REVISED GENETIC DIAGRAMS FOR NATURAL GASES BASED ON A GLOBAL DATASET OF 15,000+ GAS SAMPLES

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Petroleum geochemists routinely analyse molecular and isotopic composition of gaseous hydrocarbons to interpret their origin (microbial vs. thermogenic), maturity and alteration. Such interpretations are primarily based on genetic diagrams using stable C and H isotope composition of methane (CH_4) and molecular ratios, i.e., $\delta^{13}C$ of CH_4 vs $CH_4/(C_2H_6+C_3H_8)$ (Bernard et al., 1977) and $\delta^{13}C$ of CH_4 vs $\delta^{2}H$ of CH_4 (Schoell, 1983 and Whiticar et al., 1986). However, thousands of natural gas samples were collected from conventional and unconventional petroleum reservoirs and analysed after these genetic diagrams were published (Fig. 1). As more gas data became available, including those from surface gas seeps and samples from igneous rocks, some researchers attempted to modify the genetic fields to better characterize the origin and alteration of natural gases. For example, Milkov (2011) introduced genetic fields to identify secondary microbial gas, and Etiope and Sherwood Lollar (2013) expanded the genetic field of abiotic gas. We suggest that genetic diagrams should be further revised using a larger global dataset of natural gases to encompass the entire variety of natural gas compositions and origins known to date.

We compiled a global dataset of more than 15,000 gas samples using >400 published papers and reports as well as publicly available government databases. Using this dataset, we revised the genetic fields of biotic (primary microbial, secondary microbial and thermogenic) and abiotic gases. We proposed the genetic field for gases affected by Thermal Sulphate Reduction. We also found that gases originating from Type II and Type III kerogen overlap on the "Bernard" plot and cannot be reliably distinguished.

References

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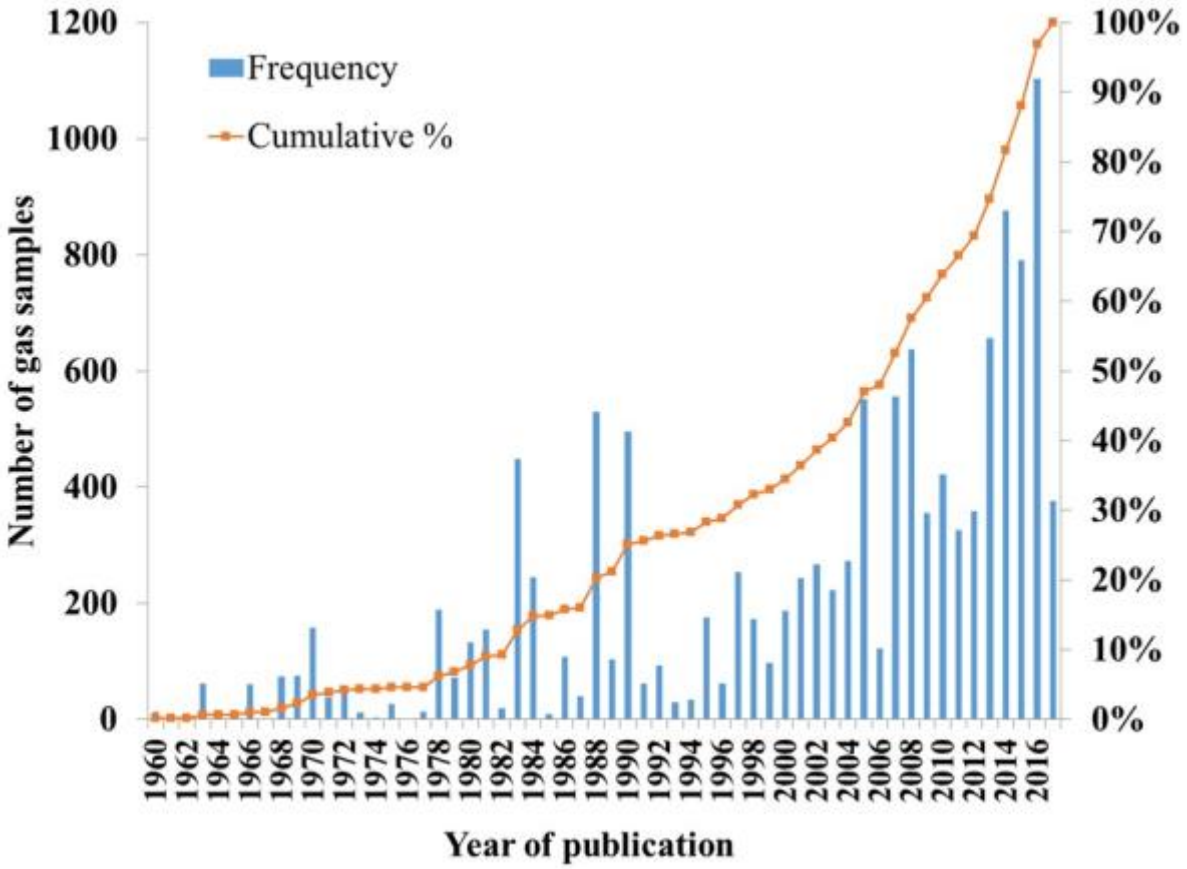

Figure 1 *Number of reservoir gas samples for which molecular and/or isotopic composition data were published each year since 1960. Note that data for about 85% of all samples were published after the genetic diagrams of Bernard et al. (1977), Schoell (1983) and Whiticar et al. (1986) were proposed. Data for 2017 are incomplete.*