Turmeric (Curcuma longa), is a perennial herb and belongs to the family Zingiberaceae (ginger) family. The plant of this species is cultivated extensively in Asian countries. An important constituent of turmeric has shown its ability to inhibit carcinogenesis at three different stages: tumor promotion, angiogenesis, and tumor growth (Louay, 2014).

Turmeric, as a dried powder of the rhizome of Curcuma longa, has been used for centuries in different parts of the world. It possesses numerous biological activities such as antioxidant, anti-inflammatory, anticancer, antigrowth, antiarthritic, antiatherosclerotic, antidepressant, anti-aging, antidiabetic, antimicrobial, wound healing, and memory-enhancing activities. One of the most important component turmeric is curcumin, which has been characterised and used extensively since the past decade (Aggarwal et al., 2013).

Hossain and Ishimine (2005) cultivated in pot containing dark red soil (pH 5.2), grey soil (pH 7.4), and red soil (pH 4.4) at Okinawa Japan and growth, yield and quality of turmeric was evaluated. Similarly its growth has also been tested in different soils. The soils were collected from the 50 cm deep layer of the fields and for cultivation not any chemical or biofertilisers were used. Turmeric was cultivated in dark red soil and it had attained the highest plant height, root biomass, and shoot biomass as compared to other soil types. Turmeric on dark red soil had the highest yield with deep yellow colour and had high curcumin content (0.20%). The yield and content of turmeric depend on soil characteristics. Rhizomes of turmeric had high content of Ca, Mg, and K when it was cultivated in grey soil, whereas Fe was the highest in amount cultivated in dark red soil. To gain high yield and high content of curcumin, dark red was found suitable for cultivation of turmeric.

Besides above, a field experiment was conducted at Mattuvarayapuram (Coimbatore District, Tamil Nadu) to evaluate the effect of lignite humic acid (HA) on growth and yield of turmeric (Curcuma longa) in analfisol. The study revealed that application of 100% NPK 050:60:108 kg ha\(^{-1}\) with HA applied to
soil (00 kg ha⁻¹) and foliar spray (HA 0.1%) + rhizome dipping (HA 0.1%) have significantly enhanced the growth and yield attributes (Baskar and Sankaran, 2005).

The field experiment was carried out to evaluate the performance of 11 new released varieties on the basis of planting date sunder mild-tropical climatic conditions at ICAR-RC-NEH Region, at Mizoram Centre, Kolasib, Mizoram. The planting of turmeric showed better plant growth, higher fresh and dried rhizome yield, and greater curcumin content in the last week of April in Mizorum. Shifting date or delaying in planting significantly affects on the yield as well as quality of rhizomes (Singh et al., 2013).

Similarly at three consecutive years (1991-93) with four varieties of turmeric viz., Suvarna, Suguna, Sudarshana and Alleppey were grown after application of different levels of NPK fertilizers and two levels of micronutrients, under rain fed conditions. The variety Alleppey followed by Sudarshana and Suguna were superior with regard to yield of rhizome, curcumin recovery and economics. Due to application of NPK at 60, 50, 120 kg/ha with micronutrient showed optimum yield for the varieties Suvarna, Suguna and Alleppey, whereas less amount of NPK 50, 40, 100 kg/ha with micronutrients showed optimum growth and yield Sudarshana (Sadanandan and Hamaza, 1996).

Overall, application of 270:135:180 kg N:P2O5:K2O per ha has recorded higher growth attributes over other levels. Influence of different irrigation methods, varieties selection and fertilizer levels have been considered as important factor for turmeric weight of mother, primary, secondary and tertiary rhizome per plant and yield (Satyareddi and Angadi, 2014).

Besides the application of fertilisers, different levels of S and Mg micronutrients showed significant enhance in the weight of the mother rhizome at 44 kg/ha of S and 22 kg/ha of Mg respectively. Results show that use of micronutrients like S and Mg with the fertilization schedule dramatically improved in the fresh yield (Bose et al., 2008).

Similarly like other elements, both zinc and boron have exerted significant effect on the growth and yield rhizome of turmeric either in single mode or in combination. Boron at rate of 3.0 kg/ha and Zn 4.5 kg/ha along with blanket
A dose of \( N_{130}P_{35}K_{80}\) kg/ha and CD5 t/ha was found to be suitable for maximum yield of turmeric in South-Eastern Brawn Hill Soils of Chittagong Hill Tracts region comparison to the region (Halder et al., 2007).

The production of curcumin as a constituent, contents in turmeric depends on geographical locations. Due to this reason, peoples of different regions are either unable to screen the good quality of turmeric or inequality to receive curcumin by body for medicinal uses.

