Global Conference on Aquaculture 2010

Farming the waters for People and Food

22-25 September 2010, Phuket, Thailand

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Global Conference
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Expert Panel Presentation 3.1:

Promoting responsible use and conservation of aquatic biodiversity for sustainable aquaculture development

by Dr. John A. H. Benzie

22–25 September 2010, Phuket, Thailand

AQUATIC GENETIC RESOURCES

Rich diversity of aquatic genetic resources are available

How can this be exploited sustainably and wild resources protected?

What genetic knowledge or technologies are available to aid sustainable production?

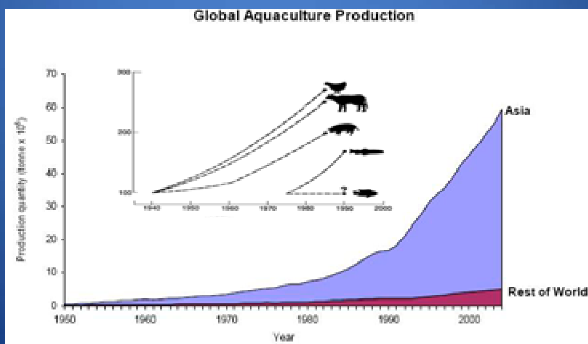
AQUATIC GENETIC RESOURCES IN AQUACULTURE

PRODUCTION
how aquatic genetic resources have been used
which genetic technologies have been applied
what genetic changes occur in culture

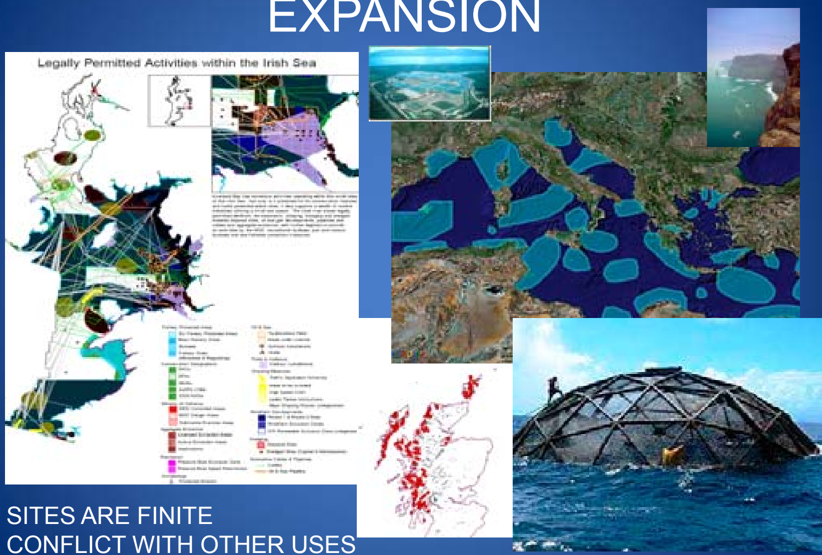
IMPACT
the wild resource and evolutionary biology
the genetic impacts of aquaculture
technologies/strategies for reducing impact

THREEFOLD INCREASE NEEDED IN AQUACULTURE PRODUCTION

10% annual growth in aquaculture achieved by accessing new areas of production, farming new species and increasing efficiencies

