [M_x(t) B_y(t) \times M_y(t) B_x(t)] - [M_z(t) - M_0]/T_1 \\ dM_x(t)/dt &= \gamma [M_y(t) B_z(t) \times M_z(t) B_y(t)] - M_x(t)/T_2 \\ dM_y(t)/dt &= \gamma [M_z(t) B_x(t) \times M_x(t) B_z(t)] - M_y(t)/T_2 \end{aligned} \quad (21)$$

The terms in equation (21) that do not involve either T_1 or T_2 are the result of the cross product in equation (20). Equation (21) describes the motion of magnetization in the “laboratory frame”, an ordinary coordinate system is stationary. Mathematically, the laboratory frame is not the simplest coordinate system, because the magnetization is moving at a frequency $\omega_0 = \gamma B_0$ in the x-y (transverse) plane. A simpler coordinate system is the “rotating frame”, in which the x-y plane rotates around the z-axis at a frequency $\Omega = -\gamma B_0$. In the rotating frame, magnetization “on resonance” does not precess in the transverse plane. The transformation of equation (21) to the rotating frame is achieved by replacing each B_z (defined as B_0) by Ω/λ :

$$\begin{aligned} dM_z(t)/dt &= \gamma [M_x(t) B_y^r(t) - M_y(t) B_x^r(t)] - [M_z(t) - M_0]/T_1 \\ dM_x(t)/dt &= -\Omega M_y(t) - \gamma M_z(t) B_y^r(t) - M_x(t)/T_2 \\ dM_y(t)/dt &= \gamma M_z(t) B_x^r(t) + \Omega M_x(t) - M_y(t)/T_2 \end{aligned} \quad (22)$$

In equation (22), the components of B have been written with r superscripts to denote that it is a rotating frame^[17-23].

PHYSICAL INTERPRETATION OF BLOCH EQUATIONS

We shall examine the behavior of equation (22) under two different limiting conditions, the effect of a short RF pulse and free precession. The RF pulse will be assumed to be very short compared to either relaxation times T_1 and T_2 , as well as the angular frequency Ω . This assumption is valid for many typical pulsed NMR experiments, in which the pulse lengths can be as short as 5 μ s. If the

RF pulse is applied along the x-axis, these conditions will allow us to neglect terms in equation (22) that contain T_1 , T_2 , Ω , and B_y .

$$\begin{aligned} dM_z/dt &= -M_y(t) \gamma B_x(t) \\ dM_x(t)/dt &= 0 \\ dM_y(t)/dt &= M_z(t) \gamma B_x(t) \end{aligned} \quad (23)$$

Before solving equation (23), we need to discuss the meaning of $B_x(t)$ and $B_y(t)$. We can recall that B_0 is the static magnetic field strength oriented along the z-axis. $B_x(t)$ and $B_y(t)$ are magnetic fields oriented along the x- and y-axes that are generated by rf pulses. By analogy to $\omega_0 = \gamma B_0$ defining the frequency of the NMR transitions in the static magnetic field, we can see that the terms $\gamma B_x(t)$ and $\gamma B_y(t)$ are frequencies of the magnetization rotating around the x- or y-axis. Thus, applying these frequencies for different periods of time will allow for different degrees of rotation around the x- or y-axis. If we introduce a frequency of rotation about the x-axis as $\omega_x = \gamma B_x(t)$, solutions to equation (23) can now be given as:

$$\begin{aligned} M_z(t) &= M_0 \cos(\omega_x t) \\ M_x(t) &= 0 \\ M_y(t) &= M_0 \sin(\omega_x t) \end{aligned} \quad (24)$$

Finally, if we let $\theta = \omega_x t$ be the pulse angle, equation (24) shows that application of a magnetic field (RF pulse) along the x-axis causes the magnetization that was originally along the z-axis to rotate toward the y-axis by an angle θ . Note that when $\theta = 0$, $M_z(t) = M_0$ and $M_y(t) = 0$ (all the magnetization is still pointing along the z-axis). When $\theta = 90^\circ$, $M_y(t) = M_0$ and $M_z(t) = 0$ (all the magnetization is still pointing along the y-axis). These have described the effects of a simple RF pulse. The second limiting condition for equation (22) is free precession in the absence of any applied pulse. In that case, B_x and B_y are both equal to zero, and equation (22) becomes:

$$\begin{aligned} dM_z(t)/dt &= -[M_z(t) - M_0]/T_1 \\ dM_x(t)/dt &= -\Omega M_y(t) - M_x(t)/T_2 \\ dM_y(t)/dt &= -\Omega M_x(t) - M_y(t)/T_2 \end{aligned} \quad (25)$$

The solutions to equation (25) can be given as:

$$\begin{aligned} M_z(t) &= M_0 (1 - e^{-t/T_1}) \\ M_x(t) &= M_0 \cos(\Omega t) e^{-t/T_2} \\ M_y(t) &= M_0 \sin(\Omega t) e^{-t/T_2} \end{aligned} \quad (26)$$

Equation (26) describes magnetization precessing in the x-y plane at a frequency Ω , while it is relaxing along the z-axis at a rate of $1/T_1$ and relaxing in the x-y plane at a rate $1/T_2$ ^[17-19,21,24].

THE GENERAL BLOCH NMR FLOW EQUATION

The Bloch NMR flow equations can be written as^[25,26]:

$$\partial M_x / \partial t + v \partial M_x / \partial x = -M_x / T_2 \quad (27)$$

$$\partial M_y / \partial t + v \partial M_y / \partial x = \gamma M_z B_1(x) - M_y / T_2 \quad (28)$$

$$\partial M_z / \partial t + v \partial M_z / \partial x = -\gamma M_x B_1(x) + (M_0 - M_z) / T_1 \quad (29)$$

From equation (28 and 29), we have

$$\begin{aligned} v^2 \frac{\partial^2 M_y}{\partial x^2} + 2v \frac{\partial^2 M_y}{\partial x \partial t} + v \left(\frac{1}{T_1} + \frac{1}{T_2} \right) \frac{\partial M_y}{\partial x} + \left(\frac{1}{T_1} + \frac{1}{T_2} \right) \frac{\partial M_y}{\partial t} \\ + \frac{\partial^2 M_y}{\partial t^2} + \left[-\frac{1}{T_1 T_2} + \gamma^2 B_1^2(x, t) \right] M_y = \frac{\gamma B_1(x, t) M_0}{T_1} \end{aligned} \quad (30)$$

Equation (30) is a general second order, non-homogeneous, time dependent differential equation that can be applied to any fluid flow problem. At any given time t , we can obtain information about the system, provided that appropriate boundary conditions are applied. From equation (30), we can obtain the diffusion equation, the wave equation, telegraph and telegraph equations, Schrödinger's equation, Legendre's equation, *etc.*, and solve them in terms of NMR parameters by the application of appropriate initial or boundary conditions. Hence, we can obtain very important information about the dynamics of the system. It should be noted, however, that the term $F_0 \gamma B_1(x, t)$ is the forcing function ($F_0 = M_0/T_1$). If the function is zero, we have a freely vibrating system; otherwise, the system is undergoing a forced vibration.