It is established fact that turmeric producing important metabolites curcumin is an important anticancer agent and has important role in controlling the cancerous activities. In this regard finding of \( H. \) pylori is one of cancer causing bacteria is needed to be controlled. Inhibition of \( H. \) pylori activities required to be mention in relation to turmeric as drug. \( H. \) pylori transmission always remains uncertain due to technical difficulties in detecting outside the stomach. According to Canadian Arctic communities contamination of the natural environment is responsible for the high prevalence of \( H. \) pylori infection to the population of mankind of different regions. Associations between exposure to potential environmental sources of biological contamination and prevalence of \( H. \) pylori infection in Arctic Canada have analysed. Using data from 3 community-driven \( H. \) pylori projects in the North west and Yukon Territories effects of environmental exposures on \( H. \) pylori prevalence have been estimated by using odds ratios (OR) and 95% confidence intervals (CI) from multi level logistic regression models by adjusting the household and community effects. Environmental exposures were untreated drinking water; livestock; dogs; cats; mice or mouse dropping in the home and cleaning fish or game. However multilevel models showed high \( H. \) pylori clustering within households, and environmental exposures accounted for little of this clustering; instead, much as it was accounted for especially infected household members along with number of children. Scientific literature could not completely ruled out environmental reservoirs of \( H. \) pylori; and topic remains a priority for future research. It has been suggested that \( H. \) pylori prevention research should seek strategies for reducing direct transmission from person to person (Emily et al., 2014).
Subsequently, *Helicobacter pylori* (HP) and diet are both risk factors for gastric cancer. Among dietary approaches, relationship between energy intake and carbohydrate with *H. pylori* infection has shown significant prevalence. For example a direct association has been found between daily intakes of sausage and burgers with HP infection while low intake of fresh vegetables and fruits also showed the most significant risk factors. Possibly, some dietary factors may increase the chances of severity of *H. pylori* infection such as consumption of fast foods and low intake of fresh vegetables (Mard et al., 2014).

*H. pylori* causing peptic ulcer is also associated with climatic change. The incidence of PUB (peptic ulcer bleeding) in cold climates is higher than that in hot climates. The protein expression levels of occludin, HSP70, NOS and EGFR in the extreme cold climate are lower than those in the extreme hot climate. The gastric acid secretion is also higher in the extreme cold climate than in hot climate. It has been indicated that low expression of HSP70 in the gastric mucosa and reduced gastric mucus thickness may play a major role in the mechanism of PUB in extreme cold climates. The significant decrease in barrier factors and increase in damage in extreme cold climates are regulated with the seasonal variations of peptic ulcers (Xiao-Gang et al., 2015).

After the description of regulation and controlling factors of population, to understand the mechanisms of infection is also needed. It has been well established that the *Helicobacter pylori* infection is the most common cause of many gastric diseases. One of its pathogenic mechanism leads to the production of a wide spectrum of alterations in different components of the gastric enteric nervous system. Changes in neural circuitry encompass structural abnormalities, sensitive, motor function impairment, altered content and release of neurotransmitters are seem to be related rather to the inflammatory response of gastric wall than the bacterial colonization. Although gathered data provide new insights into the complex mechanisms underlying the interactions between HP and enteric nervous system. Therefore, it has been suggested that impaired neural activity have a potential role in development of gastric cancer (Sticlaru, et al., 2014).
The discordant prevalence of *Helicobacter pylori* and its related diseases, fostered certain enigmatic situations has been observed since a long time in the countries of the southern world. Variation in *H. pylori* infection rates and disease outcomes among different populations in multi-ethnic Malaysia provided a unique opportunity to understand the dynamics of host–pathogen interaction and genome evolution. In a study, it has been extensively analyzed to compare the genomes of 27 Malaysian *H. pylori* isolates and recognised as three major phylogeographic lineages (hspEastAsia, hpEuropeand hpSouthIndia). The analysis of the virulence genes within the core genome, reveals a comparable pathogenic potential of the strains. Moreover, four genes have been identified and limited to strains of East-Asian lineage. Other strain-specific genes encoding restriction modification systems have been identified and outlined 311 core genes under differential evolutionary constraints, among the strains representing different ethnic groups. The prominently presence of cagA and vacA genes in the *H. pylori* also vary in accordance with the host genetic background of the strains and restriction modified genes have been found to be significantly enriched. An understanding of variations in the genome also provides various adaptive and host modulation strategies harnessed by *H. pylori* effectively persisting in a host specific manner (Kumar et al., 2015). The cagA gene as one of the important virulent factor leads to gastric cancer in the infected persons. Chances of risk of gastric cancer in human population by *H. pylori* depend on distribution of cagA strains all over world.