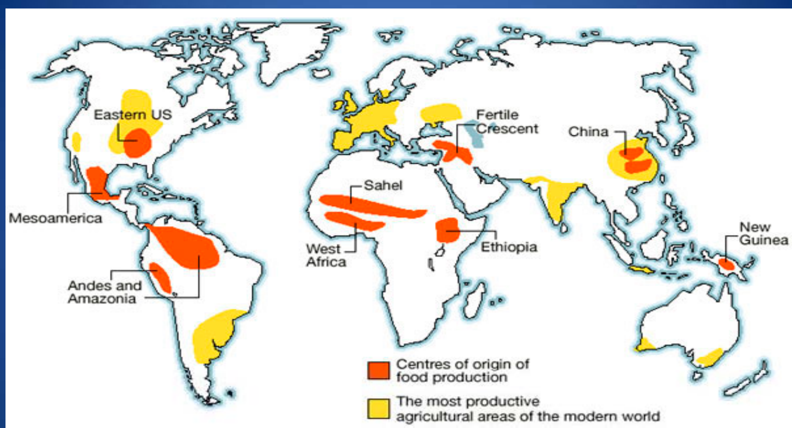


RESTRICTIONS ON AQUACULTURE EXPANSION



- SITES ARE FINITE
- CONFLICT WITH OTHER USES
- DEMANDS INCREASES IN EFFICIENCY, HUSBANDRY, DOMESTICATION, GENETIC IMPROVEMENT

DOMESTICATION IN AGRICULTURE



Few centres of origin
Centres of production elsewhere

DOMESTICATION IN AGRICULTURE

RAPID SPREAD OF DOMESTICATED STOCKS
Restricted wild distribution – one domestication event
Broader wild distribution – several domestication events
Barriers to exchange – domestication of related species
Those species domesticated were useful AND EASY to domesticate
(Diamond 2002)

FEW DOMESTICATED SPECIES

	Wild	Domesticated	
		Major	90%
Higher plants	200,000	100	5
Large herbivores	148	14	<5

Diamond 2002

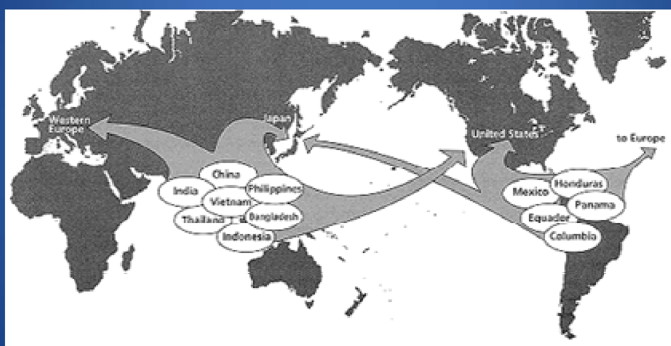
FEW FARMED AQUATIC SPECIES

	Wild Species*	Cultured	Production 99%	80%
Finfish	31,000	227	44	9
Molluscs	85,000	77	19	6
Crustaceans	47,000	35	11	4
Seaweeds	13,000	>20	2	2
Total		359	76	21
			21%	6%

*World Conservation Union (2010)

GERMPLASM MOVEMENT

- Breeding programs often developed far from the source and major production areas

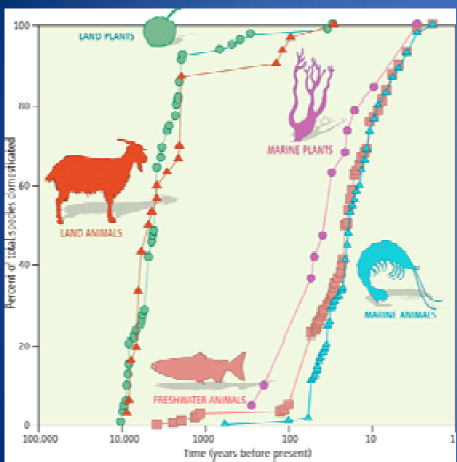


ALL 76 SPECIES USED FOR MAJOR PRODUCTION HAVE BEEN SPREAD REGIONALLY, AND THE MAJORITY GLOBALLY

IMPACT

- FERAL POPULATIONS OF ALIEN SPECIES
- GENETIC EXCHANGE OF AQUACULTURE ESCAPEES WITH WILD STOCKS
- INTROGRESSION OF GENES ADAPTATED TO CULTURE ENVIRONMENT
- DEVELOP ENDEMIC SPECIES?

