International Conference on Science and Technology for Sustainable Development 2006

< Session 4 : Creating Innovation Based on Science and Technology >

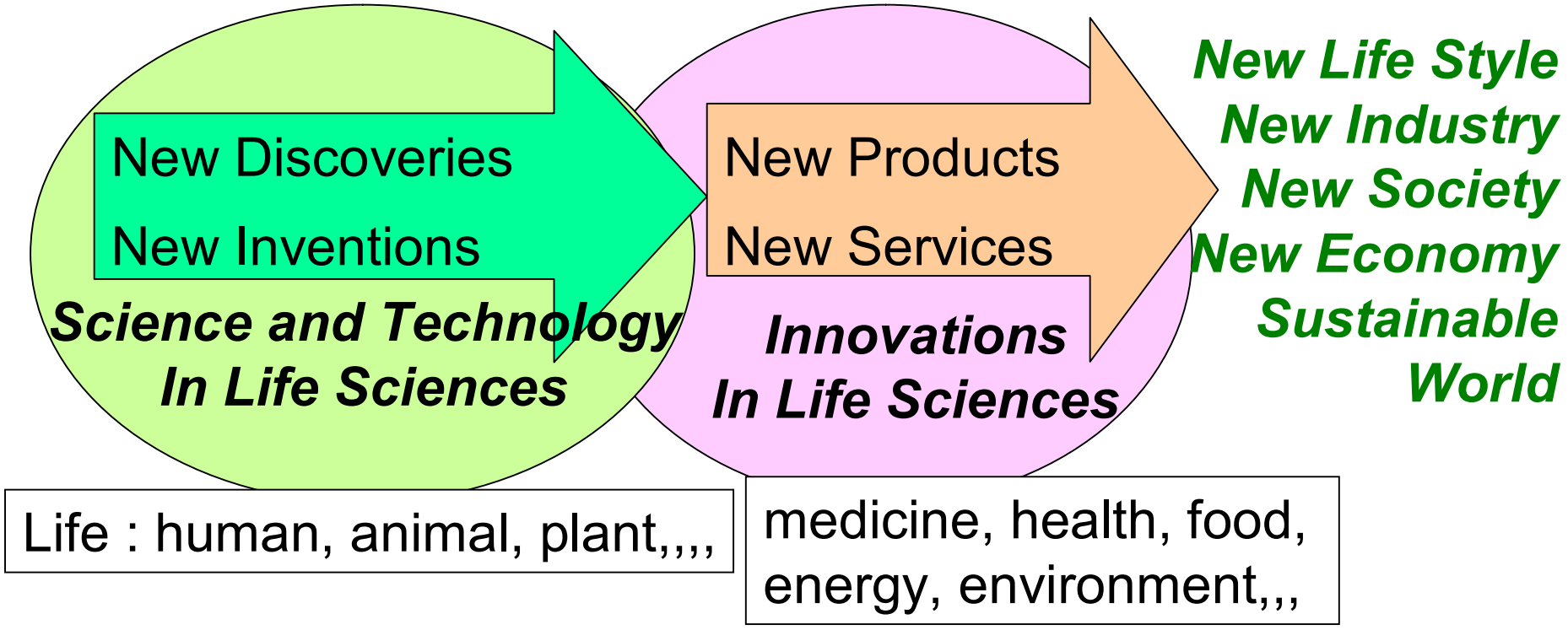
Innovation in the Life Sciences

TAKEDA Kenji

Executive Director,
RIKEN
Japan

September 9, 2006

The life sciences are the driving force for innovation in the 21st century



Death Valleys in the Life Sciences




SPring-8 NMR Supercomputer Auto-Crystallizing Robot

Research Facilities in RIKEN

The Kobe Medical Industry Cluster

Advanced Protein Research

Overcome Refractory Disease Drug Development

Diagnostic Method・Device

Preventive Medicine・Service

Robot Technology

Super computer

NMR

Radiation Light

Valley of Disciplines

Valley of Regulations

TR