*Helicobacter pylori* infection triggers a sequence for gastric alterations starting from an inflammation of the gastric mucosa leading to gastric cancer. Still effective vaccination are not been available, therefore there is need to explore alternative therapies in the background of nutritional field. It has been demonstrated an up-regulation of the expression of inflammatory cytokines and chemokines, as well as of toll-like receptors (TLRs) and MyD88 in mice and treatment with curcumin able to decrease the expression of mediators and no inflammation in mice tissues was observed by histological study. In addition, curcumin exerted a significant anti-inflammatory effect on *H. pylori*-infected mucosa, and suggested that a promising role of nutritional approach in the prevention of *H. pylori* induced deleterious inflammation. This provides an
alternatives source of vaccine non-availability for eradication or prevention of colonization (António et al., 2015).

*Helicobacter pylori* infection results into diverse clinical conditions ranging from chronic gastritis and ulceration to gastric adenocarcinoma. Among the multiethnic population, Indians have consistently higher *H. pylori* prevalence in comparison to Chinese and Malays. Despite the high prevalence of *H. pylori*, Indians showed a relatively low incidence for peptic ulcer and gastric cancer disease. Whereas, above both the diseases incidence are high in Chinese. These differences explain that the *H. pylori* Chinese strains predominantly belong to the hspEAsia subpopulation while Indian/Malay strains mainly belong to the hspIndia subpopulation. By comparing the genome of 27 Asian strains from different subpopulations have identified, where six genes associated with risk of *H. pylori*-induced peptic ulcer and gastric cancer. This study provided an important information for future researches to understand about the role of virulent factors in *H. pylori*-induced gastro-duodenal diseases (Gunaletchumy et al., 2014).

Besides above, cytotoxin-associated geneA (cagA)-positive *H. pylori* strains increase the risk of gastric pathogenesis. The carcinogenic potential of CagA has found to be associated with its polymorphic EPIYA motif variants. The cagA-positive *H. pylori* is highly prevalent in southern Mexico, and all variants are to be associated with western type. It has been evidenced that cagA alleles coding EPIYA-ABCC motif patterns associated with peptic ulcers and gastric cancer (Beltrán-Anaya et al., 2014).

It has been proved that *Helicobacter pylori* is the main risk factor for the development of chronic gastritis, gastric ulcer, and gastric cancer depending on various factors, like bacterial components, immune response, and environmental influence according to clinical study. The IFN-γ (interferon) expression as a factor has been compared among *H. pylori* vacA and cagA genotypes in patients with chronic gastritis and gastric cancer and indicated its IFNγ expression depending on distribution of *H. pylori* vacA and cagA genotype, though it has not been followed in case of chronic gastritis or gastric cancer (Martínez-Carrilloa et al., 2014).
Total cagA has been detected 99.2% where East-Asian-type cagA (62%) and vacAs1c (64.7%) are predominant genotypes in Laos. Whereas, vacA s1c-m1b genotype is significantly higher in GU (gastric ulcer) than gastritis (53.8% vs. 24.1%) and vacA s1a m2 genotype are occurred higher only in DU. East-Asian type cagA and vacAs1c are significantly higher in highland than lowland of Laos (100% vs. 55.8% and 88.2% vs. 61.5% respectively) and indicated as common infection pattern similar to other countries of Southeast Asia. The cagA gene has been demonstrated in most of Laos patients and indicated that cagA and vacA genotypes could be possible important factors for *H. pylori* infection and disease outcome in Laos (Vannarath et al., 2014).

According to previous reports, *Helicobacter pylori* is distributed worldwide, but the prevalence of infection, virulence factors, and clinical presentation vary widely among on population. In Brazil, a continental country having several ethnicities and cultural habits showed a variation in the infection behaviour. The infection with cagA-positive *H. pylori* strains in a group of children and adolescents which lead to esophagogastroduodenoscopy in Porto Alegre, and Rio Grande do Sul. In comparison, they found statistically significant differences in clinical or demographic characteristics or technically like endoscopic and histological features of patients infected with cagA-positive strains as compared with those infected by cagA-negative strains. There was no relation between the presence of cagA-positive strains and severe clinical presentations in the studied sample (Juliana et al., 2014).

