

## Enhancing Syngas Conversion Selectivity with Dynamic Confinement in OXZEO Composite Catalysts

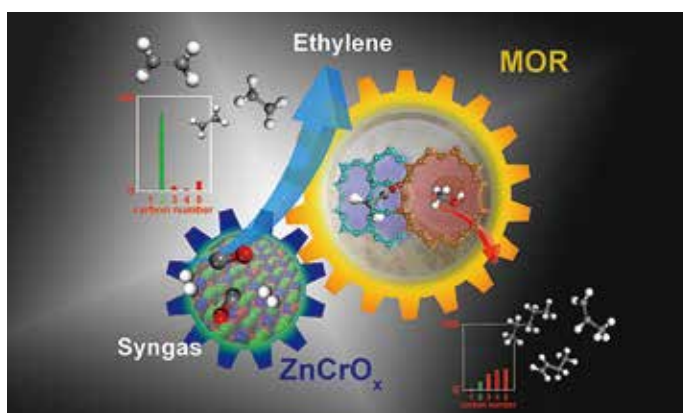
Scientists from the Dalian Institute of Chemical Physics (DICP) of the Chinese Academy of Sciences have reported for the first time the induction period in syngas conversion over an OXZEO composite catalyst, ZnCrO<sub>x</sub>-SAPO-17. During this period, a dynamic confinement develops within the SAPO-17 cage, which enhances the selectivity of ethylene and suppresses that of C<sub>4+</sub> hydrocarbons.

The study entitled “*Dynamic confinement of SAPO-17 cages on the selectivity control of syngas conversion*” was published in *National Science Review* on July 26.

Converting syngas, a mixture of hydrogen and carbon monoxide, into liquid fuels has been the focus of much academic and industrial research in the field. One promising alternative to traditional Fischer-Tropsch synthesis (FTS) is the OXZEO bifunctional catalyst concept, which offers a more effective solution to the challenge of selectivity encountered in FTS.

The OXZEO process, which involves the use of SAPO-34 zeolite and ZnCrO<sub>x</sub> oxides, has been shown to convert syngas into mixed light olefins (C<sub>2</sub><sup>=</sup>-C<sub>4</sub><sup>=</sup>) with a selectivity of up to 80%. The high selectivity of this process is due to the disconnected CO/H<sub>2</sub> activation and C-C bond coupling on the two spatially separated active sites.

The selectivity of the OXZEO process can be



Mordenite zeolite (MOR) with 8-member-ring pores (blue-colored) favors ethylene formation with high selectivity. (Image by JIAO Feng)

further modulated by the shape selective zeolitic pores and the morphology of the zeolites. For instance, zeolites with 8-member ring pores favor the synthesis of mixed light olefins, while zeolites with 10–12-member ring pores favor gasoline ranged hydrocarbons. Additionally, the channel structure and morphology of the zeolites can fine-tune the hydrocarbon distribution.

These findings demonstrate the potential of the OXZEO process as a promising technology for the efficient and clean utilization of carbon resources. Further research is needed to fully realize the potential of this technology and to find practical applications for it.

## Boosters Show Promise Against Omicron Variant

A study published in the July 21 issue of the *New England Journal of Medicine* has found that the current vaccines against the coronavirus disease 2019 (COVID-19) may not be as effective against the omicron variant and its subvariants (doi: 10.1056/NEJMc2206900).

In this study, a research team led by George F. Gao at the Institute of Microbiology of the Chinese Academy

of Sciences (IMCAS) assessed the neutralizing antibody levels in individuals who received either inactivated virus vaccines or the protein-subunit vaccine ZF2001. They found that all vaccinated groups had lower neutralizing antibody levels against the Omicron variant compared to the prototype strain. The findings indicate substantial immune escape for the omicron





they have higher hemoglobin content and red blood cell count. They have bigger lungs and hearts than those of age-matched domestic cattle. They also have more abundant blood vessels in the lung tissue. Yet, what exact genomic changes enable their high-altitude adaption remains to be explored.

Next-generation sequencing has proven to be a powerful tool for studying genomic changes. However, the limitation of the genome assembly using short reads makes it impossible to accurately detect the genomic changes that come at a big scale, such as deletions, insertions, duplications, and inversions.

Using the Nanopore technique for long reads and the Hi-C technology for genome assembly, the team successfully get two long-read genome assemblies of wild and domestic yak.

By comparing these long-read genomes with a high-quality reference genome of domestic cattle, researchers found that many genomic changes lie in

the noncoding sequences, including promoter and untranslated regions (UTR), which usually regulate the expression of nearby genes. They suggested that the yaks may benefit from the genomic changes in the promoters of hypoxia-related genes.

They also identified a yak-specific endothelial cell subtype using single-cell transcriptome sequencing, a technique widely used for grouping cells with similar mRNA expression profiles. These unique cells can enhance the medial thickness of micro-vessels and the formation of elastic fibers in yak lungs.

Researchers believe that their findings would have important implications for understanding the physiological and pathological responses of large mammals and humans to hypoxia.

“These high-quality genomes and single-cell RNA-seq data serve an important source for future research on bovine species,” say the researchers.