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# Molecular Evolution of APP Gene in Alzheimer's Disease

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# ALZHEIMER'S DISEASE

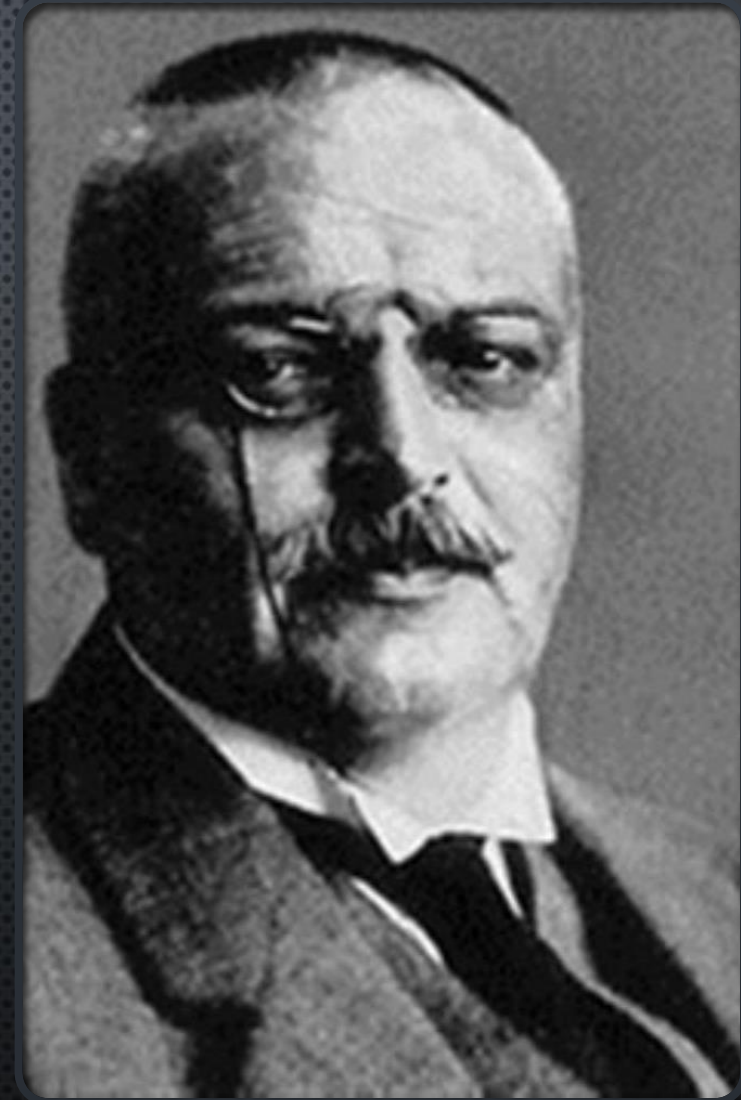
BY: MARY HUSK

# BACKGROUND

- ALZHEIMER'S DISEASE:
  - DEGENERATIVE BRAIN DISEASE OF UNKNOWN CAUSE
  - PROGRESSIVE MEMORY LOSS, IMPAIRED THINKING, DISORIENTATION, CHANGES IN MOOD AND PERSONALITY
- BECAME GENERALLY ACCEPTED AS MOST COMMON BASIS FOR SENILE DEMENTIA IN 1960'S (BLESSED, TOMLINSON, AND ROTH)
- FOUND ON CHROMOSOMES 21, 14, AND 1
- MAJOR LEADING CAUSE OF DEMENTIA IN ELDERLY

# ALOIS ALZHEIMER

- DISCOVERED ALZHEIMER'S DISEASE
- A GERMAN PSYCHIATRIST AND NEUROPATHOLOGIST
- 1901: MET AUGUSTE DETER; 51 YEAR OLD FEMALE
- 1906: DETER DIED; ALZHEIMER HAD BRAIN AND RECORDS SENT TO HIM IN MUNICH
  - AUTOPSY REVEALED SHRINKING OF CORTEX AND PRESENCE OF NEUROFIBRILLARY TANGLES AND NEURITIC PLAQUES
  - DIAGNOSED AS SENILE DEMENTIA (LATER KNOWN AS ALZHEIMER'S DISEASE)

