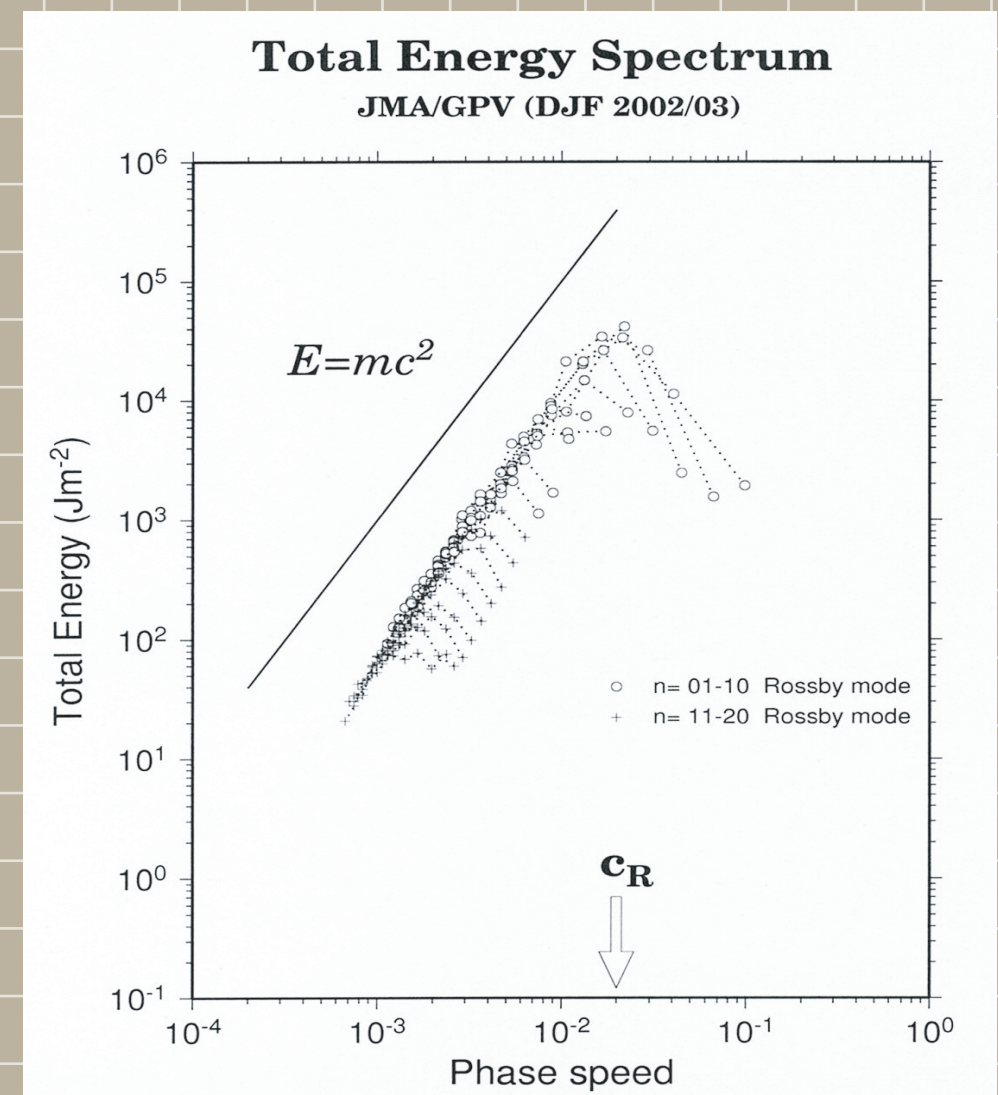# Division of Global Environment and Biological Sciences