DOMESTICATION IN AQUACULTURE



Recent and rapid

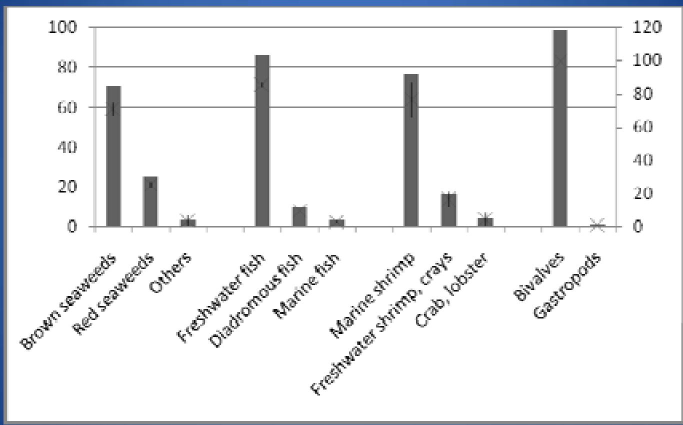
Because aquatic species are easy to reproduce in culture

10 years of R&D to domesticate a species

(Duarte et al 2007)

However, domestication is more than closing the life cycle. It is reproduction from adults reared in culture over several generations (Bilio 2007)

BIOLOGICAL CONSTRAINTS TO AQUACULTURE DOMESTICATION



Proportion of aquaculture production, by weight, of major taxonomic groups over the last 20 years (1988-2008) is given to the nearest whole percent, after FAO (2000, 2009), using only data from production assigned to specific classes

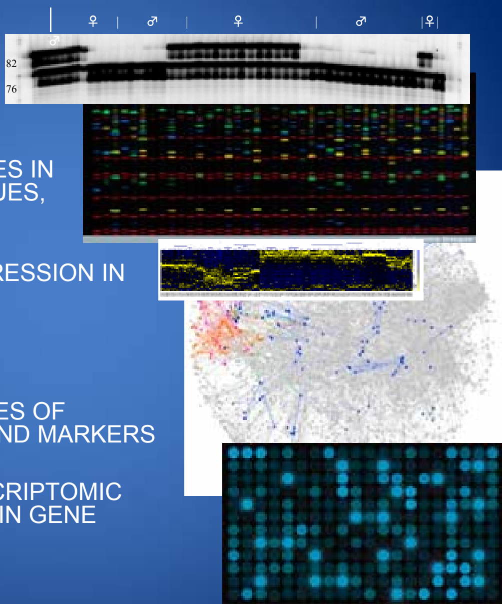
CURRENT STATUS OF DOMESTICATION AND GENETIC IMPROVEMENT IN AQUACULTURE

SELECTIVE BREEDING IS CENTRAL

- IMPROVEMENT IS DEPENDENT ON WELL MANAGED BREEDING PROGRAMS
- THESE DEPEND ON QUANTITATIVE GENETICS APPROACHES
- ESTIMATION OF GENETIC PARAMETERS (HERITABILITY, GENETIC CORRELATION)
- CALCULATION OF BREEDING VALUES

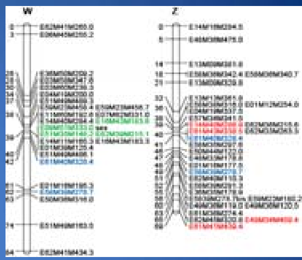
MOLECULAR TOOLS

- SEX IDENTIFICATION
- PARENT TRACKING
- GENE EXPRESSION CHANGES IN DIFFERENT SAMPLES (TISSUES, ENVIRONMENTS)
- RELATED CHANGES IN EXPRESSION IN GENE NETWORKS
- EST LIBRARIES ARE SOURCES OF SEQUENCE INFORMATION AND MARKERS
- MICROARRAYS AND TRANSCRIPTOMIC TOOLS TEST DIFFERENCES IN GENE EXPRESSION
- GENOME SEQUENCING