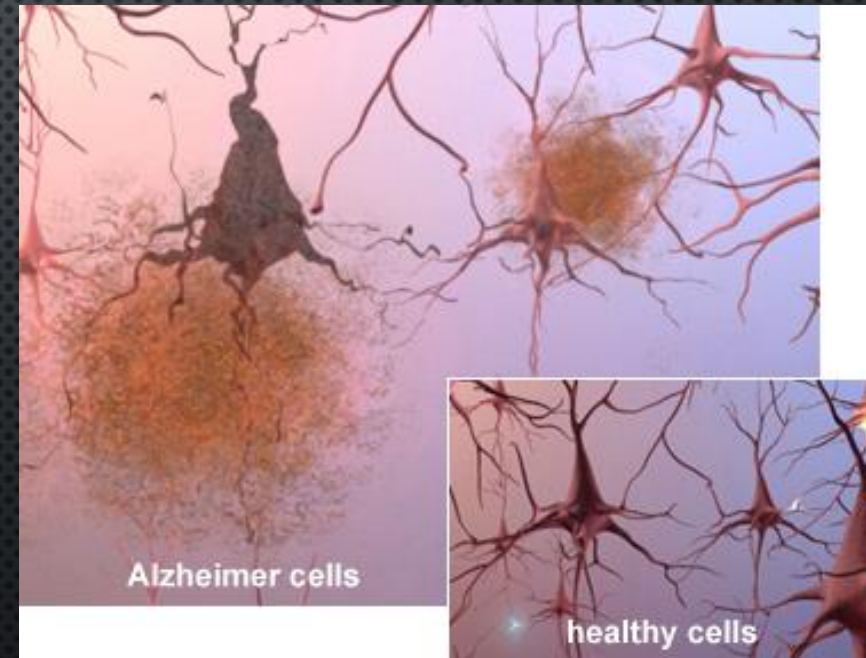


# DOWN SYNDROME TO ALZHEIMER'S DISEASE

- A STRONG HOMOLOGY BETWEEN THE AMYLOID B PROTEIN PEPTIDES FROM DS AND AD BRAINS WAS FIRST INDICATION OF COMMON GENETIC MECHANISM
  - BOTH FOUND ON CHROMOSOME 21
- PATIENTS WITH DS INEVITABLY DEVELOP CHARACTERISTIC ALZHEIMER'S DISEASE
- PEOPLE WITH DOWNS SYNDROME HAVE AN EXTRA COPY OF CHROMOSOME 21 WHICH DUPLICATES THE APP GENE