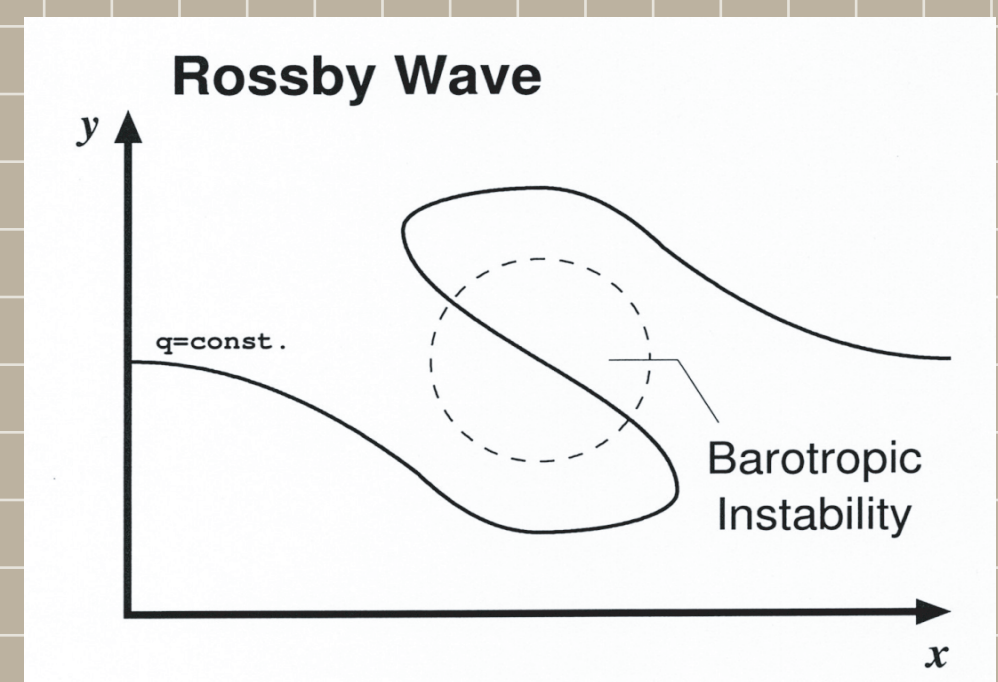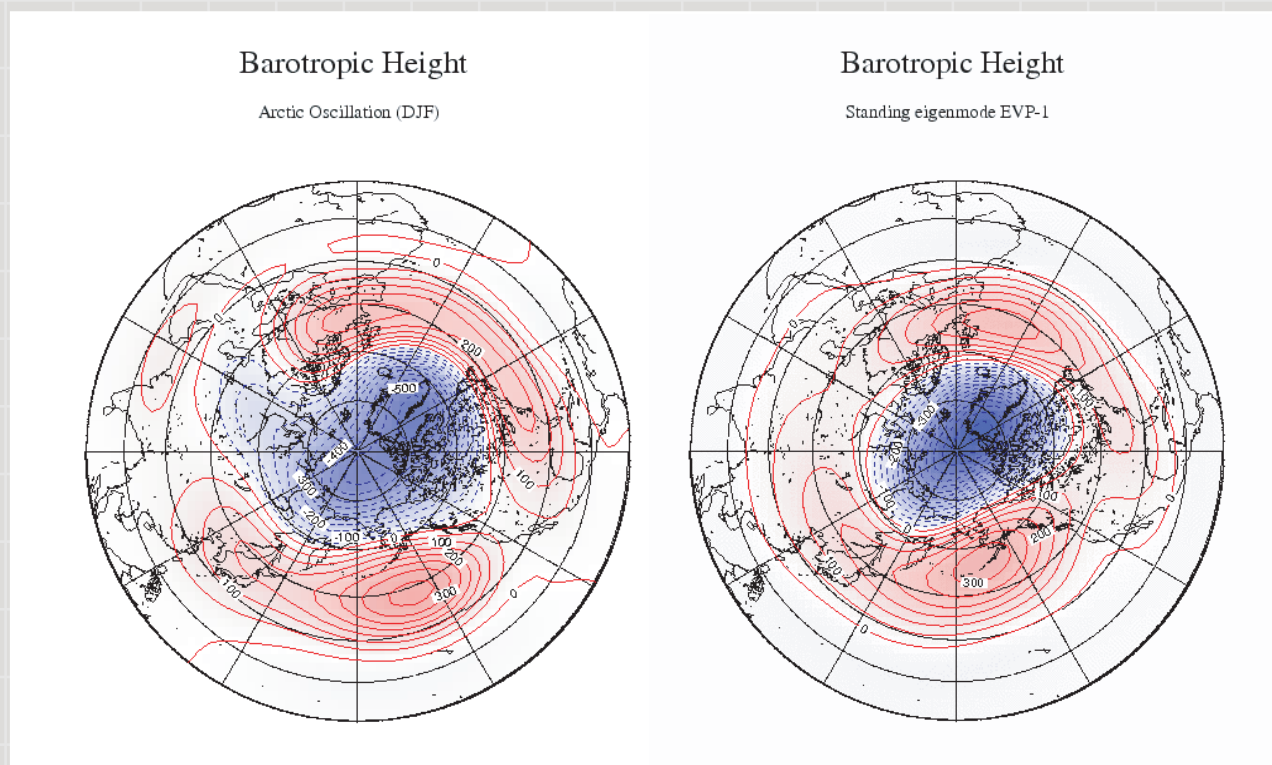
Energy Spectrum of the Global Atmosphere