NMR DIFFUSION EQUATION

A diffusion equation can easily be obtained from equation (30) if we assume that the NMR wave is a plane wave such that:

$$M_y(x, t) = A e^{\mu x + \eta t} \quad (31)$$

subject to the following MRI experimental conditions:

$$\gamma^2 B_1^2(x, t) < 1/(T_1 T_2) \quad (32)$$

where μ and η are dependent on the NMR parameters. Taking

$$\eta^2 = T_2 \text{ and } 2\eta = T_0 \quad (33)$$

Equation (30) becomes

$$v^2 \frac{\partial^2 M_y}{\partial x^2} + T_0 \frac{\partial M_y}{\partial t} = F_0 \gamma B_1(x, t) \quad (34)$$

If we write

$$\begin{aligned} D &= -v^2/T_0 \\ v &= (-D T_0)^{1/2} \end{aligned} \quad (35)$$

Then equation (34) becomes

$$\partial M_y / \partial t = D \frac{\partial^2 M_y}{\partial x^2} + F_0/T_0 \gamma B_1(x, t) \quad (36a)$$

Equation (36a) can be written in generalized co-ordinates as:

$$\partial M_y / \partial t = D \nabla^2 M_y + F_0/T_0 \gamma B_1(t) \quad (36b)$$

If D represents the diffusion coefficient, then Equation (36) is the equation of diffusion of magnetization as the nuclear spins move. The function $F_0/T_0 \gamma B_1(x, t)$ is the forcing function, which shows that application of the RF B_1 field has an influence on the diffusion of magnetization within a voxel. It is interesting to note that the dimension of equation (35) exactly matches that of the diffusion coefficient.

Equation (36) is only applicable when D is non-directional. That is, we have a constant diffusion coefficient (isotropic medium). Equation (36) can be considered for

restricted diffusion in various geometries^[25,26]. This model would work quite well for molecules that move very short distances over a very considerable amount of time; where

$$\begin{aligned}\Omega &= T_g + \gamma^2 B_1^2(x, t); \\ F_0 &= M_0/T_1; \\ T_g &= 1/(T_1 T_2) \\ \text{and } T_0 &= 1/T_1 + 1/T_2\end{aligned}\quad (37)$$

where γ is the gyromagnetic ratio, D is the diffusion coefficient, v is the fluid velocity, T_1 is the spin lattice relaxation time, T_2 is the spin relaxation time, M_0 is the equilibrium magnetization, $B_1(x, t)$ is the applied magnetic field and M_y is the transverse magnetization. Solutions to equation (36) have been discussed by applying a number of analytical methods^[26], and for the present purpose it is sufficient to design the NMR system in such a way that the transverse magnetization M_y , takes the form of a plane wave.

MATHEMATICAL CONCEPT OF ROTATIONAL DIFFUSION MRI AND MOLECULAR DYNAMICS OF BIOLOGICAL FLUIDS

The random re-orientation of molecules (or larger systems) is an important process for many biophysical probes. By the equipartition theorem, larger molecules re-orient more slowly than do smaller objects and, hence, measurements of the rotational diffusion constants can give insight into the overall mass and its distribution within an object. In this study, the mathematical concept of rotational diffusion MRI and molecular dynamics of biological fluids is presented. This approach ensures the analytical solution of the Bloch NMR flow equation, which enables us to obtain the NMR transverse magnetization in terms of spherical harmonic functions and NMR relaxation parameters for measuring rotational diffusion at the molecular level.

Theoretical and experimental studies to determine rotational diffusion coefficients using Fluorescence Correlation Spectroscopy, fluorescence anisotropy, flow birefringence, dielectric spectroscopy, NMR relaxation and other biophysical methods that are sensitive to picosecond or slower rotational processes have been published earlier studies^[1-12].

In this study, we have presented a new method based on the Bloch NMR flow equation to measure rotational diffusion of biological fluids. The approach ensures that analytical solutions to the Bloch NMR flow equation yield the NMR transverse magnetization in terms of spherical harmonic functions and NMR relaxation parameters. The NMR/MRI technique can generate exquisite images of the soft tissue anatomy of the human body; therefore, this method is expected to become an efficient and reliable technique for measuring rotational diffusion at the molecular level for application in nanomedicine.

We consider a tumbling molecule that can be completely described by a rotational diffusion equation where the radius is fixed ($r = R$). It would be very important to derive the diffusion system directly from equations (36). Equations (36) within a spherical cavity is given by

$$\frac{\partial M_y}{\partial t} = D \left[\frac{1}{r^2} \frac{\partial}{\partial r} \left(r^2 \frac{\partial M_y}{\partial r} \right) + \frac{1}{r^2 \sin^2 \theta} \frac{\partial^2 M_y}{\partial \phi^2} + \frac{1}{r^2 \sin \theta} \frac{\partial}{\partial \theta} \left(\sin \theta \frac{\partial M_y}{\partial \theta} \right) \right] \quad (38)$$

A tumbling molecule exhibits rotational diffusion that describes the tumbling motion of the molecules. In this case, the radius is fixed ($r = R$) and equation (38) becomes the rotational diffusion equation (the radial differential terms disappear):

$$\frac{\partial M_y}{\partial t} = D_r \left[\frac{1}{\sin^2 \theta} \frac{\partial^2 M_y}{\partial \phi^2} + \frac{1}{\sin \theta} \frac{\partial}{\partial \theta} \left(\sin \theta \frac{\partial M_y}{\partial \theta} \right) \right] \quad (38)$$

where $D_r = D/R^2$ is the rotational diffusion coefficient and R is the fixed radius of a sphere. The parameter D is called translational diffusion coefficient. The NMR transverse magnetization M_y of the diffusing molecule which is making a tumbling motion is the general solution of equation (39) obtained by the method of separation of variables:

$$M_y(\phi, \theta, t) = A e^{-D_r l(l+1)t} Y_l^m(\phi, \theta) \quad (40)$$

Equation (40) can be related to the correlation time constant τ :

$$1/\tau_l = D/R^2 l(l+1) = D_r l(l+1) \quad (41)$$

Equation (40) becomes:

$$M_y(\phi, \theta, t) = A e^{-t/\tau_l} Y_l^m(\phi, \theta) \quad (42)$$

MOLECULAR HYDRODYNAMICS IN NMR OF PROTEINS

If we sum over all possible values of m and l , equation (42) gives

$$M_y(\phi, \theta, t) = \sum_{l,m} A e^{-t/\tau_l} Y_l^m(\phi, \theta) \quad (43)$$

The rotational correlation time τ_l , is the characteristic time constant associated with the Brownian rotation diffusion of a particle in a solution. This is the time it takes the particle to rotate by one radian and it is a function of the particle size. For globular proteins, a spherical approximation can be used and the rotational correlation time is given by equation (44)^[21]

$$\tau_l = 4\pi \eta R^3 / (3kT) \quad (44)$$

where η is the viscosity of the solvent, R is the effective hydrodynamic radius of the protein molecule, k is the Boltzmann constant and T is the temperature. From the molecular weight (MW) of the protein (M), the hydrodynamic radius can be calculated as follows:

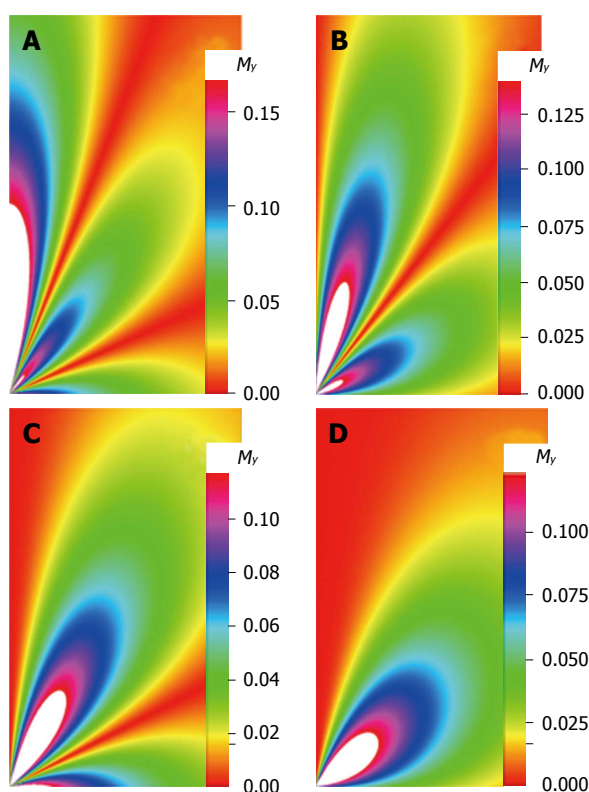
$$R = [3M/(4\pi \rho N_a)]^{1/3} + R_w \quad (45)$$

where ρ is the average density for proteins (1.37 g/cm^3), N_a is the Avogadro's number and R_w is the hydration ra-

