Chemometric Recognition of Genetically Distinct Oil Families in the Los Angeles Basin, California

K.E. Petersa,b*, T.L. Wrightc, L. Scott Ramosd, J.E. Zumbergee

a Schlumberger Information Solutions, Mill Valley, CA 94941
b Department of Geological & Environmental Sciences, Stanford University, Palo Alto, CA 94305
c Chevron Corporation (retired), San Anselmo, CA 94960
d Infometrix, Inc., Bothell, WA 98011

*eGeoMark Research, Houston, TX 77095

*peters2@slb.com

Introduction

The prolific Los Angeles basin is a classic transform-margin basin that may be the most petroliferous province on Earth per volume of sedimentary fill. Since Brea-Olinda in 1880, 67 fields were discovered, including three super-giants at Wilmington, Long Beach, and Huntington Beach. Little exploration has occurred since the early 1970s, although significant potential likely remains in deep, especially offshore areas. Because most exploration in the basin occurred prior to the advent of modern geochemical methods, genetic relationships among the various petroleum accumulations and their source rocks remain speculative.

This paper uses source-related biomarker and isotope ratios to evaluate genetic relationships among ~150 crude oil samples from the basin. The extent of biodegradation for each sample was assessed in order to identify a “training set” where the source-related ratios are unaffected and can be used to identify genetic oil families. The training set was used to create a chemometric decision tree (multivariate statistics) that allows automated genetic classification of additional oil or source-rock extracts that might be collected, including samples where some of the source-related ratios were altered by biodegradation. The chemometric analysis also allows quantitative assessment of the degree of certainty for each genetic assignment. Finally, the geochemical data and stratigraphic occurrence of each oil family were used to infer their source-rock organofacies.

Methods

Procedures are similar to those in Peters et al. (2007). Asphaltenes were removed from the oil samples using n-hexane. Saturate and aromatic hydrocarbons were separated by column chromatography using hexane and dichloromethane, respectively. Stable carbon isotope ratios were determined using a Finnigan Delta E isotope ratio mass spectrometer. C15+ saturated biomarkers were analyzed on a Hewlett-Packard (HP) 5890 gas chromatograph interfaced to a HP 5971 mass spectrometer. The HP-2 column (50 m x 0.2 mm id, 0.11-mm film thickness) was programmed from 150 to 325°C at 2°C/min. Mass spectrometry was in SIM mode for m/z 177, 191, 205, 217, 218, 221, 231, and 259. Response factors were determined by comparing m/z 221 for a deuterated standard (d4-C29 20R sterane; Chiron Laboratories, Norway) with terpane (m/z 191) and sterane (m/z 217) standards.

Samples excluded from the training set included: (1) heavily biodegraded oils (rank 5 or more on the 1–10 scale of Peters and Moldovan, 1993), and (2) highly mature condensates, where biomarkers are low (e.g., <10 ppm steranes). Source-related biomarker and carbon isotope ratios for the remaining 112 non- or mildly biodegraded oil samples were used to define the training set.

Chemometric (multivariate statistics) software (Pirouette and InStep, Infometrix, Inc.) was used to create a multi-tiered decision tree that identifies genetic oil families. We used geochemical expertise and principal component loadings to select 24 source-related parameters that differentiate the samples (details of the method are described in Peters et al., 2005, 2007).

Results and discussion

Hierarchical cluster analysis and the decision tree identify six tribes and 12 genetic oil families (Figure 1).

Introduction

The families within each tribe have different bulk properties (e.g., API gravity, sulfur, and metal content) that were previously explained as mainly due to secondary processes, such as biodegradation or thermal maturity (e.g., Jeffrey et al., 1991). However, the decision-tree classification is based on differences in genetic properties that reflect distinct petroleum systems.

The oil families occur in different reservoirs from different parts of the basin, consistent with origins from distinct pods of active source rock (Figures 2-3). The source-rock depositional environment for each oil family can be inferred using biomarker and isotope ratios (e.g., Peters et al., 2005). Carbon isotope data for saturate and aromatic hydrocarbons in the samples suggest Miocene marine source rocks. Tribes 1-2 straddle the Central Trough, occur mainly east of the Newport-Inglewood Fault Zone (NIFZ), and show evidence of clay-rich source rock deposited under suboxic conditions with elevated higher-plant and angiosperm input. Unlike tribes 1-2, tribes 3-6 occur west of the NIFZ and show evidence of more distal, clay-poor source rocks deposited under anoxic conditions. Tribes 3-5 include the giant Wilmington, Long Beach, and Huntington beach fields, which account for ~60% of the conventional reserves in the basin.

Figure 1. Hierarchical cluster analysis dendrogram based on 24 source-related biomarker and isotope ratios identifies six oil tribes.
Anoxic Upper Miocene (M.-U. Puente) marl source rock generated tribe 3 west of NIFZ.

Anoxic Mohnian (?) marl generated tribe 4 west of NIFZ.

Anoxic M.-U. Miocene (L. Puente “nodular shale”) marl with significant terrigenous plant input generated tribe 5 southwest of NIFZ.

Anoxic M.-U. Miocene (L. Modelo “nodular shale”) marl with significant terrigenous plant input generated tribe 6 at low maturity northwest of NIFZ.

Conclusions
Six genetically distinct Miocene petroleum systems (12 families) occur in different parts of the Los Angeles basin. The Newport-Inglettwood Fault Zone separates tribes 1-2 (families 11-12, 13, 21-22) to the east from tribes 3-6 (families 31-33, 41-42, 5, 6) to the west. Chemometric analysis of biomarker and isotope ratios and distinct stratigraphic occurrence help identify the source rock for each family. Oil families in the Los Angeles basin retain the geochemical fingerprint of the vertical and lateral organofacies variations in their source rocks.

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References


Peters, K.E. et al., 2013. Chemometric differentiation of crude oil families in the San Joaquin Basin, California. AAPG Bulletin97, 103-143.


In summary, geochemistry and stratigraphy of the oil families suggest the following source rocks:

Suboxic Upper Miocene (Delmontian) shale with significant angiosperm input generated tribes 1-2 in the Central Trough east of NIFZ.