INTRODUCTION:

Cataract

According to the definition of WHO Cataract is clouding of the crystalline lens of the eye which prevents clear vision. In all over the world Cataract causes blindness and visual impairment. Globally it was estimated that in 2010 cataract was responsible for 51% of world blindness. The lens, being an avascular structure, cannot develop an inflammatory disease. The commonest disease is a degenerative process leading to opacity of lens fibers, known as cataract.

Classification of cataract- A) Congenital and Developmental-It includes Blue-dot cataract, Coronary cataract, Capsular or Polar cataract, Sutural cataract, Coralliform cataract, Floriform cataract, Central cataract, Lamellar or Zonular cataract etc.

B) Acquired Cataract – It includes – Senile cataract, Traumatic cataract, Endocrine cataract, Cataract due to systemic diseases like Myotonic dystrophy, generalized dermatitis.

Senile cataract- Usually it develops in above 50 years persons, and equal in both the sexes, it appears bilateral but develops earlier in one eye.

Heredity- Genetic influence is marked. In hereditary cases the cataract appears at earlier ages in subsequent generations. Near about 55% blindness is due to senile cataract.

With the age increasement prevalence of age-related cataract also increases and after forty years prevalence of cataract doubles with decades, so that everyone in their nineties is affected. In some parts of Asia it is common for appearance of cataract in earlier ages .As the lens ages, it increases in weight and thickness and decreases in accommodative power. As new layers of cortical fibres are formed concentrically, the lens nucleus undergoes compression and hardening (nuclear sclerosis). Modification of the chemical nature of nuclear proteins also increases
pigmentation, such that the lens increasingly takes on a yellow or brownish hue with advancing age.

**Pathogenesis**- Cataract is caused by the degeneration and opacification of the lens fibers already formed the formation of aberrant lens fibres or deposition of other material in their place. The loss of transparency occurs because of abnormalities of the lens proteins and consequent disorganization of the lens fibers.

Biochemically three factors are evident in the process of cataract formation. In the early stages of cataract, particularly the rapid developing forms, hydration is a prominent feature so that frequently actual droplet of fluid gathers under the capsule forming lacunae between the fibers, and the entire tissue swells and becomes opaque. To some extent, this process may be reversible and opacities thus formed may clear up as in juvenile insulin dependent diabetic patients whose lens becomes clearer after control of hyperglycaemia. The second factor is denaturation of lens proteins. If the lens protein denatured with an increase in insoluble proteins, a dense opacity is produced, a process which is irreversible, opacities thus constituted do not clear up. Such an alteration occurs typically in the young lens or the cortex of the adult lens where metabolism is relatively active. It is rarely seen in older and inactive fibers of the nucleus. Here the usual degenerative change is rather of third type, one of slow sclerosis. Clinically, when the first process is predominant the condition is called a soft cataract; the third is described as a hard cataract.

**Risk Factors for Cataract**

There are various risk factors for cataract. These include: Increasing age, severe diarrhoeal dehydration, Diabetes, Sunlight (especially the ultraviolet-A and UV-B components) radiation, Smoking, Vitamins A, C, E deficiency, medications such as steroids and topical intra-ocular pressure lowering agent and Genetics.
Genetic Risk Factors for Cataract

DNA repair enzymes like 8-oxoguanine glycosylase-1, Apurinic/apyrimidinic endonuclease 1, and X-ray repair cross-complementing-1 continuously monitor chromosomes to correct damaged nucleotide residues generated by exposure to carcinogens and cytotoxic compounds. Studies have confirmed that polymorphisms of DNA repair genes decreased their ability to repair DNA damage, leaving human body a greatly increased susceptibility to cancer or age-related diseases. For DNA repair pathways base excision repair (BER) has a crucial role. As the key enzymes of the BER pathway, association between 8-oxoguanine glycosylase-1 (OGG1), AP endonuclease-1 (APE1) and X-ray repair cross-complementing-1 (XRCC1) genes polymorphisms.

APE1 Gene- Through both its endonuclease and its phosphodiesterase activities, Apurinic/apyrimidinic endonuclease 1 (APE1) plays a central role in the repair of apurinic apyrimidinic sites of DNA.

Function- The human apurinic/apyrimidinic endonuclease (APE), APE1 (also known as APE, APEX, and REF-1), is involved in the BER pathway. Location of APE1 gene is on chromosome 14q11.2-q12. APE1 produces normal 3′-hydroxyl nucleotide termini by hydrolyzing 3′-blocking fragments from oxidized DNA, that are necessary for DNA repair synthesis and ligation at single- or double-strand breaks. A total of 18 polymorphisms in APE1 have been reported, but the most extensively studied polymorphism is the T to G transversion (T1349G, also known as Asp148Glu, rs3136820).

Activity- apurinic/apyrimidinic endonuclease

Location- Chromosome 14q12
**XRCC1 Gene**- X-ray repair cross-complementing protein 1 (XRCC1) is DNA repair protein. In human this protein is encoded by XRCC1 gene. Wherever DNA repair is complexes with DNA ligase III XRCC1 also involved.

**Function**- Due to the exposure to ionizing radiation and alkylating agents, DNA single-strand breaks and those are efficiently repair by XRCC1. XRCC1 protein participates in the base excision repair pathway due to interaction with DNA ligase III, polymerase beta and poly (ADP-ribose) polymerase. It also plays a role in DNA processing during meiogenesis and recombination in germ cells. The XRCC1 protein acts as a scaffolding protein, so that it interacts with multiple repair enzymes. Due to scaffolding, repair enzymes carry out their enzymatic steps in repairing DNA. XRCC1 has a crucial role in single-strand break repair, base excision repair and nucleotide excision repair.

**Activity**- Main ligation function

**Location**- Chromosome 19q13.2

**OGG1 Gene**

**Oxoguanine glycosylase (OGG1)** is a glycosylase enzyme; it is encoded by the OGG1 gene in human. It is also involve in base excision repair mechanism. It is found in bacterial, and eukaryotic species.

**Function**- Due to the exposure to reactive oxygen species (ROS) a mutagenic byproduct occurs that is 8-oxoguanine, and for excision of 8-oxoG OGG1 is primary enzyme. OGG1 is able to both cleave the glycosidic bond of the mutagenic lesion and cause a strand break in the DNA backbone that’s why it act as a bifunctional glycosylase. N-terminus of OGG1 gene contains a mitochondrial targeting signal in eukaryotes, it is essential for mitochondrial localization.

**Activity**- 8-oxoguanine opposite C
**Location**- Chromosome 3p26.2

**Management of cataract**

Nowadays treatment is surgery and in cataract surgery we have to remove the pacified crystalline lens and insertion of a synthetic intraocular (IOL) lens. If an intraocular lens cannot be used, contact lenses or eyeglasses must be worn to compensate for the lack of a natural lens. The main aim of Cataract surgery is to rehabilitate blind or visually impaired persons by restoring their eye sight so that their quality of life and ability to function will improve.