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Mapping the Dairy Cattle Genome Using Somatic Cell Hybrids and Recombinant DNA Technology

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TABLE OF CONTENTS

	<u>Page</u>
1.0 Abstract	1
2.0 Objectives	1
3.0 Scientific Accomplishments (Reprints and Preprints)	2
3.1 Restriction fragment length polymorphism among Israeli Holstein-Friesian dairy bulls	3
3.2 Restriction fragment length polymorphisms in dairy and beef cattle at the growth hormone and prolactin loci	4
3.3 Molecular Markers In The Genetic Improvement of Farm Animals	5
3.4 Mapping of bovine prolactin and rhodopsin genes in hybrid somatic cells	6
3.5 Detection of linkage between marker loci and loci affecting quantitative traits in crosses between segregating populations	7
3.6 Symposium: Cytogenetics and Cell Biology	8
3.7 The bovine gene map	9
3.8 Restriction fragment length polymorphisms for growth hormone, prolactin, osteonectin, α crystallin, γ crystallin, fibronectin and 21-steroid hydroxylase in cattle	10
3.9 Somatic Cell Mapping of the Bovine Somatostatin Gene	11
3.10 Genetic and Synteny Mapping of Parathyroid Hormone and Beta Hemoglobin in Cattle	12
3.11 (TG) _n Uncovers a Sex Specific Hybridization Pattern in Cattle	13
4.0 Cooperation	14
5.0 Evaluation of Research Achievements	14
6.0 List of Publications	15

ABSTRACT

In the three years of this project, we have expanded the bovine gene map from a syntenic map of less than 50 genes to one of 140 genes on all the chromosomes. Furthermore, at least 30 restriction fragment length polymorphisms (RFLPs) have been described in our laboratories. Moreover, three new minisatellite probes for bovine fingerprints were discovered and a binary (TG) n sequence was found to hybridize bovine Y-specific fragments. These important contributions to the bovine map are summarized in this report in the form of preprints, reprints and abstracts from work in the cooperating laboratories.

OBJECTIVES

1. To search for restriction fragment length polymorphisms (RFLPs) in cattle, principally in the dairy cattle of Israel.
2. To map the same genes to cattle chromosomes, principally by use of hybrid somatic cells derived in the Texas laboratory.

COOPERATION

Cooperation between the laboratories has facilitated the efficient and timely syntenic mapping of genes for which polymorphisms have been discovered in the Israel laboratories. The Hallerman et al (1988) paper resulted from the visit of an Israel post-doctoral fellow (E.M. Hallerman) to the U.S. laboratory. Probes for prolactin and rhodopsin, developed for use in the Israel dairy cattle populations, were applied to the U.S. panel of hybrid cells. Physical mapping of both genes to different syntenic groups was the result. Further collaboration between the groups is evidenced by participation of the principal investigators in international conferences for planning bovine mapping initiatives (Fries et al, 1989).

EVALUATION OF RESEARCH ACHIEVEMENTS

Bovine gene mapping is in its infancy. Nevertheless, its importance is now generally recognized and major research initiatives are coming forth from several countries. We have provided much of the foundation for the map of the future. Our achievements were consistent with our original objectives and the result is a physical map of anchor gene loci, many of which are polymorphic. The next step, the filling of the gaps with hypervariable markers, has been made possible by this work.

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