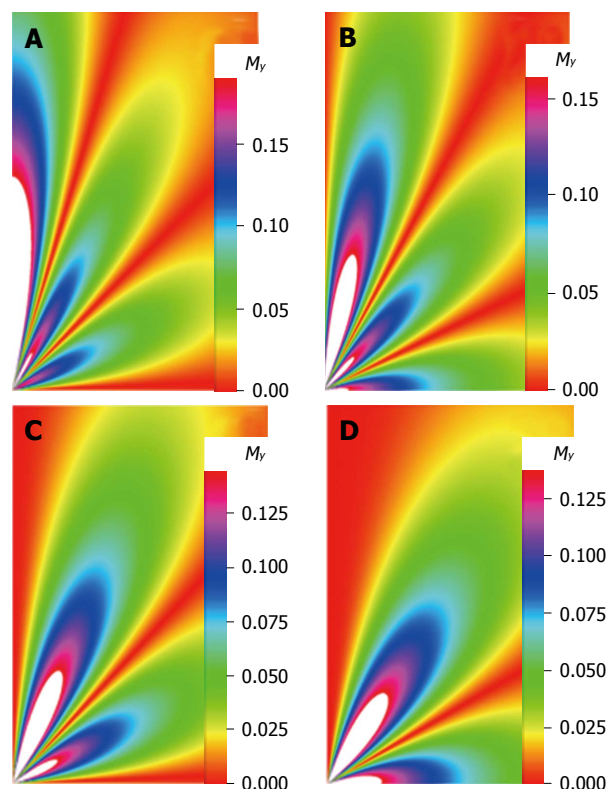
Table 3 Nuclear magnetic resonance determined rotational correlation time values for known monomeric NESG targets^[19]

NESG target (isotope labeling)	MW (kDa)	¹⁵ N T ₁ (ms)	¹⁵ N T ₂ (ms)	<i>I</i> = T ₁ /T ₂	τ _{<i>l</i>} (ns)
PsR76A (NC5)	7.2	478	128	3.734375	5.1
VfR117 (NC)	11.2	605	119	5.084034	6.3
SyR11 (NC5)	12.4	630	104	6.057692	7.1
ER541-37-162 (NC5)	15.8	729	66.5	10.96241	10.0
ER540 (NC5)	18.8	909	66.5	13.66917	11.3
SoR190 (NC)	13.8	697.5	100.9	6.912785	7.7
TR80 (NC5)	10.5	612.8	102.9	5.955296	7.0
Ubiquitin (NC)	9	441.8	144.6	3.055325	4.4
HR2873B (NC)	10.7	492	115	4.278261	5.7
B-domain (NC)	7.2	423.5	153.3	2.762557	4.05
BcR97A (NC)	13.1	705.8	80.6	8.756824	8.8
PfR193A (NC)	13.6	733.9	80.9	9.071693	9.0
MvR76 (NC)	20.2	1015	64.5	15.73643	12.2
DvR115G (NC)	10.9	608.7	115.6	5.265571	6.5
MrR110B (NC5)	11.8	707	99.2	7.127016	7.8
VpR247 (NC5)	12.5	661.2	88.3	7.488109	8.05
BcR147A (NC)	11.9	645	104	6.201923	7.2
WR73 (NC5)	21.9	1261	41.3	30.53269	13.0
NsR431C (NC5)	16.8	855.5	71.2	12.01545	10.6
StR82 (NC)	9.2	537.3	100.4	5.351594	6.6

MW: Molecular weight.


Figure 4 Image from the transverse magnetization as it varies with time, *t* = 3 ns, and the relaxation parameters τ_{*l*} = 5.1 ns, *I* = 3.734375 for (A) *m* = 0; (B) *m* = 1; (C) *m* = 2; (D) *m* = 3.

dus (1.6Å to 3.2Å). For rigid protein molecules, in the limit of slow molecular motion (τ_{*l*} >> 0.5 ns) and high magnetic field (500 MHz or greater), a closed-form solution for τ_{*l*} as a function of the ratio of the longitudinal (T₁) and transverse (T₂) ¹⁵N relaxation times is


Figure 5 Image from the transverse magnetization as it varies with time, *t* = 3 ns, and the relaxation parameters τ_{*l*} = 6.3 ns, *I* = 5.084034 for (A) *m* = 0; (B) *m* = 1; (C) *m* = 2; (D) *m* = 3.

$$\tau_l = 1 / (4\pi \omega_N) (6T_1/T_2 - 7)^{1/2} \quad (46a)$$

where ω_N is the ¹⁵N resonance frequency (Hz). Average ¹⁵N T₁ and T₂ relaxation times for a given protein can be measured using 1D ¹⁵N-edited relaxation experiments. To minimize contributions from unfolded segments, each 1D spectrum is integrated over the downfield backbone amide ¹H region (typically 10.5 to 8.5 ppm) and the results are used to fit an exponential decay as a function of delay time. One then computes the correlation time and compares it to a standard curve of τ_{*l*} vs protein MW obtained at the same temperature on a series of known monomeric proteins of varying size. The T₁/T₂ method is suitable for proteins with MW of up to MW ≈ 25 kDa. Accurate measurement of the diminishing ¹⁵N T₂ becomes difficult for larger proteins and cross-correlated relaxation rates are measured instead^[21].

The parameter *I* is a dimensionless constant; therefore, it may be appropriate in this study to define *I* as

$$I = T_1/T_2 \quad (46b)$$

Values of rotational correlated time for some monomeric NESG (North East Structural Genomics Consortium) targets are shown in Table 1.

The density images below are obtained for the first three isotopes of Table 3, for M₀ = 1, *m* = 0, 1, 2, 3, and a time of 3 ns. The plots shown in Figures 4-7 are made with the assumption that the spins move across rigid spheres whose radii (= R) are in the range {0, 8^{1/2}}. Figures 4-7 give the density mapping of the transverse magnetization for specific correlation times (*i.e.*, for selected

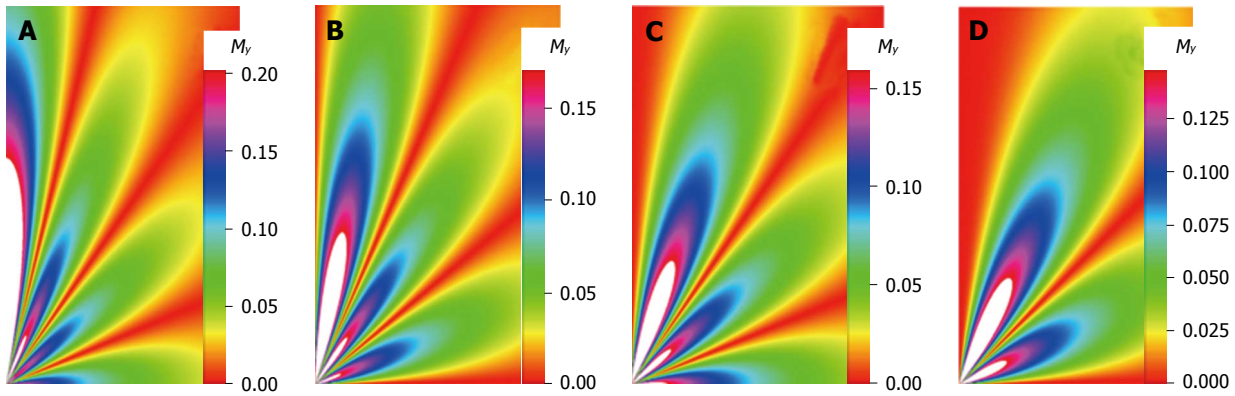


Figure 6 Image from the transverse magnetization as it varies with time, $t = 3$ ns, and the relaxation parameters $\tau_r = 7.1$ ns, $l = 6.057692$ for (A) $m = 0$; (B) $m = 1$; (C) $m = 2$; (D) $m = 3$.

