

## Influence of major hydraulic projects on saltwater intrusion in the Yangtze River estuary

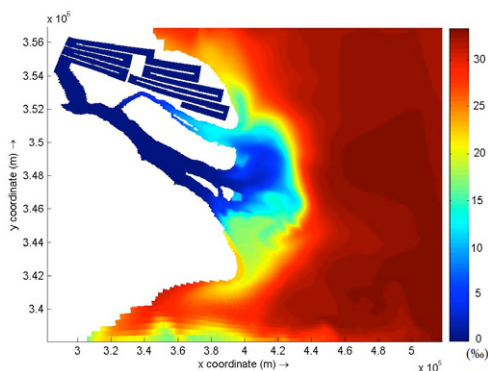
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To understand the influence of the Three Gorges Project (TGP) and South-to-North Water Diversion Project (SNWDP) on saltwater intrusion in Yangtze River estuary, a depth-averaged 2D numerical model, loosely coupled with geographic information system (GIS), is developed to compute and analyze the hydrodynamics and salinity field about the estuary water. The model is validated through observed data. Then combined simulations under multiple hydrologic conditions considering different regulation schemes of the hydraulic projects as well as varied tidal ranges in the outer sea are carried out. Furthermore, the numerical output is rendered dynamically in GIS environment, and the distribution behaviours and variation trend of salinity are analyzed. The result shows that the salinity of north branch is higher than that of south branch (fig.1), and the change of salinity is mostly affected by river discharge. The maximum water diversion scheme of 1000 m<sup>3</sup>/s of SNWDP will aggravate saltwater intrusion, while the increased discharge of TGP in dry season will restrain saltwater intrusion in the estuary.



**Figure 1:** simulated salinity field of Yangtze River estuary in dry season

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## Methodology and foreground of metalloprotein

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Metalloproteins is proposed as a new omics to follow genomics, proteomics and metabolomics. Researchs on metalloproteins not only answer the question of the chemical compose of metals and proteins, but also pioneer a new way for probing into the mechanisms of life substances such as metalloproteins in life activity. In Metalloproteins, metalloenzymes and othe metalcontaining biomolecules are defined as "Metallomes". Syntheses and metabolic functions of genes and proteins cannot be performed without the aid of various metal ions and metalloproteins. The main research targets of metallomics are to identify the metallomes and elucidate their biological or physiological functions in biosystem. Chemical speciation analysis is a key technology in metalloproteins study.

Some new trends in the study of metalloproteins and metalloenzymes have been described from aspects of metal ions-related diseases (especially the neurodegenerative diseases), the roles of metalions in folding, aggregation and assembly of proteins, the design and reconstruction of metallochaperons and metalloproteins, interactions between metalloproteins and DNA.

Now, metallomics is focused on analytical techniques and methods, particularly the so-called hyphenated techniques which combine a high-resolution separation technique (gel electrophoresis/laser ablation, chromatography or capillary electrophoresis) with a highly sensitive detection method as elemental (inductively coupled plasma, ICP) or molecular (electron spray ionization (ESI) or matrix-assisted laser desorption/ionization (MALDI)) mass spectrometry, or nuclear X-ray fluorescence/absorption spectrometry. The applications of these advanced analytical methods in the identification of metallo-/phosphor-/seleno-proteins, probing of relationships between structure and function of metalloproteins, and study of clinically used metallodrugs will be selectively outlined, along with their advantages and limitations.