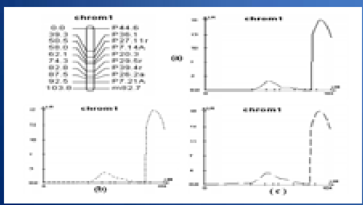


BENEFITS OF MOLECULAR TOOLS

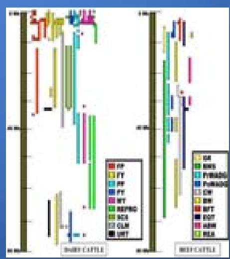
- **MARKER ASSISTED SELECTION**
- **MORE ACCURATE/EFFICIENT BREEDING FOR EXISTING TRAITS**
- **SELECTION ON ADDITIONAL TRAITS** (SEXES WHERE THE PHENOTYPE IS NOT EXPRESSED, CHARACTERS DIFFICULT OR IMPOSSIBLE TO OBSERVE)
- **WHOLE GENOME SELECTION**



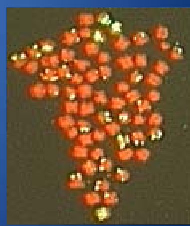
GENETIC MAP



QTLs



PHYSICAL MAP –
large insert libraries



CHROMOSOMES

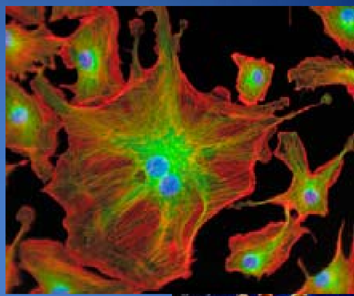
CATTLE EXPERIENCE

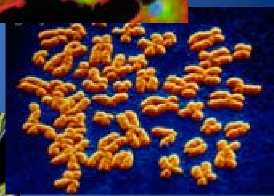
WHOLE GENOME SELECTION

- PEDIGREE FROM SNP ANALYSIS MORE ACCURATE THAN PAPER TRAIL (THOUSANDS OF MARKERS)
- SELECTION MORE ACCURATE EXCLUDING PHENOTYPIC DATA
- POTENTIALLY SAVE COST OF OBTAINING PHENOTYPIC DATA FROM TEST POPULATIONS

CHROMOSOMAL SET MANIPULATION

- SEX MANIPULATION/REVERSAL – TO PRODUCE ONE SEX (E.G. BEST GROWING)
- USE ONLY THE FEMALE GENES - GYNOGENESIS
- USE ONLY THE MALE GENES - ANDROGENESIS
- CREATE CLONAL LINES
- CHANGE PLOIDY - NUMBER OF CHROMOSOME SETS - (E.G. TRIPLOIDY)
- INSERT SPECIFIC GENES