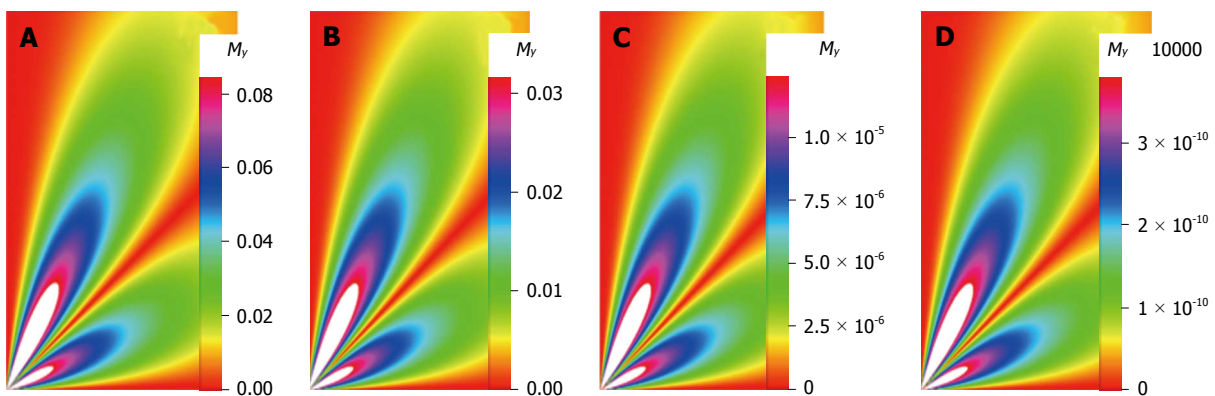


Figure 7 Image from the transverse magnetization as it varies with $m = 3$, and the relaxation parameters $\tau_r = 7.1$ ns, $l = 6.057692$ for (A) $t = 5$ ns; (B) $t = 10$ ns; (C) $t = 50$ ns; (D) $t = 150$ ns.

NESG targets) and NMR relaxation parameters.

ROTATIONAL FRICTIONAL COEFFICIENT AND MOLECULAR NMR

When a particle moves in a fluid, either under the influence of an applied force or torque, or due to Brownian motion, it experiences frictional resistance. The proportionality between particle velocity and frictional resistance is the frictional coefficient.

It may be significant to note that the rotational diffusion coefficient D_r can be defined from equation (39) as

$$D_r = D/R^2 = k_B T / (R^2 f_r) \quad (47)$$

where k_B is the Boltzmann's constant, f_r is the rotational frictional coefficient, R is the hydrodynamic radius of the molecule being observed and T is the absolute temperature. Equation (47) becomes discretized when the time constant is introduced:

$$1/\tau_l = k_B T / (R^2 f_r) l(l+1) \quad (48)$$

$$f_r = k_B T \tau_l / R^2 l(l+1) \quad (49)$$

Therefore, for the NESG target PsR76A (NC5)^[21], the rotational friction coefficient can easily be calculated:

$$f_r = 90.16765 \times 10^{-9} k_B T / R^2$$

It may be very important to note from equations (35,

39) that

$$D = -v^2 / T_0 = D_r R^2 \quad (50a)$$

And

$$D_r = -v^2 / (T_0 R^2) = -\omega^2 / T_0 \quad (50b)$$

where

$$\omega = v/R$$

is the angular velocity. Hence, we have:

$$f_r = k_B T T_0 / v^2 \quad (50c)$$

The angular drift velocity can be defined as

$$\Omega_d = d\omega / dT_0 = F_\omega / f_r \quad (51)$$

Equation (50b) defines the angular deviation in terms of the T_1 and T_2 relaxation parameters for rotational diffusion about a single axis

$$\omega^2 = D_r T_0 \quad (52)$$

Equation (52) describes the response of the angular drift velocity to an external torque F_ω assuming that the flow stays non-turbulent and that inertial effects can be neglected.