► Energy spectrum of the large-scale atmospheric motions is examined in the framework of the 3D normal mode decomposition. The representative horizontal scale of disturbance is measured by the phase speed of Rossby waves c. According to the result of the observational analysis, we obtain a characteristic energy spectrum with its peak at the spherical Rhines speed c_R, and the slope can be derived from the criterion of Rossby wave breaking, $\partial q / \partial y < 0$, where q is potential vorticity. With a proportional constant m, describing a total mass of the atmosphere for unit area, we have shown that the barotropic energy spectrum of the general circulation can be represented as $E = mc^2$.

Total Energy Spectrum
JMA/GPV (DJF 2002/03)

$E = mc^2$

Total Energy (Jm^2) vs Phase speed

○ n= 01-10 Rossby mode
• n= 11-20 Rossby mode

c_R

Arctic Oscillation explained by singular eigenmode

► Most dominant low-frequency variability of the global atmosphere is the Arctic Oscillation (AO). Abnormal weather and global warming often appear with the characteristic pattern of the AO. We have shown that the AO eigenmode of the global is an atmosphere with zero eigenvalue, which can be excited by arbitrary steady forcing.

Barotropic Height
Arctic Oscillation (DJF)

Barotropic Height
Standing eigenmode EVP-1

Rossby Wave

q=const.

Barotropic Instability

Phylogenetic Inference on the Universal Tree of Life

► The central focus of our research is to gain insight into origin and early evolution of eukaryotes, the most important open problem in evolutionary biology. One of the goal of this research is to reconstruct the Universal Tree of Life including diverse organisms on the Earth, based on molecular phylogenetic approach. Since a reliable phylogenetic inference simultaneously requires numerous genes and species, a large scale scale data analysis using high performance computers plays a key role in our study.

| 1 species

Maximum likelihood tree of eukaryotes

Analysis was performed by using 22 protein genes with more than 6,000 amino acid positions and the tree was selected as the best tree among 10,395 possible alternatives for 8 taxonomic groups.

Euglenozoa Heterolobosea [2.5]

a (59)

Alveolata Stramenopiles [4.1]

b (47)

Plantae [4.0]

c (50)

Amoebozoa [2.5]

(45)

(BPs) [averaged No. of species]

Opisthokonta [10.3]

Trichomonas vaginalis

Giardia intestinalis

(86)

Parabasala [1.1]

Representative organisms

Diplomonadida [1.3]

Outgroup [4.6]

0.1 substitutions/sites