Clinical Trial

Protein Research

Molecular Biology

Biochemistry

Chemistry

Engineering

Physics

Math

Medical Science

Biology

Industries

Government

Research Institute

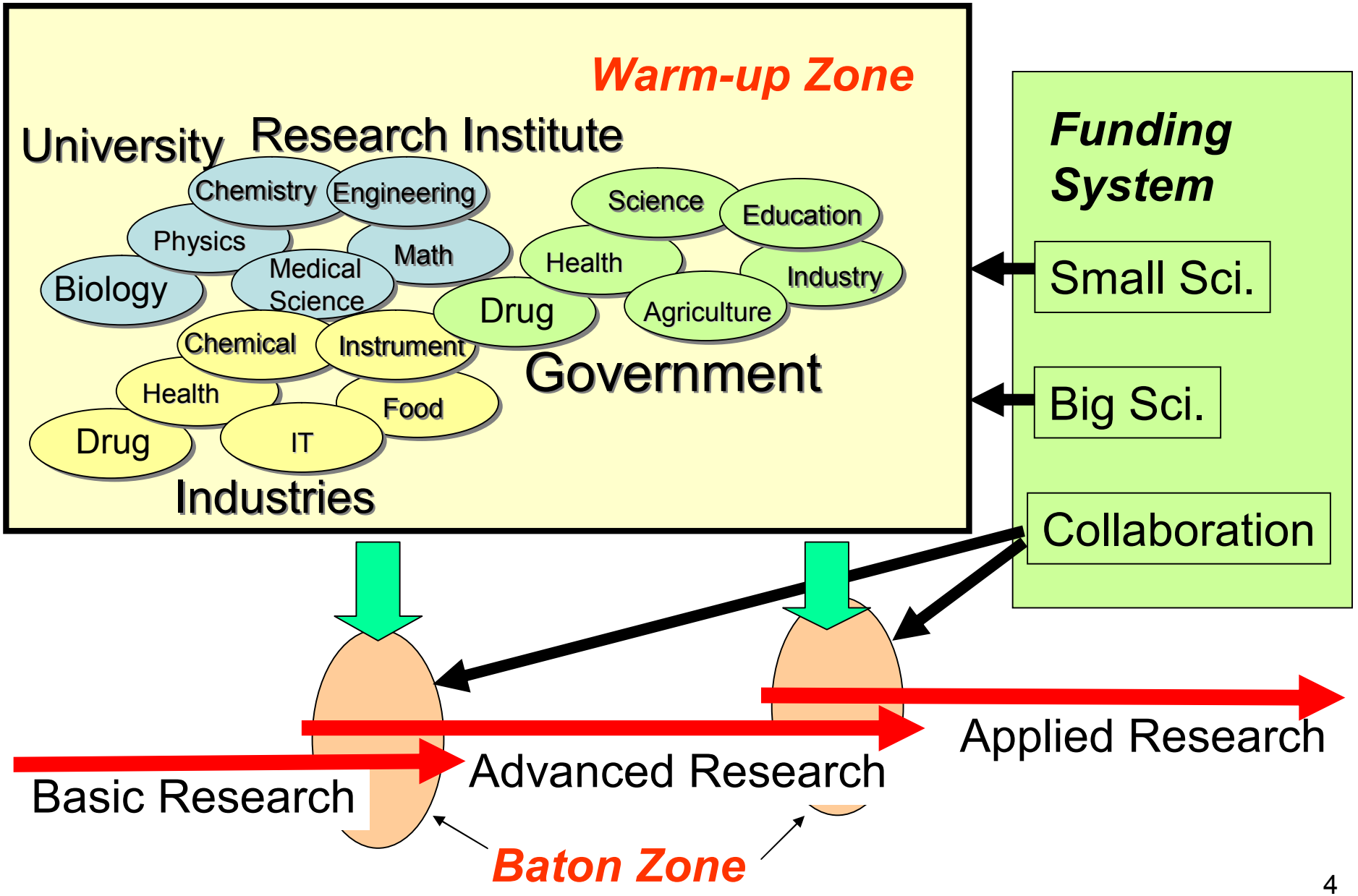
University

Applied Research

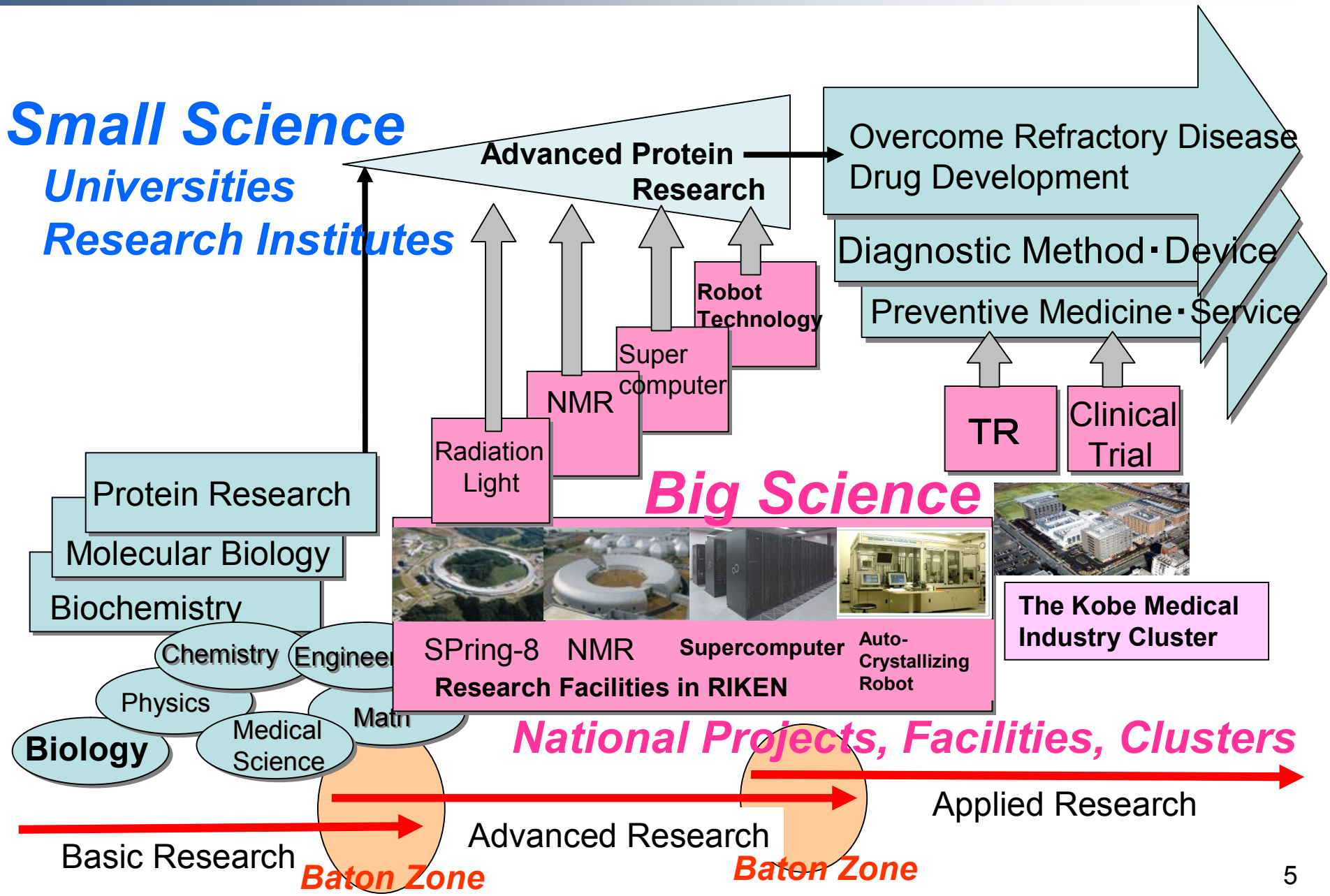
Advanced Research

Basic Research

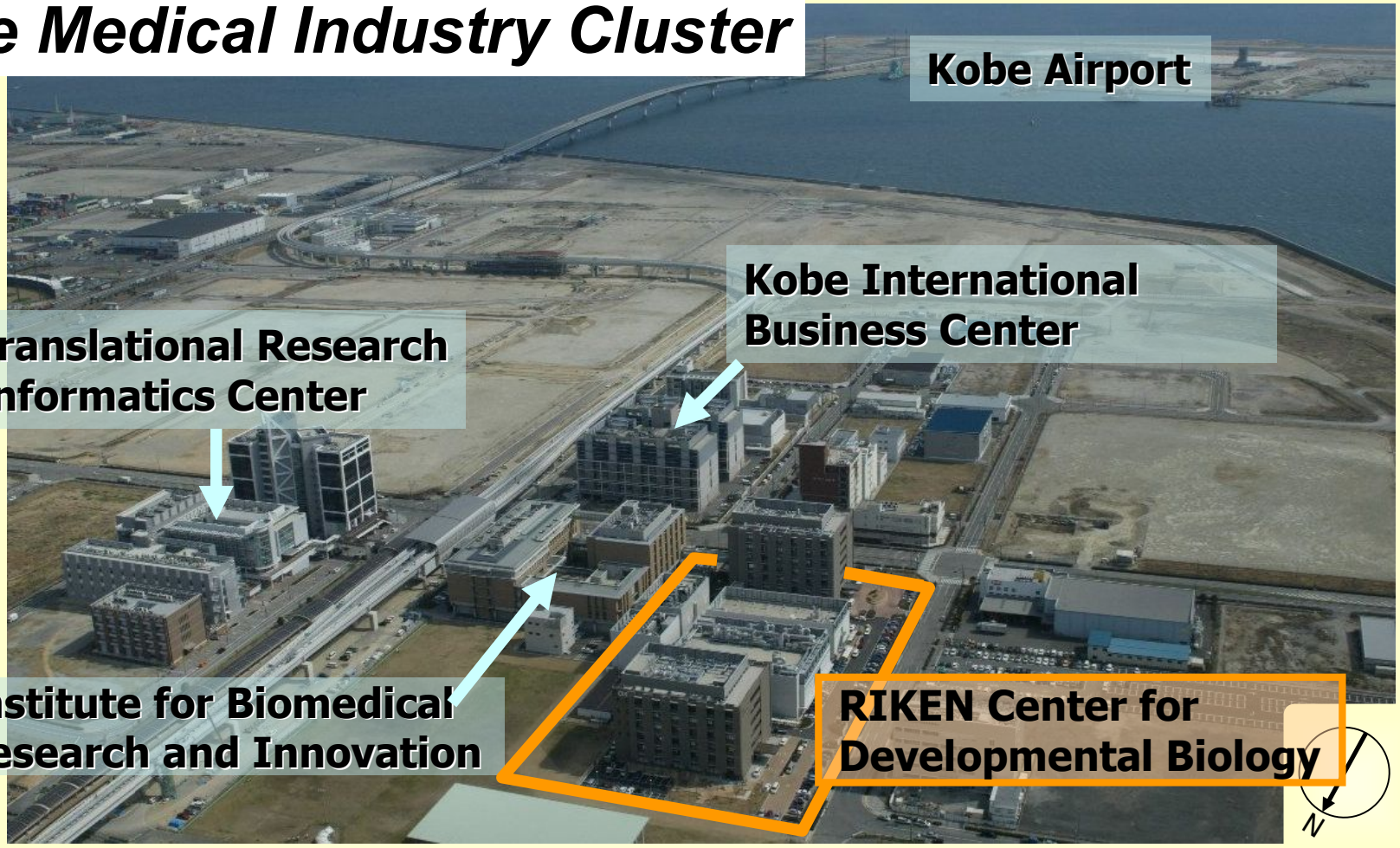
Warm-up Zones and Baton Zones



Small Science and Big Science



Kobe Medical Industry Cluster



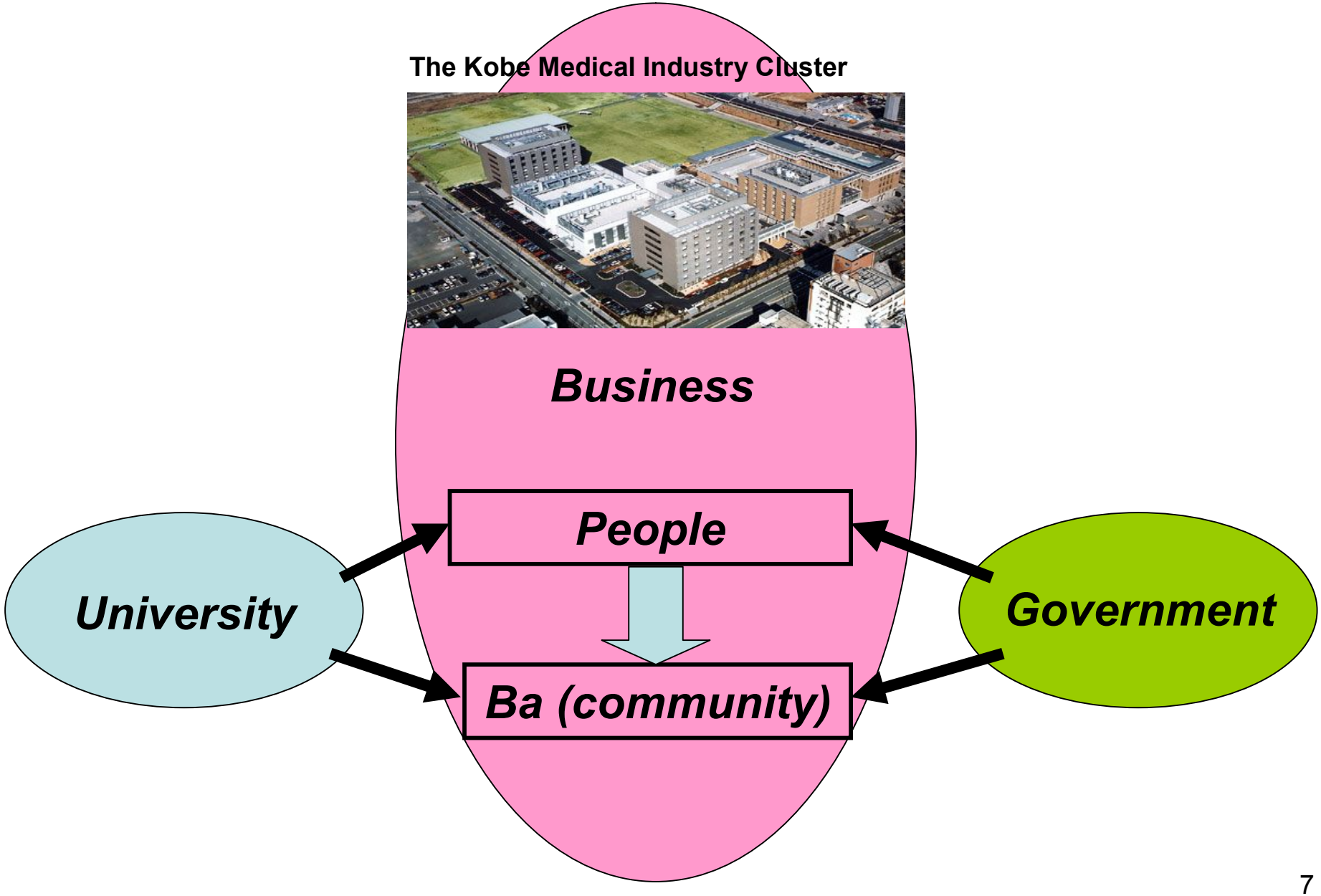
Kobe City **Kobe Citizens Hospital**

Kobe Univ., Kyoto Univ., Osaka Univ.

Big Enterprises **Small Ventures**

As of April 2005

Clusters for Innovation (2)



International Cooperation and Partnership (1)

Major Scientific Contributions of the RIKEN GSC since 2004