RELAXATION STUDIES OF DIATOMIC MOLECULES IN ROTATIONAL DIFFUSION

Rotational diffusion is a process by which the equilib-

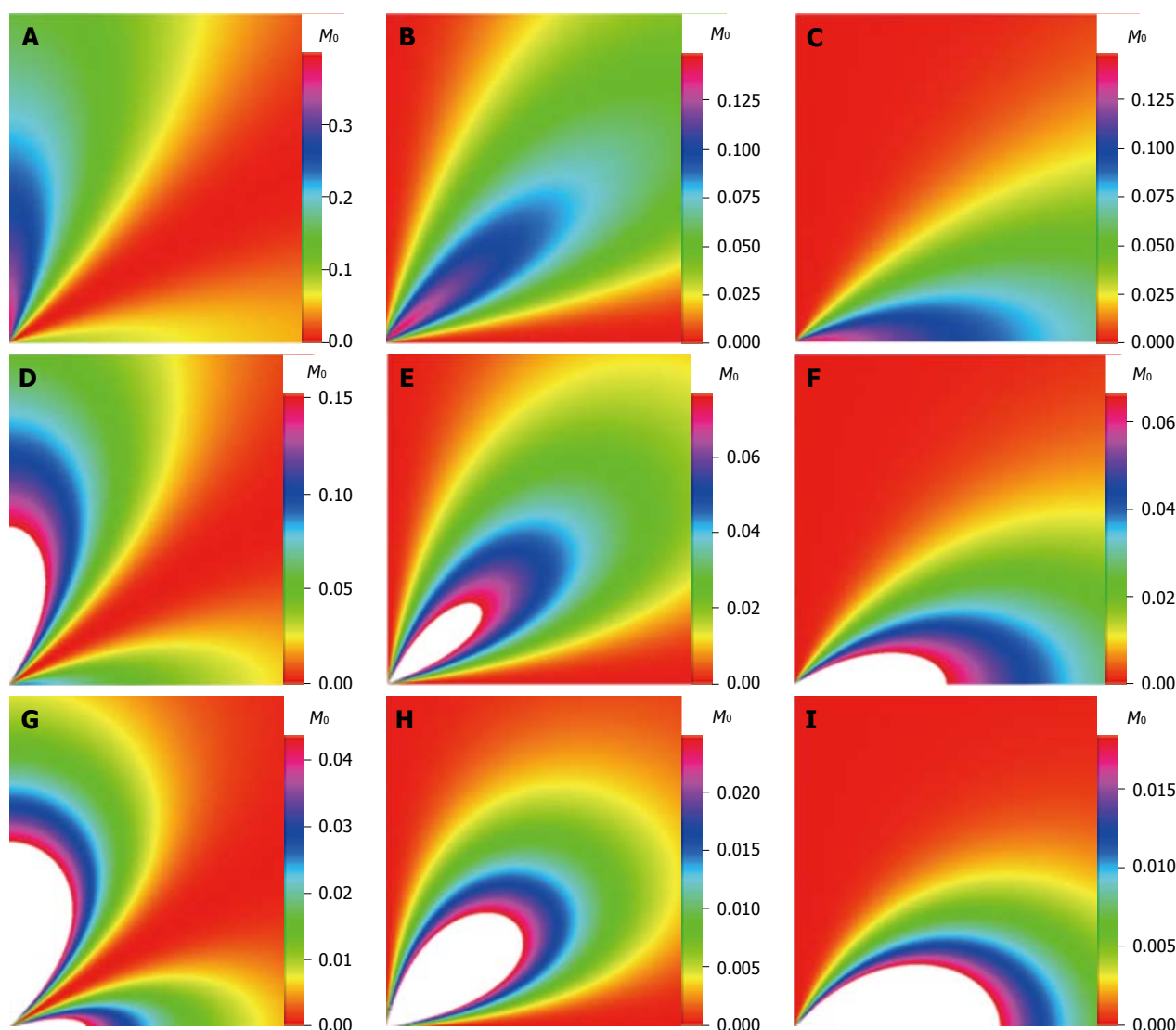


Figure 8 Density maps of M_0 using Equation (8) for $l=2$ and (A) $m=0, 0 \leq R \leq 2^{1/2}$; (B) $m=1, 0 \leq R \leq 2^{1/2}$; (C) $m=2, 0 \leq R \leq 2^{1/2}$; (D) $m=0, 0 \leq R \leq 8^{1/2}$; (E) $m=1, 0 \leq R \leq 8^{1/2}$; (F) $m=2, 0 \leq R \leq 8^{1/2}$; (G) $m=0, 0 \leq R \leq 32^{1/2}$; (H) $m=1, 0 \leq R \leq 32^{1/2}$; (I) $m=2, 0 \leq R \leq 32^{1/2}$.

rium statistical distribution of the overall orientation of molecules is maintained or restored. The random re-orientation of molecules is an important process for many biophysical probes. The rotational diffusion of molecules in the presence of static magnetic and RF fields can be described by the NMR diffusion equation. The NMR diffusion equation within a spherical cavity has been described in equation (42).

The radial parameter R is constant; therefore, we may assume that $\mathcal{A} = M_0 e^{-R}$. If we sum over all m and l , we have:

$$M_y(\phi, \theta, t) = \sum_{l,m} M_0 e^{-R_{lm}} e^{-t/\tau_l} Y_l^m(\phi, \theta) \quad (53)$$

If at $t=0$, $(\phi, \theta) = (\phi_0, \theta_0)$, we write:

$$M_y(\phi, \theta, 0) = \sum_{l,m} M_0 e^{-R_{lm}} Y_l^m(\phi, \theta) = \delta[(\phi, \theta) - (\phi_0, \theta_0)] \quad (54)$$

Then, the delta function may be expanded such that:

$$\begin{aligned} \delta[(\phi, \theta) - (\phi_0, \theta_0)] &= \sum_{l,m} Y_l^{m*}(\phi_0, \theta_0) Y_l^m(\phi, \theta); \\ M_0 e^{-R_{lm}} &= Y_l^{m*}(\phi_0, \theta_0) \end{aligned} \quad (55)$$

$$M_y(\phi, \theta, t) = \sum_{l,m} Y_l^{m*}(\phi_0, \theta_0) Y_l^m(\phi, \theta) e^{-t/\tau_l} \quad (56)$$

For this system, the autocorrelation function may be given as:

$$G(t) = 12\pi/20 [\mu_0/(4\pi)]^2 \eta^2 \gamma^4 / r^6 [Y_2^{m*}(\phi, \theta) Y_2^m(\phi, \theta) e^{-t/\tau_l}] \quad (57)$$

The angle bracket is the average over the transverse magnetization of the rotating molecules. This average is given as:

$$\begin{aligned} 1/4 \int d(\phi, \theta) \int d(\phi_0, \theta_0) \sum_{l,m} Y_l^{m*}(\phi_0, \theta_0) Y_l^m(\phi, \theta) \\ Y_2^{m*}(\phi_0, \theta_0) Y_2^m(\phi, \theta) e^{-t/\tau_l} \end{aligned} \quad (58)$$

If we perform the integral, we obtain^[27-31]:

$$G(t) = K/3 e^{-t/\tau_l} \quad (59)$$

where $\tau_l = R^2/(6D) = 1/(6D)$, and $K = 9/20 [\mu_0/(4\pi)]^2 \eta^2 \gamma^4 / r^6$ is the second moment of interaction and r is the separation between two nuclear spins. The spectral density function is the Fourier transformation^[27-31] of equation (53):

$$J(\omega) = 2/3 [K\tau_l/(1 + \omega^2\tau_l^2)] \quad (60)$$

$$\frac{1}{T_1} = K\tau_l \left(\frac{2/3}{1 + \omega^2\tau_l^2} + \frac{8/3}{1 + 4\omega^2\tau_l^2} \right)$$

$$\frac{1}{T_2} = K\tau_l \left(1 + \frac{5/3}{1 + \omega^2\tau_l^2} + \frac{2/3}{1 + 4\omega^2\tau_l^2} \right) \quad (61)$$

MAPPING OF EQUILIBRIUM MAGNETIZATION

From equation (55), we can map M_0 as a function of the radius of the rigid rotator R (which is also dependent on θ_0 and ϕ_0). At the point when RF B_1 field is just removed, M_0 starts building up from its lowest value. For multi-voxel imaging, R may be changing with different tissue conditions. This may have very important influence on the changes in M_0 . Figure 8 show the changes in M_0 with assumed ranges for R .

CONCLUSION

We have presented the basic principle of NMR/MRI in a way that can be easily understood and that may fascinate researchers into the field of NMR/MRI. After a very brief history of the subject, a second order non-homogeneous, time dependent differential equation derived from the Bloch NMR equation was presented. Note that equation (30) uniquely assembles all the NMR, MRI, MRA and magnetic resonance spectroscopy parameters in an exciting way ready to be explored. The NMR signals as represented by equations (40-42) and Figures 4-7 are greatly influenced by the T_1 and T_2 relation times and the NMR parameter m . As l increases the motion gets faster and as m is increased, the particle's motion moves closer to orbiting the equator. This can greatly motivate further research into the use of rotational motion of nanoparticles to perform medical procedures inside the human body, noninvasively. Equations (40-42) are also the solutions for a rigidly rotating diatomic molecule. They are the angular parts of the hydrogen atom wave functions. These functions are important in many theoretical and practical applications, particularly in the computation of atomic orbital electron configurations, representation of gravitational fields, geoids, and the magnetic fields of planetary bodies and stars, and characterization of the cosmic microwave background radiation. In 3D computer graphics, spherical harmonics play a special role in a wide variety of topics including indirect lighting (ambient occlusion, global illumination, pre computed radiance transfer, *etc.*) and recognition of 3D shapes. The concept presented in this study can also be used to analyze the Earth's magnetic resonance. Application of this concept to nanomedicine will be the focus of our next investigation. Towards this goal, we derived the standard parameters of NMR relaxometry of diatomic molecules directly from the NMR diffusion equation. The advantage of this is that we are able to obtain the autocorrelation function and the spectral density function without the use of the

rigorous method of probability distribution function.

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Translational medical mycology guides clinical and laboratory practice on fungal diseases

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Abstract

Patients with fungal infection having skin lesions may consult a dermatologist, which is a diagnostic and therapeutic challenge. Dermatologists take samples from the lesion to check the fungal elements under a microscope by KOH preparation and then treat the patient. This model has advanced from bedside to bench and from bench to bedside (B to B to B), which is defined as Translational Medical Mycology. Dermatologists have an advantageous position in finding, isolating and identifying the pathogenic fungi and treating the patient with antifungal drugs. Samples should be cultured in different media with or without chloramphenicol and cycloheximide and incubated at room temperature or 37 °C. Non-culture techniques such as polymerase chain reaction based molecular identification, transmission electron microscopy, scanning electron microscopy, biochemistry tests and histopathology are also necessary to confirm the identification of the species, especially when the routine culture is negative. We start treatment upon obtaining evidence of fungal infection,

i.e., positive KOH examination. Antifungal drugs such as itraconazole, fluconazole, terbinafine and amphotericin B can be used alone or in combination based on the fungal species and the location of the lesion. Practice on fungal infection includes screening of the patient, merging all of the laboratory techniques and methods from the microbiologists, pathologists, molecular researchers, identification of the pathogen and determination of the optimum antifungal drug.