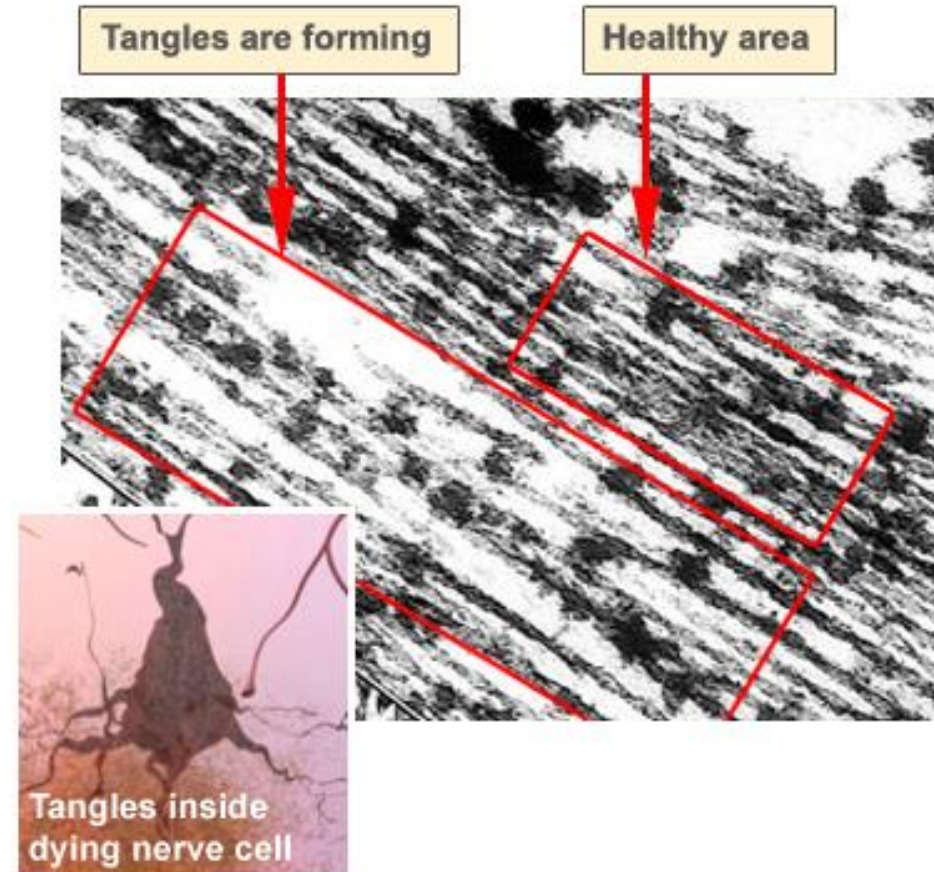
# PLAQUES

- PLAQUES OCCUR WHEN PIECES OF BETA AMYLOID CLUMP TOGETHER
- INDIVIDUALS WITH ALZHEIMER'S DISEASE DEVELOP PLAQUES AT AN INCREASED RATE
- USUALLY START IN AREAS OF THE BRAIN DEALING WITH LEARNING



# TANGLES

- A PROTEIN CALLED TAU HELPS KEEP THE TRACKS STRAIGHT
- TAU COLLAPSES INTO TWISTED STRANDS CALLED TANGLES
- THEY FALL APART AND DISENTIGRATE



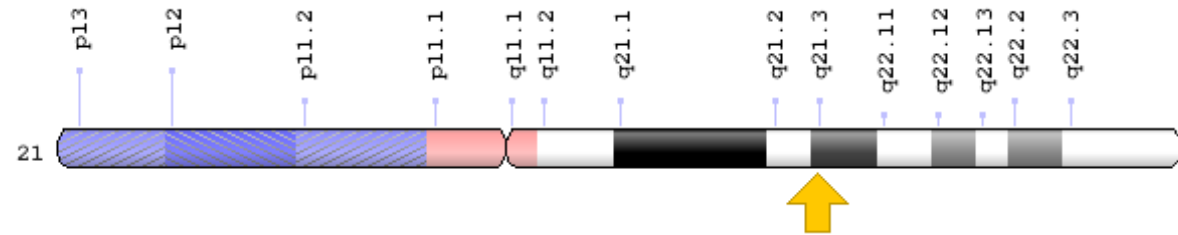
# GENES





# APP GENE

- LOCATED ON CHROMOSOME 21
- PROVIDES INSTRUCTIONS FOR MAKING PROTEIN CALLED AMYLOID PRECURSOR PROTEIN
- FOUND IN MANY TISSUES LIKE BRAIN AND SPINAL CORD
- APP IS CUT BY ENZYMES TO CREATE SMALLER FRAGMENTS, SOME OF WHICH ARE RELEASED OUTSIDE OF THE CELL