Recently non-availability of suitable treatment can be a major reason for the increasing prevalence of *Helicobacter pylori*-related gastroduodenal diseases like gastritis, peptic ulcer, and gastric cancer. Presently, curcumin (diferuloylmethane) as a compound in turmeric, has been found as a inhibitor of *H. pylori* growth. During study of growth, the MIC of curcumin was determined ranging between 5 µg/ml and 50 µg/ml, and showed its effectiveness against *H. pylori* growth in vitro irrespective of the genetic makeup of the strains. Curcumin exhibited immense therapeutic potential against *H. pylori* infection as shown experimentally in eradication of *H. pylori* from infected mice as well as restoration of *H. pylori* induced gastric damage. This study provides a novel insights into the therapeutic effect of curcumin against *H. pylori*.
*pylori* infection and explored as potentiality alternative therapy (De et al., 2009).

Presently researches are being focused to develop and characterize mucoadhesive microspheres of curcumin for the potential use for treating gastric adenocarcinoma, gastric and duodenal ulcer developed by *Helicobacter pylori* infection. The prolonged time of curcumin mucoadhesive microspheres in stomach may play a role in complete eradication in combination with other antimicrobial agents of *H. pylori* infection (Ali et al., 2015).

Recent therapy-regimens for treatment of *Helicobacter pylori* (Hp) infections have shown considerable failure rates and adverse side effects, that urge the quest for an effective alternative therapy. Curcumin has proved to be potential to eradicate Hp-infection in mice. Curcumin suppresses MMP-3 and -9 expression in Hp infected human gastric epithelial (AGS) cells depending the doses applied. Hp-eradication by curcumin-therapy consistently involves significant downregulation of MMP-3 and -9 activities and expression in both cytotoxic associated gene cag+ve and cag-ve Hp-infected mouse gastric tissues. Moreover, it has been demonstrated that the conventional triple therapy (TT) to alleviate MMP-3 and -9 activities are less efficient than curcumin. Curcumin’s action on MMPs links to decrease proinflammatory molecules and protein-1 activation in Hp-infected gastric tissues. Curcumin has capability to enhance peroxisome proliferator receptor-c and the inhibitor of kappaB-a. Above curcumin actions indicate that curcumin-mediated healing of Hp infection is possible by regulation of MMP-3 and -9 activities (Kundu et al., 2011).

Human epidermal growth factor receptor tyrosine kinase (HER-TK) is an useful target for cancer therapy. Despite a number of effective EGFR inhibitors that are constantly expanding and still different methods are employed to obtain novel compounds, although the search for newer EGFR inhibitors is still a major scientific challenge. Currently, computational approaches a molecular docking and molecular dynamics investigation are carried out with an ensemble of EGFR-TK structures against a synthetically feasible library of curcumin analogs to explore the potent EGFR inhibitors. To resolve protein flexibility issue has been resolved by taking 5 EGFR wild type crystal structures during
docking which improved the possibility of identifying an active compound than using a single crystal structure. This was identified curcumin as five analogs representing different scaffolds serve as lead molecules. Finally, the 5 ns molecular dynamics simulation demonstrated that knoevenagel condensate of curcumin specifically C29 and C30 are used as starting blocks and effective leads capable of inhibiting EGFR was developed (Yadav et al., 2014).

With repeated established fact and Curcumin, a natural anticancer agent, has capability to inhibit cell growth in a number of tumor cell lines and animal models. These outcomes provided clues to find out the anticancer mechanisms of curcumin. By exploring more potent molecular targets expected to be helpful for the development of new drugs (Cia et al., 2013).

Besides above, human epidermal growth factor receptor2 (HER2) has an important role in cancer aggressiveness and poor prognosis. Therefore, factor HER2 is used as a drug target to diagnose cancers. In particular, to treat effectively of HER2-positive cancer, small molecule inhibitors are needed to target HER2 kinase. Where curcumin has been used and the efficacy of curcumin and its analogs have been evaluated against HER2 expression using in vitro and in silico studies. The specificity of selected curcumin analogs are examined from the docking against human breast cancer cell lines. The screened curcumin compounds have been subjected to molecular dynamics simulation and for increasing the protein-ligand affinity, the curcumin analogs are modified. The series of modifications made the possibility of the new drug design as potential effective inhibitors of HER2-TK (Yim-im et al., 2014). The dietary approaches of turmeric reveals the inhibitory role for HER2 level in blood of gastric cancer patients infected with *H. pylori*. Such inhibition of HER2 level in blood due to presence of curcumin may be associated with mechanism as above previous reports.