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Key words: Translational; Mycology; Bedside; Bench; Fungal infections

Core tip: "Translational medical mycology" has transformed vastly in recent years, which is aimed to solve clinical problems. This transformation is a dynamic, multi-level, multi-directional and continuously improving process. There are different processes in translational medicine, with the main objective being translation journey from bench to bedside to the community. We can solve a clinical problem by using a number of new technologies with the help of advanced laboratories and professionals, which will eventually promote the overall progress of medical mycology and ultimately provide an access to the effective treatment and prevention of the fungal disease.

Lama J, Ran X, Ran YP. Translational medical mycology guides clinical and laboratory practice on fungal diseases. *World J Transl Med* 2014; 3(1): 31-36 Available from: URL: <http://www.wjgnet.com/2220-6132/full/v3/i1/31.htm> DOI: <http://dx.doi.org/10.5528/wjtm.v3.i1.31>

INTRODUCTION

As modern science continuously spawns even more dra-

matic discoveries about human health, more research with the help of new technology and advanced laboratories is increasingly encouraged to find the practical application that can improve human lives. The problems encountered in clinical situation undergo laboratory studies through the problem-solving process (such as finding etiology and pathogenesis to find a key factor against the development of the cause or drugs) and then return to clinical guided treatment, and this process is summarized as from the bedside to the laboratory and vice-versa (Bench to Bedside and Bedside to Bench, *i.e.*, B to B to B, defined as Translational Medicine). Furthermore there are different processes in translational medicine, with the main objective being translation journey from bench to bedside to community. As the medicine enters the era of translational medicine, medical mycology as an important part of medicine has become translational medical mycology^[1,2].

Although in translational medical mycology the patient's history and clinical manifestations are important clues to clinical diagnosis, sample collection from lesion sites is a crucial step in order to identify patients with fungal infection specimens (scales, pus, sputum, blood, cerebrospinal fluid, *etc.*). Obtaining high quality specimens to meet the laboratory requirements for etiological diagnosis is critical, including professional training in mycology, biologically secure laboratory conditions, preparation of different media, culture incubator (24 °C-26 °C and 37 °C), and most importantly avoidance of contamination during the procedure. Microscopic computer image acquisition and processing system is the basic premise of fungal microscopic examination, specimens are processed (KOH preparation) to observe fungi (hyphae/spores, different shapes and size), and for further inquiry there is also molecular identification. It is estimated that there are more than 1.5 million kinds of fungi on the Earth. So far more than 100000 kinds have been described, but only just over 100 kinds are known as common pathogenic fungi, suggesting that there is a great development space for medical mycology.

The rapid developed molecular biology techniques are used for molecular identification of not only fungi isolated in culture but also those from non-culture specimens, like direct DNA extraction using universal fungal primers by polymerase chain reaction (PCR) amplification/sequencing; further pathological examination (Periodic acid-Schiff or Methenamine-silver staining) can be used to identify the fungus and its special structures. Electron microscopy is used to observe the ultra-structure and fungal pathogens for species identification and study of pathogenesis. For translational medical mycology, molecular biology and individualized treatment should include both the host and the fungus. To perform host susceptibility analysis to the pathogenic species and the virulence factors, molecular biology techniques are required to analyze the host susceptibility genes, environmental and exposure factors. DNA from the fungal specimens (isolated colonies in culture, non-cultured clinical specimens or pathological paraffin block specimens) for molecular am-

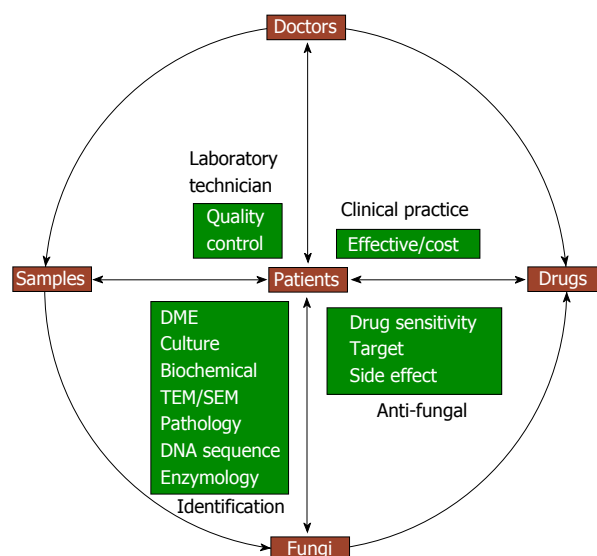


Figure 1 Essential factors for translational medical mycology. DME: Direct microscopic examination; TEM: Transmission electron microscopy; SEM: Scanning electron microscopy.

plification and sequencing of pathogenic fungi is equally important. For identification, common fungal universal primers to amplify the internal transcribed spacer 1/4 region and D1/D2 domain are used, but species-specific primers can also be designed.

Various comprehensive detection techniques are designed to quickly identify pathogenic fungi for administration of antifungal therapy on time. Antifungal drug sensitivity test is a superior choice to select drugs to which the particular strain is highly sensitive, but at the same time, drug interactions, safety and drug prices should be taken into consideration. Each link has a puzzle challenge with a variety of problems and each clinical problem is transformed into medical mycology research topic. The essential factors for translational medical mycology and their relationship are summarized in Figure 1.

With the improvement in patient acceptance and the rate of positive fungal results^[3], we can improve the traditional methods for sample collection. In one patient with Candidosis intertrigo in the groin, specimens were collected using a cotton swab, tape and blunt scraping of scales, respectively, for direct DNA extraction by PCR/sequencing. The results confirmed that the three different methods all identified the pathogenic fungi as *Candida albicans*, and the results were verified by cultured colony identification. The new method for sample collection by using a cotton swab, tape and using blunt scraping of scales for direct DNA extraction by PCR/sequencing does not only solve the problem of sample collection from sensitive parts, but also can be used for early identification of pathologic fungi and treatment accordingly, which in turn saves time^[4]. Direct DNA extraction from the clinical samples (hair or nail) for identification of the pathogenic strains has also been successfully developed to distinguish between tinea capitis^[5] or onychomycosis. In one case, hair samples collected from a 6-year-old girl

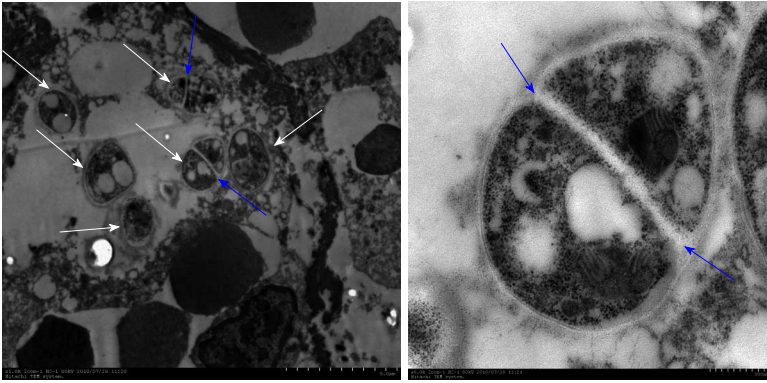


Figure 2 In transmission electron microscopic examination, there are 6 organisms with cell wall (white arrows), of which 2 have septated wall (blue arrows) within a macrophage. This specific structure of *Penicillium marneffei* helped to clarify the pathogen as *Penicillium marneffei*.

