THE INTERNATIONAL POULTRY GENOME MAPPING PROJECT

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SUMMARY

This paper is a summary of the current status of poultry genome mapping worldwide and is based on an international workshop held in Interlaken, Switzerland (Society News, 1993).

INTRODUCTION

During the last two years there has been dramatic progress towards producing a genetic linkage map of the chicken genome. This has been due to an international collaboration based on two mapping populations in the USA and UK (Crittenden et al., 1993; Bumstead and Palyga, 1992). Key mapping laboratories are: Roslin Institute (UK), Institute of Animal Health (UK), East Lansing (USA), Leicester University (UK), Wageningn University (Netherlands), Michigan State University (USA), Avian Disease and Oncology Laboratory (USA) and Hebrew University (Israel).

OBJECTIVES OF POULTRY GENOME MAPPING PROJECTS

1. Isolate and share information on molecular markers.
2. Prepare a detailed molecular map of the chicken genome to a resolution of at least 10 cM.
3. Set up an International Poultry Genome Mapping database.
4. Cytogenetic mapping of molecular markers to unify physical and genetic linkage maps.
5. Develop a DNA panel based on the parents of various resource populations to assess the polymorphic content of molecular markers.
6. Develop an Index Microsatellite Marker Set to scan poultry genomes for marker-trait associations.
7. Use whole genome mapping strategies to scan chicken genomes for markers linked to traits of agricultural and medical interest.
8. Develop chromosome-specific libraries, micro-dissection, chromosome scrapping, etc to facilitate the isolation of chromosome and sub-chromosome specific markers.
9. Construction of large inserts libraries (e.g. YAC and P1) to facilitate the isolation of trait genes.
10. Identification of novel genes by cDNA sequencing and sequence comparison.
11. Transfer chicken genome mapping technology to other poultry species.

GENE MAPPING POPULATIONS AND GENETIC LINKAGE MAPPING

Two backcross populations have been used as reference panels for mapping polymorphic markers.

Compton, UK: A reference population based on a backcross between outbred (line N) and inbred (line 15I) White leghorn lines (Bumstead and Palyga, 1992), which differ in susceptibility to a number of diseases.

East Lansing, USA: A reference population produced by backcrossing a partially inbred Red Jungle Fowl (JF) line to a highly inbred White Leghorn (WL) line (Crittenden et al., 1993). The parental lines were chosen to maximise the expected genetic polymorphism between them.

Molecular Markers: Expressed sequences (cloned genes, random cDNAs) and anonymous markers (random genomic clones, microsatellites, minisatellites and other PCR-based markers).

Linkage Analysis: Over 400 loci have been mapped using the UK and USA reference panels (February 1994). Currently the major focus is on mapping microsatellite markers to both crosses to facilitate the construction of a consensus map.

PHYSICAL MAPPING

Physical mapping has been slow due to the complex nature of the chicken karyotype (38 autosomes plus the Z and W sex chromosomes). Progress should be more rapid now with a standardised banding scheme for macrochromosomes (International Committee for the Standardization of the Avian Karyotype - Guelph, 1993). The issue of microchromosomes has not been resolved and will be discussed at a later date (ISAG - Prague, 1994). It is likely to involve a standard based on marker probes assigned to specific microchromosomes. 35 genes have been assigned to the macrochromosomes and 20 to the microchromosomes by a range of in situ techniques (Ponce de leon and Burt, 1993). This has allowed the chromosomal assignment of some of the linkage groups.

COMPARATIVE GENE MAPPING

In contrast to expectations, significant conservation of synteny is found between the maps of the chicken and mammals. For example, seven conserved syntenic groups can be identified from the comparison of human and chicken maps: HU-4 and GG-6; HU-4 and GG-E33+C11; HU-6 and GG-E2+C1; HU-6 and GG-17; HU-7 and GG2; HU-8 and GG-2; HU-12 and GG-1 (Table 1). Overall these comparisons highlight the fact that rodents are unusual and may have undergone extensive inter-chromosomal exchanges since the radiation of mammals 80 million years ago. This paper however does not address the possibility of intra-chromosomal rearrangements which have certainly occurred since the divergence of avian and mammalian species.

INTERNATIONAL POULTRY GENOME DATABASE

A Poultry Genome Database is being developed at the Roslin Institute based on a set of tables and an adapted version of G-BASE, the mouse database. This database contains a summary of chicken mapping data: (a) alphabetical listing of chicken gene loci and nomenclature rules; (b) classical genetic loci; (c) loci defined by random genomic fragments, cloned genes, anonymous expressed DNA sequences, microsatellites, anonymous RAPD markers, anonymous CR1 repeats, anonymous minisatellites; (d) gene assignments to macro- and microchromosomes; (e) information on resource populations; (f) directory of researchers in poultry genetics; (g) references to published material. In the long term, this database will contain information on all poultry genomes to facilitate comparative genome mapping.

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Table 1. Comparative Gene Mapping in Vertebrates.

LOCUS	CHICKEN	HUMAN	BOVINE	PIG	SHEEP	MOUSE
PGR	1	11				9
LYZ	1	12	5	5	3	
GAPD	1	12	5		3	6
H1H5	1	12				13
IGF1	1	12	5	5	3	10
CYP19	1	15				9
GH1	1	17	19	12	11	11
BMP6	2	6				13
EGFR	2	7				11
ACTB	2	7				
CA2	2	8	14		9	3
CALB1	2	8				4
MYC	2	8	14		9	15
HBB	2	11	15			7
HBE	2	11	15			7
YES1	2	18	24			
PGM2	6	4	6	6	6	5
PPAT	6	4			6	
ALB	6	4	6	8	6	5
GC	6	4	6	8	6	5
TAP2	17	6				17
HLA@	17	6				17
TGFB2	E2, C1	1				1
ODC1	E2, C1	2				12
FYN	E2, C1	6				10
TCP1	E2, C1	6	23		23	17
CD8A	E33, C11	2	11			6
MSX1	E33, C11	4				5
ANX5	E33, C11	4				