

03-621 Week 3

Advanced Quantitative Genetics

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Mutations (Continued)

- Synonymous Substitutions Can Alter Phenotypes

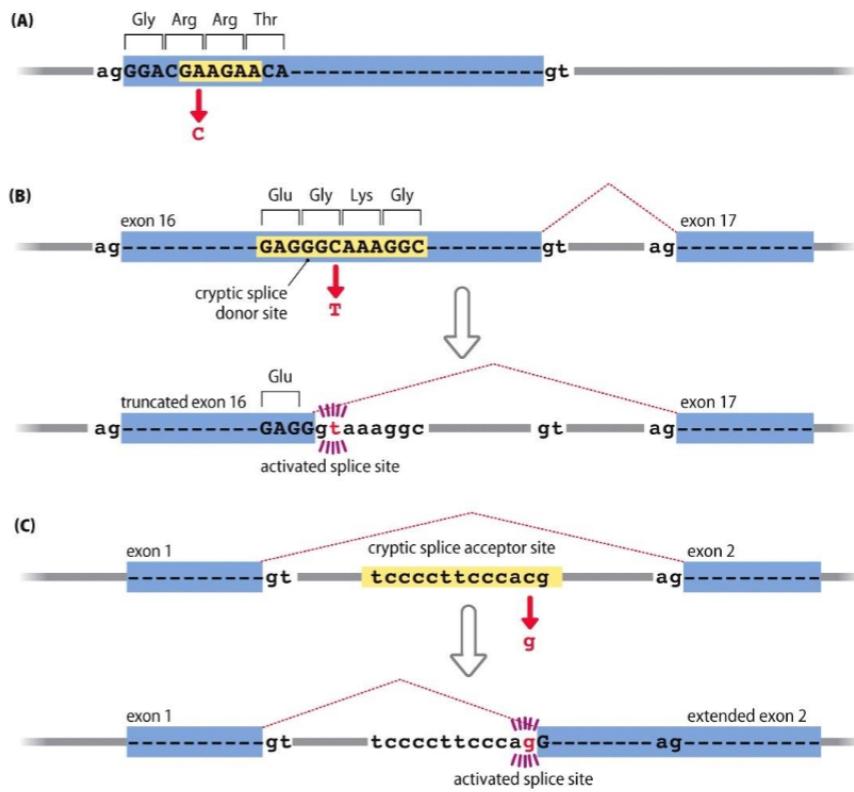
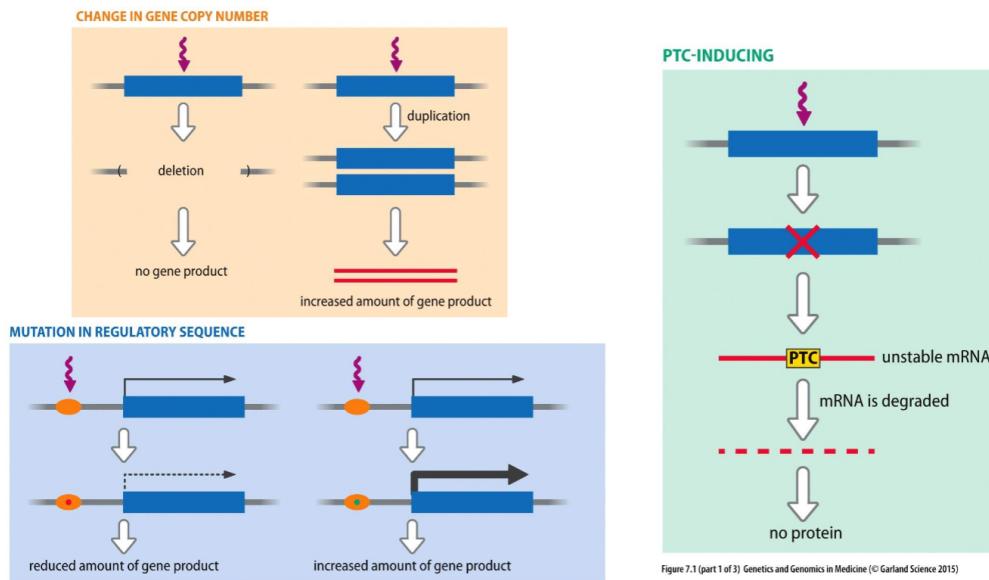


Figure 7.4 Genetics and Genomics in Medicine (© Garland Science 2015)

- Single-gene disorders can also be caused by mutations in **non-coding** RNA genes
- Large Copy Number Variations (CNVs) are common in the human genome
 - One section of DNA is duplicated many times
 - About 10-15% of the genome displays copy number variation
 - 1000 bp - 5 mbp in length
 - Most are in non-coding regions, but some contain genes
 - Too large for PCR analysis, can be detected using a microarray

- Variable nucleotide tandem repeats (VNTR) and short tandem repeats (STR) are inherited repeating stretches of DNA
 - Different individuals may have different numbers of repeats at a given locus.
 - If the number of base pairs in a repeated section is not a multiple of three, tandem repeats may cause frameshift errors.
- Some mutations that cause disease do not change the sequence of a gene product but alter the amount of gene product
 - For example, mutations in promoters or enhancers
 - Mutations in transactors (e.g., histones)
 - Gene duplication or deletion



- Gene dosage changes via Meiotic Non-disjunction
 - Frequency: in all recognized pregnancies
 - 8% of *recognized* pregnancies have major chromosomal abnormalities. > 94% of this 8% undergo spontaneous abortion.
 - Aneuploidies change the amount of gene product expressed ("gene dosage"), across many genes.
 - Among the fetuses in 100000 recognized pregnancies, about 8000 have major chromosomal abnormalities, 7500 of these undergo spontaneous abortion, and 500 are born alive.

Meiosis I Non-disjunction