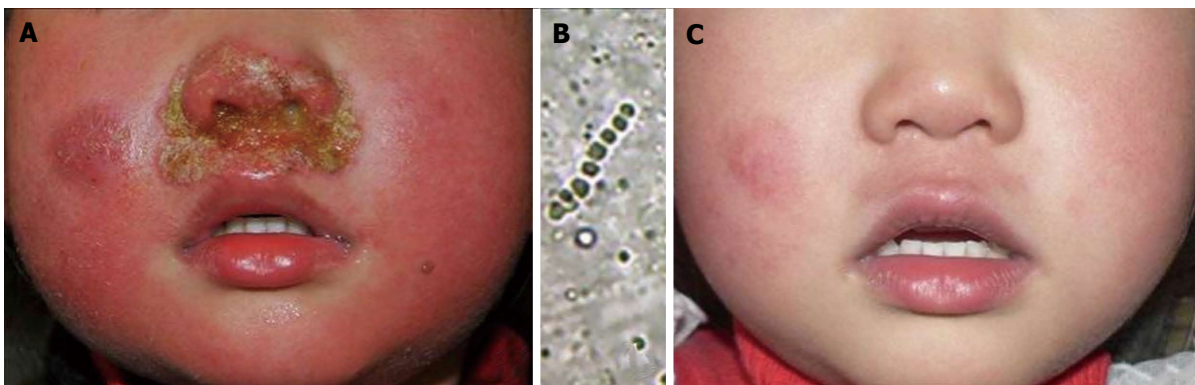


Figure 3 A 3-year-old girl was consulted with impetigo-like lesions around the nostrils. A: Pustules and erythema around nostrils; B: Hyphae and clustered spores in the crust but the culture was negative. The pathogenic agent was identified as *Arthroderma vanbreuseghemii* (a teleomorph of *Trichophyton interdigitale*) using polymerase chain reaction-based sequencing of the crusts; C: The pustules and erythema disappeared after 35 d of antifungal treatment.

who suffered from kerion were divided into two parts for culture dependent and independent methods, respectively. Since the patient was already on terbinafine, the culture grew slowly. Two sequences from the hair and the culture were both identified as *Arthroderma vanbreuseghemii*. Hence, PCR based molecular biological validation of DNA directly from the sample can rapidly identify the pathogenic fungus, especially after the use of antifungal drugs. Pathological examination is important in the field of medical mycology, but it has its own limitations. It is important to verify the results since specific fungal strains cannot be determined by pathological reports. In a patient with oral ulcers, histopathology reported a diagnosis of “Leishmaniasis”, but the review of the pathological section found that “*Leishmania*” is more like *Penicillium marneffei* yeast cells. The oral specimens were negative for fungal culture. To rule out the “Leishmaniasis” and to establish a new diagnosis as “Penicilliosis marneffei”, paraffin-embedded tissue was used to extract DNA using universal primers for PCR, and the obtained sequence was compared with the sequences in database by Blast and found to share a 99% similarity to the *Penicillium marneffei*. In addition, the paraffin-embedded tissue was prepared for transmission electron microscopy observation, which showed the septated wall, the specific structure for *Penicillium marneffei* yeast in tissue (Figure 2). The diagnosis was

confirmed as a case of HIV-negative primary, localized, penicilliosis marneffei by the non-culture method^[6].

The fungal culture result can be influenced by various factors like culture media, incubation conditions, the volume and quality of inoculation, previous history of use of antifungal drugs and the technique of the inoculation, which lead to unsuccessful attempt to isolate the pathogenic fungi. Direct extraction of DNA is a useful method for guiding treatment in these cases where microscopic tests are positive and cultures are negative. We have encountered some cases in which there was no growth in fungal culture but a significant treatment effect was achieved with antifungal agents^[7]. A 3-year-old girl was consulted with impetigo-like lesions around the nostrils. KOH examination showed hyphae and clustered spores in the crust but the culture was negative. The pathogenic agent was identified as *Arthroderma vanbreuseghemii*, a teleomorph of *Trichophyton interdigitale* using PCR-based sequencing of the crusts taken from the lesion. She recovered from the infection after oral and topical antifungal agents (Figure 3).

Regarding the treatment, whenever the direct microscopic examination with KOH is positive, the antifungal treatment should be started immediately without waiting for the fungus to be isolated or the species be identified. As this might take weeks and the patient's

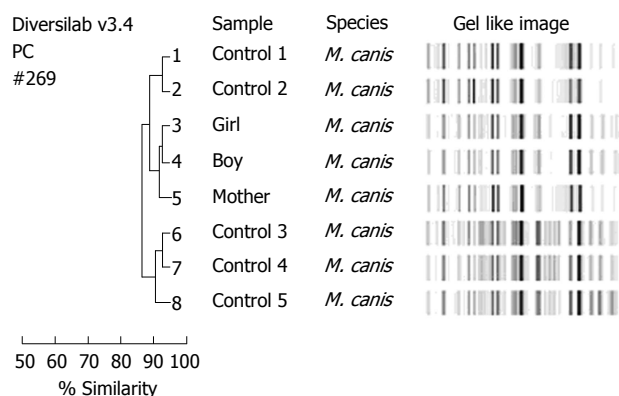


Figure 4 Molecular typing of eight *Microsporium canis* isolates showed distinct and similar fingerprint patterns visualized by the gel-like image and as indicated by a > 90% similarity coefficient in the dendrogram. The three isolates from patients of a same family (number 3, 4, 5) were grouped together with a $\geq 98\%$ similarity compared with the control isolates of *M. canis*. *M. canis*: *Microsporium canis*.

condition might deteriorate. More importantly, sample collection from the lesions for culture and pathology should be conducted just before starting the antifungal agents. As the treatment progresses, a fungal culture (the conventional method and subsequent identification and susceptibility testing) and direct extraction of DNA for molecular identification should be performed in addition to the weekly follow-up. Samples should be collected and examined until the culture becomes negative before stopping the antifungal treatment^[8].

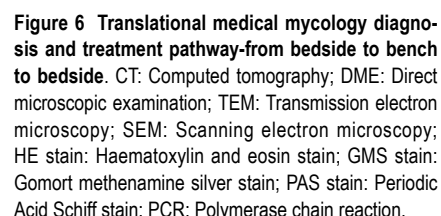
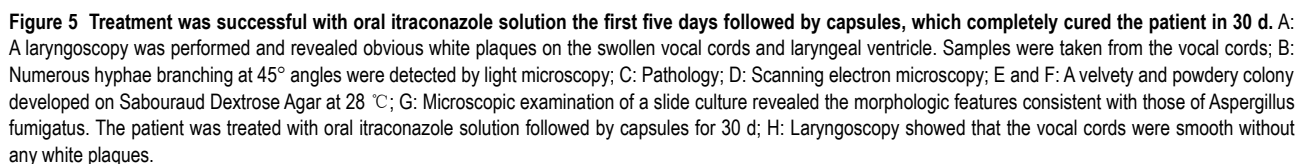
Antifungal drugs are the key factor in the treatment of fungal infection. Commonly used topical antifungal drugs consist of allylamines (such as terbinafine, naftifine, butenafine), imidazoles (such as ketoconazole and bifonazole) or a mixture of the two (naftifine with ketoconazole), and some are even mixed with steroids (triamcinolone acetonide with econazole or miconazole nitrate). Topical drugs are made by mixing various concentrations of antifungal agents with matrices composed of different vehicles and formula. The antifungal spectrum and activity of this mixture (final product) are determined by applying a fixed volume directly to the pathogenic fungus, and then observing and comparing the size of the inhibition zone around the well containing the tested cream. This modified agar diffusion method is a practical agar-based method, which enables determination of the activity of various antifungal drugs against an array of fungal genera and species. It is useful to assess antifungal activity and spectrum against fungal skin infection and to determine the *in vitro* spectrum and activity of different topical antifungal creams by studying their direct inhibition activity against clinical isolates. We can select the product with the best effect/cost potency ratio from the commercial antifungal creams based on the comparison of the inhibition zone in the same condition to the same species of pathogenic fungus^[9,10].

