DEPENDENCE OF DRAWDOWN PRESSURE ON THE HYDRATE REFORMATION DURING METHANE HYDRATE PRODUCTION AND ITS INHIBITION WITH KINETIC HYDRATE INHIBITORS

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ABSTRACT
Methane gas from marine hydrate deposits can be produced by one or a combination of three methods: depressurization, thermal stimulation, and injection of inhibitors. Since residual hydrate structures known as hydrate precursors will exist in the water phase after dissociation, the risk of hydrate re-formation has to be evaluated during the production and transportation of methane gas from natural gas hydrate deposits. One viable option to avoid hydrate re-formation is the injection of hydrate inhibitors. However the selection of chemicals must be done carefully, as its impact on the production economics can be enormous. The use of kinetic hydrate inhibitors (KHI) has recently become popular. These inhibitors are generally water soluble polymers and delay initial hydrate nucleation. The required concentration for KHI is commonly in a range of 0.5~5 wt%, which is much lower than those of conventional hydrate inhibitors, e.g. glycols of 30~60 wt%. Although the use of KHI in conventional gas production has become more widespread, its applicability to methane hydrate production has not yet been studied thoroughly, especially in the presence of residual hydrate precursors. In this work, we conduct experiments to test the performance of KHI on hydrate re-formation during the production and transportation of methane gas from marine hydrate deposits. The risk of hydrate re-formation in methane hydrate production system is also discussed.

Keywords: methane hydrates, production, dissociation, re-formation, kinetic inhibitors

INTRODUCTION
Gas hydrates are crystalline compounds formed when guest molecules are incorporated in host cages formed by water molecules through hydrogen bonding [1]. Low molecular weight gas molecules, such as methane and carbon dioxide, are captured into these cages, and each hydrate lattice consists of at least two types of polyhedral cages. Three distinct structural families, termed structure I, II, and H, are known; they show distinct structural characteristics such as cage types, distribution of guest molecules, and stability conditions.

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