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التوثيق الالكتروني والميكرو فيلم

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بالرسالة صفحات
لم ترد بالأصل

DELETIONAL DYSTROPHIN GENE MUTATIONS IN MUSCULAR DYSTROPHY IN EGYPT

*Thesis
submitted by*



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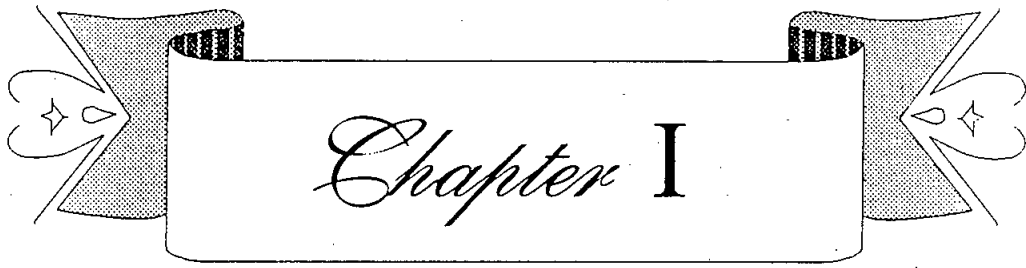
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CONTENTS

	Page
I. INTRODUCTION AND AIM OF THE WORK	1
II. REVIEW OF LITERATURE	3
Muscle	3
Dystrophin	9
Historical Review.	13
Incidence and Prevalence	14
Clinical Picture	14
Diagnosis of DMD	17
Pathophysiology of DMD.	20
Molecular Genetics of DMD Gene	
Mapping of the Gene	22
Isolation of the Gene	27
Polymerase Chain Reaction.	29
Primary Selection	33
PCR Buffer	37
Cycling Parameters	38
Amplification Plateau	39
Medical Applications	40
Detection of Deletions at DMD Locus.	42
Southern Blot	46
Western Blot	48
Immunohistochemical Studies.	49
Investigations of Relatives and Prenatal Diagnosis	50
Differential Diagnosis of DMD	51
Management and Treatment of DMD	63
III. SUBJECTS AND METHODS	68
IV. RESULTS.	80
V. DISCUSSION	114
VI. SUMMARY	132
VII. CONCLUSION	136
VIII. RECOMMENDATIONS	137
IX. REFERENCES	138
X. ARABIC SUMMARY	

Abbreviations

DMD	Duchenne muscular dystrophy
BMD	Becker muscular dystrophy
EMG	Electromyography
PCR	Polymerase chain reaction
NM	Neuromuscular disease
DNA	Deoxyribonucleic acid
cDNA	Cloned DNA
cM	Centi Morgan
Kb	Kilo base
bP	base Pair
RFLPs	Restriction fragment length polymorphisms
mRNA	Messenger Ribonucleic acid
mM	millimole
I.Q.	Intelligence quotient
CPK, CK	Creatine phosphokinase
P	Fisher exact test
del	Deletion
Fam	Family
YACs	Yeast Artificial Chromosomes
Res	Residence
N	Normal
Sub	Subnormal
LL	Lower limbs
UL	Upper limbs
Ms	Muscle
HFDRs	High frequency deletion regions.
EM	Electron microscope
CT	Connective tissue
PERT	Phenol Enhanced Reassociation Technique.



**INTRODUCTION
AND
AIM OF THE WORK**

INTRODUCTION AND AIM OF THE WORK

Duchenne muscular dystrophy is the most common and severe neuromuscular genetic disease in man (Emery et al., 1988). It has an X-linked recessive mode of inheritance, with an incidence of 1/3,500 male births. Duchenne muscular dystrophy is allelic with Becker muscular dystrophy, a clinically similar but less severe form of myopathy affecting 1/30,000 males (Worton et al., 1988). Duchenne muscular dystrophy is characterized by the inability to produce normal dystrophin, a component of membrane cytoskeleton of myofiber (Hoffman et al., 1989).

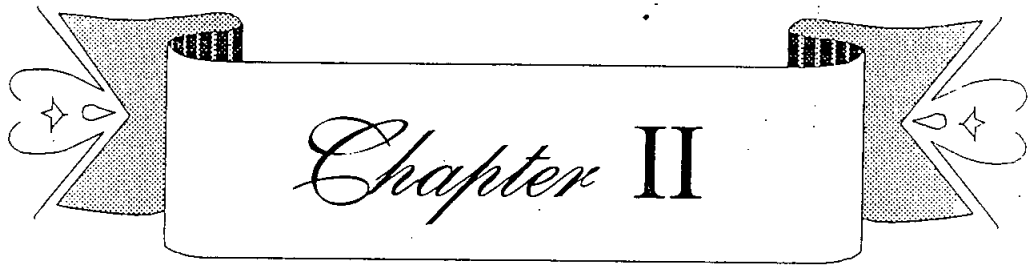
The cloning of Duchenne muscular dystrophy gene led directly to the identification of its protein (Xiuyuan et al., 1990). Because of the large size of the dystrophin gene, the restriction fragment patterns revealed by the cDNA probes are quite complex. So far, the majority of the detectable mutations at this locus are of the deletion type which accounts for about 60% of all mutations (Darras et al., 1988) resulting in the loss of one or more of the 65 exons preferentially clustered in the center of the gene and less frequently near the 5' end (Liechti-Gallatis et al., 1990).

Deletions are not uniformly distributed throughout the gene and deletion rich regions, have been identified. A strong correlation has been observed between the shift in transnational reading frame of a national transcript from such a disrupted gene and the severity of patient's disease, while the size and position of the disruption appear less important (Monaco et al., 1988).

Duplication of part of the Duchenne muscular dystrophy gene has also been revealed in a few patients (Xiuyuan et al., 1990).

Rapid detection of deletion and duplication mutations that cause Duchenne and Becker muscular dystrophy was achieved in patients and carriers after amplification of small amounts of mRNA from peripheral blood lymphocytes (Roberts et al., 1990). Such deletions are readily identified in patients by the absence of bands from Southern blots (Speer et al., 1989) or by failure of amplification of individual reactions in multiplex polymerase chain reaction (Saiki et al., 1988, Chamberlain et al., 1988). However diagnosis is complicated in carrier women by the presence of the normal chromosome which masks the results from the defective chromosome (Roberts et al., 1990).

The aim of this work is detection of the different types of deletions in the dystrophin gene that may lead to the Duchenne or Becker muscular dystrophy in affected Egyptian patients, this will greatly facilitate the arrangement for a programme of prevention through detection of carriers and prenatal diagnosis in the proband's families.



REVIEW OF LITERATUTRE