THE SURVEY

SPECIES	Wild pops (sources)	Genetic Selection D/B, Dyr,Glyr,GP	Hybrids C	H	Molecular markers Est,Par,Qtl,LIL,Mar	Genetic maps Type, No	Other genetic technologies Cr, SM, G, A, CL, Pl, GMO
Silver carp, *H. molitrix*	+ (18,50)	B*, ∞, >20, h	-	e	- , PT-, -,-	AM 483	Cr, SMe, Ge,
Grass carp , *C. idella*	+ (17,18)	B*, ∞, - h	-	e	10^{2}, -, -, -,-	Ms 279	Cr, SMe, Ge, Pb*, GMOe
Common carp, *C. carpio*	+ (12,22)	B*, ∞, >40, h,r,gxe	b*	-	10^{4}, - , -, BAC, M	MA 719	Cr, SM*, Ge, A*,CL, Pe, GMOet
Bighead carp, *H. nobilis*	+ (15,18)	B*, ∞, - , -	-	e	-	Am 153	Cre, , Pe
Crucian carp, *C. carassius*	(+) (27)	B*, -, -, -	e	e	-	-	Cre, Gb, A, CL, Pb*, GMOe
Nile tilapia, *O. niloticus*	+ (11)	B*, ∞,>20, h,r,gxe	b*	*	10^{5},- , <10, BAC,-	M 525	SMb*,Ge, - CL, Pe, GMOe,
Atlantic salmon, *S. salar*	+ (10)	B* ,∞,>39, h,r,gxe	-	e	10^{5},-, 10-20, BAC, M	A,MS 527	SMb*,Gb, Pb*,GMOet
Catla, *C. catla*	+ (28,29)	D, ∞, ? , -	-		-	-	Pe, GMOe
Pacific shrimp, *P. vannamei*	+ (4)	B*, ∞,>20, h,gc,r,gxe	-		10^{5}, PT, <10, BAC FOS, -	A,M,S 418	Cr, GMOe
Giant tiger shrimp, *P. monodon*	+ (4)	B*, ∞,>10, h,gc,r,gxe	-		10^{4}, PT, -, FOS, , -	AMo 547	Cr, GMOe
Chinese river crab, *E. sinensis*	+ (5,6,7)	-	-		10^{4}, T, -, -, , -	-	Cr,
Orient. river prawn, *M. nipponense*	+ (18,19)	-	-		-	-	-
Red swamp crawfish, *P. clarkii*	+ (10,11)	-,-,-, h	-		-	-	GMOe
Mud crab, *S. serrata*	+ (20)	D, ∞, -	-		-	-	-
Manila clam, *R. philippinarum*	+ (18,19)	B, ∞, -, -	-		-, PTe, -, -, -	-	Cre, Pe
Pacific cupped oyster, *C. gigas*	+ (9,10)	B*, ∞,>30, h,gc,r,gxe	b*	-	10^{4}, PT, <10, - , M	A,M 119	Cr, Pb*
Constr. tagelus, *S. constricta*	+ (29)	D, ∞, -, -	-		10^{3}, -, -, -, -	-	-
Blood cockle, *A. granosa*	+ (30,31)	D, ∞, -, -	-		-	-	-
Green mussel, *P. viridis*	+ (13,14)	-	-		-	-	-
Yesso scallop, *P. yessoensis*	+ (20,21)	-	-		10^{3}, PTe, -, -, -	Am 166	Pe

Abstracted from major reviews prior to 2000; reviews, data bases and recent literature to present (400+ papers), fishbase, algae base etc.

Number domesticated

	Cultured	Domesticated	
Finfish	**227**	**91**	**40%**
Molluscs	**77**	**30**	**39%**
Crustaceans	**35**	**19**	**54%**
Seaweeds	**>20**	**6**	**30%**
Total	**359**	**136**	**37%**

GENETIC IMPROVEMENT TECHNOLOGIES

	CRYOPRESERVATION SEX MANIPULATION GYNOGENESIS ANDROGENESIS CLONAL LINES PLOIDY MANIPULATION DIRECT GENE TRANSFER (GMO)	SELECTIVE BREEDING CROSS BREEDING SB	 CB	GENETIC MARKERS PARENT TRACKING EST LIBRARIES GENETIC MAPS QTLs LARGE INSERT LIBRARIES MICROARRAYS
Finfish (227)	68	24	42	44
Molluscs (77)	21	18	2	15
Crustaceans (35)	10	6	0	6
Seaweeds (20)	2	2	2	2
TOTAL (76)	40 **(53%)**	22 **(29%)**	19 **(25%)**	37 **(33%)**
TOTAL (359)	101 **(28%)**	50 **(14%)**	46 **(13%)**	67 **(19%)**

GENETIC PARAMETERS

HERITABILITY: good (0.3-0.5) for growth, some disease responses, aspects of condition and reproduction. Poor (<0.1) for other diseases.

GENETIC CORRELATIONS: high (0.8-0.9) between size, weight and growth characters. Variable, sometimes negative between disease tolerance and size/growth or reproductive characters.

RESPONSE TO SELECTION: , good, reflecting heritability, sometime >10-15% per generation, but averaging around 5% for reasonable selection intensities in finfish, molluscs, crustaceans and seaweeds.

GENOTYPE BY ENVIRONMENT INTERACTION: GxE variable, low for key species tested [one strain does well in a range of environments].