Completion of Human Genome Sequence

Chromosome 11 (Nature, March 2006), 18 (Nature, Nov. 2005)

Comparative Genomics

Human-Chimp Chr.21 (Nature, May 2004), Chr.Y (Nature, Dec. 2005)

Non-coding RNA/Transcriptome Complexity

Discovery of "RNA continent" (Science, Sept. 2005)

Complexity of Promoter Region (Nature Genetics, April,2006)

Protein 3D Structure

2500 proteins will be analyzed by the end of 2006

Mutant Mice

Public Release of 223 Lines of Mice of Interesting Phenotypes (2006)

International Cooperation and Partnership (2)

The International Hapmap Project

Contribution in the Project

Canada	**10.1%**	**2, 4p**
China	**9.5%**	**3, 8p, 21**
Japan	**24.3%**	**5, 11, 14, 15, 16,17,19**
UK	**23.7%**	**1, 6, 10, 13, 20**
USA	**32.4%**	**4q, 7, 8q, 9,12, 18, 22, X,**

Illumina	16.1
UCSF/WashU	2.0
MIT	9.7
BCM	4.6

The RIKEN SRC generated 24.3% of the genotyping data.

The largest contribution among the research centers that participated in the project.

Vol 437|27 October 2005|doi:10.1038/nature04226 nature

ARTICLES

A haplotype map of the human genome

The International HapMap Consortium*

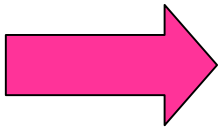
Inherited genetic variation has a critical but as yet largely uncharacterized role in human disease. Here we report a public database of common variation in the human genome: more than one million single nucleotide polymorphisms (SNPs) for which accurate and complete genotypes have been obtained in 269 DNA samples from four populations, including ten 500-kilobase regions in which essentially all information about common DNA variation has been extracted. These data document the generality of recombination hotspots, a block-like structure of linkage disequilibrium and low haplotype diversity, leading to substantial correlations of SNPs with many of their neighbours. We show how the HapMap resource can guide the design and analysis of genetic association studies, shed light on structural variation and recombination, and identify loci that may have been subject to natural selection during human evolution.

October 27, 2005

International Cooperation and Partnership (3)

Sharing new knowledge
- Genome sequence
- Protein structure
-

Exchange materials and information
- Bio resources
- Clinical data
-

Pro-Patent  ***Pro-Innovation***