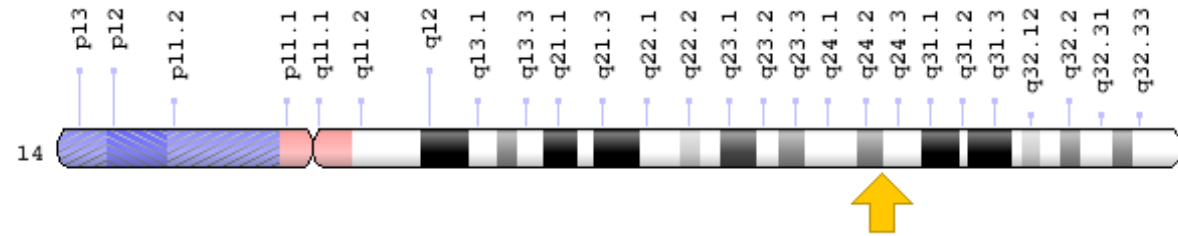


# APP GENE MUTATION

- ACCOUNTS FOR LESS THAN 10% OF EARLY ONSET CASES
- MUTATION IN APP GENE AT CODONS 717 AND 716 (NEW)
  - REPLACES AMINO ACID VALINE WITH AMINO ACID ISOLEUCINE AT 717
- DOUBLE MUTATION AT CODONS 670 AND 671
- COMMON FEATURE OF MUTATIONS IS TO INCREASE THE CONCENTRATION OF AB ENDING AT Ab42
- OVEREXPRESSION OF APP INHIBITS CELL PROLIFERATION; MAY PROMOTE AD PATHOGENESIS

# PSEN1

- LOCATED ON CHROMOSOME 14
- MAKES PRESENILIN 1 PROTEIN
- SUBUNIT OF GAMMA SECRETASE
- KNOWN AS PROTEOLYTIC SUBUNIT

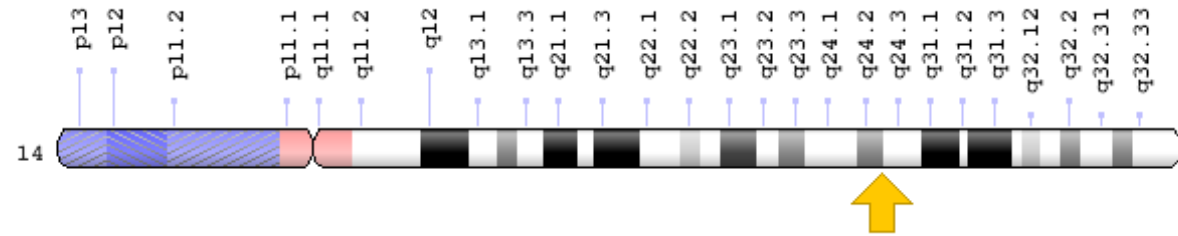


# PSEN 1 MUTATION

- MORE THEN 150 MUTATIONS
- ACCOUNTS FOR UP TO 70% OF EARLY ONSET CASES
- RESULTS IN PRODUCTION OF ABNORMAL PSEN1 WHICH INTERFERES WITH THE FUNCTION OF GAMMA SECRETASE COMPLEX
- LEADS TO LONGER, TOXIC VERSION OF AMYLOID BETA PEPTIDE

# PSEN2

- LOCATED ON CHROMOSOME 1
- BEST KNOWN FOR ITS ROLE IN PROCESSING APP
- MAKES PROTEIN PRESENILIN 2
- HELPS PROCESS PROTEINS THAT TRANSMIT CHEMICAL SIGNALS FROM THE CELL MEMBRANE INTO THE NUCLEUS
  - ACTIVATES GENES THAT ARE IMPORTANT FOR CELL GROWTH AND MATURATION



# PSEN 2 MUTATION

- AT LEAST 11 MUTATIONS
- ACCOUNTS FOR LESS THAN 5% OF EARLY ONSET CASES
- CHANGES THE AMINO ACID ASPARAGINE TO AMINO ACID ISOLEUCINE AT POSITION 141
- CHANGES AMINO ACID METHIONINE TO AMINO ACID VALINE AT POSITION 239
- DISRUPTS PROCESSING OF APP LEADING TO BUILD UP OF AMYLOID PRECURSOR PROTEIN

# PHYTOTHERAPY

- GARDEN ANGELICA (ANGELICA ARCHGANGELICA) AND CATERALL (TRECVLIA OBOVOIDEA)
  - MORE THAN 80% INHIBITION OF AChE
- TURMERIC (CURCUMA LONGA)
  - REGULATES MULTIPLE TARGETS
  - SAFE FOR HUMANS
  - TARGETS GROWTH FACTORS
  - CONSIDERABLE AFFINITY FOR AB 1-42 FIBRILS

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