A DEEPER LOOK

MOLECULAR MARKERS, GENETIC MAPS, and QTLs

- EST libraries 1000-10,000 few >100,000

  Agricultural Sp. 1 million

- Maps most <500 markers, only 1 >1,000

  Agricultural Sp. >10,000

- AFLP markers dominant and do not provide a transferable platform

- Density of markers low
- QTLs few <10 for most spp.
- Precision poor >3 cM
- 1 used in marker assisted selection (salmon disease)

A DEEPER LOOK

OTHER TECHNOLOGIES

Limited penetration

Triploidy:

Salmonids (sterility)

Oysters (sterility, better growth and condition)

Gyn/Androgenesis in carp breed formation/ conservation

Clonal lines 3 spp finfish (carps)

GMOs 2 in trials

Only 1 near regulatory approval and production ready (Atlantic salmon)

A DEEPER LOOK

SELECTIVE BREEDING PROGRAMS

Few of significant scale:

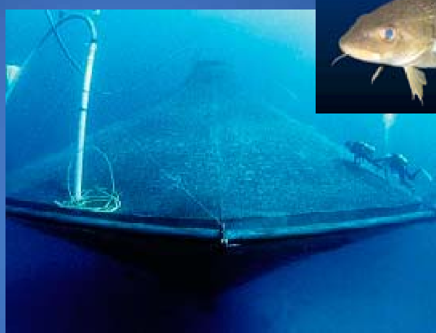
10-12 finfish

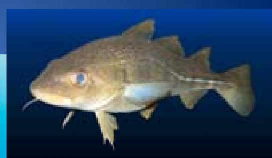
3 mollusc

3 crustacean

Need integrated rearing and production technologies, distribution networks

All have depended on a mix of: government, private sector, NGOs, sustained investment





SALMONIDS
TILAPIA
CATFISH
CARPS
SEA BASS
SEA BREAM
SHRIMPS
OYSTER
COD (developing)

INTERNATIONAL EXCHANGE AND COLLABORATION

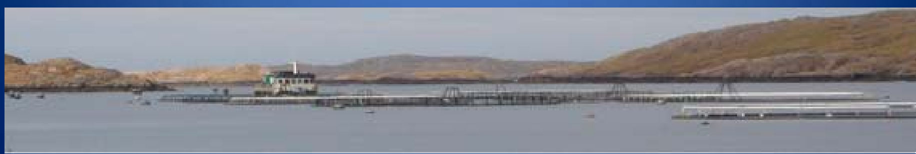
NEED EFFECTIVE MECHANISMS OF EXCHANGE AND BENEFIT SHARING

UTILISATION OF GENETICS IN AQUACULTURE

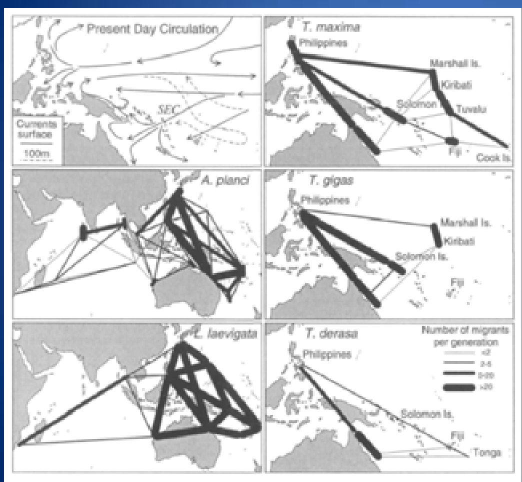
- Twenty years ago <5% of aquaculture production was from genetically improved organisms
- Today it is much more (but the actual amount is difficult to estimate given lack of statistics on strains and market penetration)

Estimates range from 38% to 73% of all production and 7% - 76% of finfish
(depends on proportion of carp production assumed from improved stock - the lower figures are more realistic)

Upper limits of 15% of mollusc, 67% of crustacean, and 99% of seaweed
More realistic limits of <10% of mollusc, 45% of crustacean