On the basis of several experiments, the interaction of curcumin with actin and their binding and thermodynamic parameters were determined by using isothermal titration calorimetry. Curcumin generally fluoresces weakly in aqueous solution, but the binding with actin enhances fluorescence several folds with a large blue shift in the emission maxima. Curcumin inhibits
microfilament formation, and inhibits the microtubule formation. A series of stable curcumina alogues are synthesised and used to examine their affinity towards virulent proteins and the process of inhibition of its self-assembly. Cell biology study suggests the disorganization of actin network leads to the destabilization of filaments in presence of curcumin. Molecular docking reveals that the curcumin closely bindings along with cytochalasin binding site of actin and molecular dynamics revealed a possible allosteric effect, where conformational changes disrupt interactions with the adjacent actin monomer, interrupting filament formation. The recognition and binding of actin by curcumin could be an example of its unique ability to target multiple receptors as yet (Dhar et al., 2015). With above explanations of molecular docking of curcumin exploration for its inhibitory potentiality against CagA oncoprotein of Helicobacter pylori has been explored by comparing binding energies of conventional drugs.

Several types of cancer accounted for 10% of total death worldwide and necessitates better therapeutic strategies. Earlier, inhibitory properties of curcumin has been described towards virulent proteins generating various cancers by computer aided virtual screening. Based on earlier literatures, twenty two receptors have been recognised as critical virulent factors in various cancers. The binding efficiencies of curcumin towards selected targets has been studied by molecular docking. Curcumin as drug showed the best results towards epidermal growth factor (EGF), virulent protein in gastric and prostate cancer; glutathione-S-transferase Pi gene (GST-PI), platelet derived growth factor alpha (PDGFA) and virulent proteins for mesothelioma and glioma as compared to other natural ligands. Whereas binding energies of docked conformations with curcumin has been found to be −7.59 kcal/mol, −7.98 kcal/mol and−7.93 kcal/mol respectively. Based on this, a comparative study described the binding efficiency of curcumin with two conventional antitumor agents, litreol and triterpene. The calculated binding energies of triterpene with EGF and PDGFA have been found to be −4.02 kcal/mol and −3.11 kcal/mol respectively, whereas in case of GSTPI had +6.07 kcal/mol, and these outcome of docking indicate poor binding of lead molecules than curcumin. This pharmacological features of curcumin elucidated to be better than litreol and
triterpene. Curcumin has better interacting properties to these cancer targets than their normal ligands and conventional antitumor agents. Above explanations pave the way for designing of curcumin as novel inhibitors against various types of cancer (Mahajanakatti et al., 2014).

According to previous findings, anomalous behaviours of activation-induced cytidine deaminase (AID) in Helicobacter pylori infected gastric epithelial cells has been postulated as one of the key mechanisms in the development of gastric cancer. The activation of nuclear factor (NF) kappa B activation by H. pylori induces for overexpression of AID in the cells and hence, inhibition of NF kappaB pathway is capable to downregulate the expression of AID. Meanwhile curcumin, as a spice-derived polyphenol has been recognised for its anti inflammatory activity by inhibiting NF-kappaB factor. Therefore, it has been hypothesized that the curcumin might suppress AID overexpression through NF-kappaB inhibitory activity in H. pylori infected gastric epithelial cells. MKN-28 or MKN-45 cells and H. pylori strain 193C isolated from gastric cancer patient are used for co-culture experiments. During the experiments they are pretreated with or without curcumin which showed apoptosis is determined by DNA fragmentation assay. Enzyme-linked immunosorbent assay has been performed to evaluate the antiadhesion activity of curcumin. Real-time polymerase chain reaction (RT-PCR) has been employed to evaluate the expression of AID mRNA and immunoblot assay is subjected for the analysis of AID, NF-kappaB, inhibitors of NF-kappaB (IkappaB), and IkappaB kinase (IKK) complex regulation with or without curcumin. The adhesion of H. pylori to gastric epithelial cells is not inhibited by curcumin pretreatment at nonbactericidal concentrations. Pretreatment with nonbactericidal concentration of curcumin downregulate the expression of AID induced by H. pylori. Similarly, NF-kappaB activation inhibitor (SN-50) and proteasome inhibitor (MG-132) also downregulate the mRNAexpression of AID. Moreover, curcumin has also showed its capability to suppress the H. pylori-induced NF-kappaB activation by inhibiting IKK activation and degrading IkappaB. It has been also demonstrated that nonbactericidal concentrations of curcumin downregulate H. pylori-induced AID expression in gastric epithelial cells by inhibiting pathway of NFkappaB. With reference to above, curcumin
has been considered as a potential chemopreventive agent against *H. pylori* related gastric carcinogenesis (Zaidi et al., 2009).

Efficacy of curcumin against virulent factors also depends on administration routes, when curcumin is administered through orally undergoes for conjugation process. Whereas, intravenously administration of curcumin undergoes for reduction process. In case of *Helicobacter pylori* infection with CagA oncoprotein, conjugated compounds of curcumin has more potential to inhibit the oncogenic activities of *H. pylori* than the reduced compounds.