Sometimes in clinical practice we might encounter multiple mixed fungal infections, which will require different media. The samples should be incubated at differ-

ent temperatures to distinguish them and we must not jump into a premature conclusion that there is a “contaminated fungus”. Generally, the fungus which invades the skin during trauma at the initial stage is considered contaminated. When the local condition becomes suitable for its growth, this “contaminated fungus” could become as the pathogenic fungus (opportunistic fungal infection). This idea leads us to find out the uncommon pathogen and the cure to the difficult cases^[11,12].

It is important to use techniques of molecular biology and electron microscopy to identify fungi from all the lesions, particularly in cases of rare fungi, where there is not much of a morphological characteristic. In one case, several samples were collected from patient’s face, neck, back, buttocks, foot as well as toenail lesions and all were isolated as *Trichophyton rubrum*. By using *Trichophyton rubrum* specific random amplified polymorphic DNA (RAPD) and tandem repeat subunit Trs-1/Trs-2 PCR product analysis, we found that the patient was infected with six different strains at various sites of the infection, proving that various strains did not occur by autoinoculation^[13]. RAPD and Trs-1/Trs-2 analysis of 8 family members showed that although *Trichophyton rubrum* can infect one member of the family to another (2 families), but more cases showed that the infections are beyond the families^[14]. The members from one family had kerion (son) and tinea corporis (father and mother), and *Arthroderma vanbreuseghemii* was isolated from their lesions. By using the morphology, rapid urease test, hair perforation experiment, random primers polymorphism and zymogram analysis, it was proved that the pathogen was the same and it was transmitted from the neighbor’s rabbit to the son and later to his parents^[15]. In another case, two children (tinea capitis) and mother (tinea corporis) were diagnosed based on the positive KOH examination. Morphological characteristics and sequencing of the internal transcribed spacers 1 and 2 amplified from primary culture isolates confirmed that their infections were caused by the zoophilic *Microsporium canis*. Repetitive sequence-based molecular typing using the DiversiLab system, secreted enzymatic activity analysis and antifungal susceptibility indicated that these isolates might share the same source (Figure 4)^[16]. Therefore, molecular identification can give us clues about the source of infection whether the infection is caused by autoinoculation, by some external sources or by close contact within the family members.

In recent years we have seen several cases of common fungi causing debilitating rare diseases, which give us a new thought about how people with normal immune system can get infected with common pathogens. In one case, a boy had scalp laceration from a road accident, and the treatment included debridement and scalp transplantation in orthopedic surgery. After the treatment, the scalp had honeycomb nodules and abscesses. Culture, morphology and molecular identification showed that it was *Microsporium gypseum* (*M. gypseum*) infection. *M. gypseum* is a geophilic fungus commonly found in soil, and it may have lurked in the scalp when the wound came in contact



that there were plaques on the vocal cord. By using microscopic examination, culture and molecular identification, the results showed *Aspergillus fumigatus* (*A. fumigatus*) and later she was cured with itraconazole^[19]. In another a woman who had hoarseness because of a lump on her vocal cord, examination of tissues extracted for scanning electron microscopy revealed that they were destroyed by the hyphae of *A. fumigatus*. In addition, we also discovered several kinds of exocrine protease activities in the specimen^[20]. The third female patient with a similar pathogen had severe hoarseness and a medical history of oral sex. The pathogen was identified by morphology and molecular identification. Treatment was successful by oral itraconazole solution for the first five days and then it was followed by capsules, which completely cured the patient in 30 d (Figure 5). This case gives us a new thought about how people with normal immune system can be infected with common airborne pathogenic *A. fumigatus*.

The vocal mucous membrane barrier which was damaged by oral sex made it easy for the colonization of the spore which later invades the tissue^[21].

Over the past one century medical mycology has had a typical “transformation” characteristic: we used to take samples from the lesion of a patient to check the fungal elements under the microscope to make the diagnosis and then treat the patient. Translational Medical Mycology is not just an empty theory and slogan, it should be in the classic “transformation” based on constantly enhanced (electron microscopy, *etc.*) and enriched contents (molecular biology, *etc.*) and individual medicine. In summary, in “translational medicine mycology” the starting point and end point are the clinical and laboratory studies, which are aimed to solve clinical problems (Figure 6). Patient is the “center” and problems that are encountered during the diagnosis and treatment are transforming medical mycology. For specific diseases, we might need to integrate microbiologists, pathologists, molecular biologists and other laboratory experts with all techniques and methods to determine the pathogenic fungi, help with susceptibility testing, remote consultation, so that we can start the treatment as soon as possible to save patient lives. Transformation is a dynamic, multi-level, multi-directional and continuously improving process. We can solve a clinical problem by using a number of new technologies, new methods and training, and then there will be an improvement in the treatment of fungal diseases. It will eventually promote the overall progress of medical mycology and ultimately provide an access to the effective treatment of the disease as well as prevention.

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WJTM publishes articles that report the results of translational medicine-related applied and basic research in fields such as immunology, physiopathology, cell biology, pharmacology, medical genetics, and pharmacology of Chinese herbs. The current columns of WJTM include editorial, frontier, diagnostic advances, therapeutics advances, field of vision, mini-reviews, review, topic highlight, medical ethics, original articles, case report, clinical case conference (Clinicopathological conference), and autobiography. Priority publication will be given to articles concerning diagnosis and treatment of translational medicine diseases. The following aspects are covered: Clinical diagnosis, laboratory diagnosis, differential diagnosis, imaging tests, pathological diagnosis, molecular biological diagnosis, immunological diagnosis, genetic diagnosis, functional diagnostics, and physical diagnosis; and comprehensive therapy, drug therapy, surgical therapy, interventional treatment, minimally invasive therapy, and robot-assisted therapy.

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- 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

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- 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

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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 *v* (in Greek), sample number as *n* (in italics), and probability as *P* (in italics).

Units

Use SI units. For example: body mass, *m* (B) = 78 kg; blood pressure, *p* (B) = 16.2/12.3 kPa; incubation time, *t* (incubation) = 96 h; blood glucose concentration, *c* (glucose) 6.4 ± 2.1 mmol/L; blood CEA mass concentration, *p* (CEA) = 8.6 24.5 μ g/L; CO₂ volume fraction, 50 mL/L CO₂, not 5% CO₂; likewise for 40 g/L formaldehyde, not 10% formalin; and mass fraction, 8 ng/g, *etc.* Arabic numerals such as 23, 243, 641 should be read 23 243 641.

The format for how to accurately write common units and quantum numbers can be found at: http://www.wjnet.com/2220-6132/g_info_20100725073806.htm.

Abbreviations

Standard abbreviations should be defined in the abstract and on first mention in the text. In general, terms should not be abbreviated unless they are used repeatedly and the abbreviation is helpful to the reader. Permissible abbreviations are listed in Units, Symbols and Abbreviations: A Guide for Biological and Medical Editors and Authors (Ed. Baron DN, 1988) published by The Royal Society of Medicine, London. Certain commonly used abbreviations, such as DNA, RNA, HIV, LD50, PCR, HBV, ECG, WBC, RBC, CT, ESR, CSF, IgG, ELISA, PBS, ATP, EDTA, mAb, can be used directly without further explanation.

Italics

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

Genotypes: *gyrA*, *arg 1*, *c myc*, *c fos*, *etc.*

Restriction enzymes: *EcoRI*, *HindI*, *BamHI*, *Kho I*, *Kpn I*, *etc.*

Biology: *H. pylori*, *E. coli*, *etc.*

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