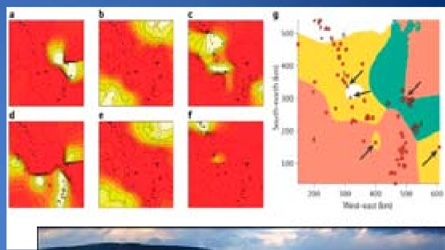
WILD GENETIC STRUCTURE



High genetic variation
Cryptic species
Geographic variation
Local adaptation

EVOLUTIONARY GENETICS

- IDENTIFYING STOCKS, ESCAPEES
- TRACKING GENE FLOW AND ADAPTATION
- UNDERSTANDING RECRUITMENT, EFFECTIVE POPULATION SIZE, GENE EXCHANGE



- Variable effects of introduction
- Variable effects of restocking
- Evolution of a stock in culture

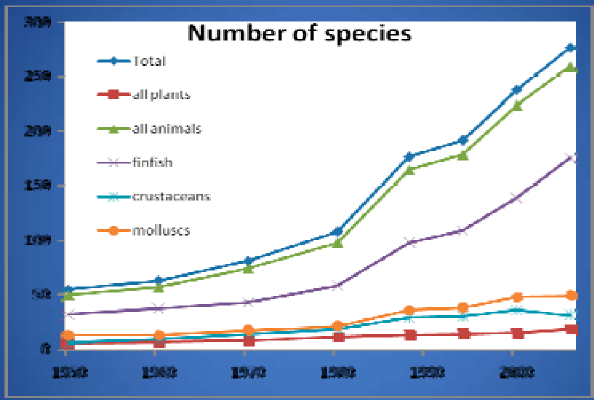
WILD GENETIC RESOURCE

	Cultured	Genetic data on wild stock	
Finfish	**227**	**162**	**72%**
Molluscs	**77**	**65**	**84%**
Crustaceans	**35**	**28**	**80%**
Seaweeds	**>20**	**6**	**30%**
Total	**359**	**261**	**73%**

BUT: many assay few populations, use poor markers, and assess diversity level only.

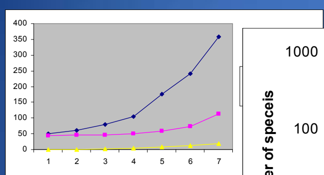
In depth studies with deep interpretation of population evolution and/or deep investigation of interaction with cultured stocks are few.

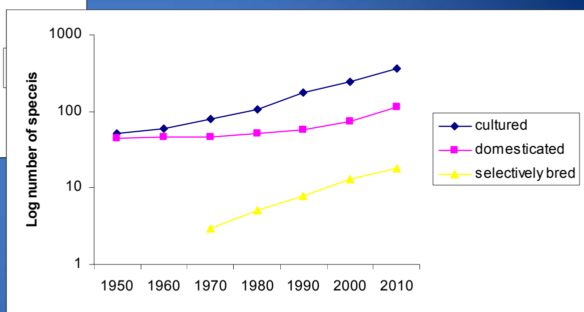
CULTURED SPECIES



Number of species cultured in each of the major taxonomic groupings for selected years between 1950 and 2006, where production was recorded for FAO statistics in that year (FAO Fish Stat Plus 2009).

DOMESTICATION AND GENETIC IMPROVEMENT





Rate: suggests 30 years for domestication, >60 for genetic improvement

SUSTAINABLE AQUACULTURE

The responsible use and conservation of aquatic biodiversity for sustainable aquaculture requires

- the use of efficient mechanisms for production: species choice, integrated technologies global cooperation; clarity of goals
- Use of technologies to minimise environmental and genetic impact: containment, reduce/eliminate gene exchange, sterility;
- Conservation restocking; gene banking.

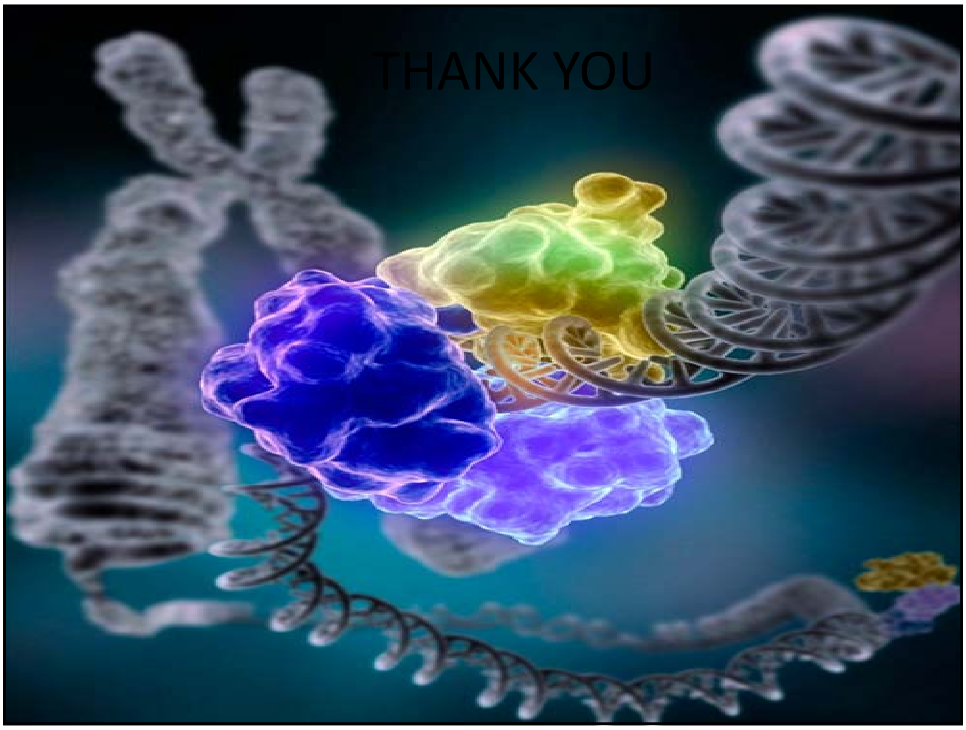
RECOMMENDATIONS

1. Improve information on the state of aquatic genetic resources including wild populations, cultured strains, rate of advance of selective breeding programs, and of impacts on wild populations including the effectiveness of technologies designed to mitigate such effects.

2. Increase investment in genetic technology development with focused development of the well-founded selective breeding programs that provide the necessary foundation for application of a variety of other technologies, and their use in production.

3. Encourage exchange among the diverse groups needed to for better understanding of aquaculture and conservation activities, improved technology transfer, and effective investment and benefit sharing.

4. Continue dissemination of sound resource material and advice already available.



DOMESTICATION AND GENETIC SELECTION

FOR SPECIES GIVING 99% OF PRODUCTION

	Domesticated	Genetic Parameters Estimated	Genetically Improved	Cross breeding	Inter-species hybrids
Finfish (44)	29	17	14	8	15
Molluscs (19)	8	5	4	1	0
Crustaceans (11)	8	6	4	0	0
Seaweeds (2)	2	2	2	2	2
TOTAL (76)	47 (62%)	30 (39%)	24 (32%)	11 (14%)	17 (22%)

MOLECULAR GENETIC TOOLS

FOR SPECIES GIVING 99% OF PRODUCTION

	EST libraries	Parent tracking	QTLs	Large insert libraries	Micro-arrays	Genetic maps
Finfish (44)	12	9	9	10	7	17
Molluscs (19)	6	4	2	0	2	4
Crustaceans (11)	5	4	2	4	0	4
Seaweeds (2)	2	2	2	0	0	0
TOTAL (76)	25 (33%)	19 (25%)	15 (20%)	14 (19%)	9 (12%)	25 (33%)

OTHER GENETIC TOOLS

FOR SPECIES GIVING 99% OF PRODUCTION

	Cryo-pres'n	Sex manip'n	Gyno-genesis	Andro-genesis	Clonal lines	Ploidy	GMO
Finfish (44)	10	9	12	4	4	18	14
Molluscs (19)	4	0	0	0	1	7	1
Crustaceans (11)	5	1	0	0	0	2	4
Seaweeds (2)	2	0	0	0	2	0	0
TOTAL (76)	21 (28%)	10 (13%)	12 (16%)	4 (5%)	7 (9%)	27 (36%)	19 (25%)