Exploring the microbial fingerprint of corrosion

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Abstract

There was a great evolution in the studies of microbial corrosion for more than twenty years. The scientific community took about 30 years from the beginning of the last Century to reach the first rigorous (electrochemical) explanation of why some bacteria induce fast steel corrosion. Hence, a half-century more was spent to reach a general agreement on the effect of biofilm in changing the electrochemical condition of metal surfaces, and electrochemical sensors to monitor biofilm were developed (it occurred in 80'-90' years particularly) [1]. Investigations of electroactive biofilm later diffused worldwide, in-field and in labs. Those studies permitted sharing the amazing discovery that living organisms "electrically" (electrochemically) communicate with conductive, wet surfaces similary all over the world [2]. Next Generation Sequencing (NGS) tools, nowadays, allowed for documenting the rich pool of uncultivable bacteria and archaea populating the biofilm of in-field MIC cases [3]. Nonetheless, a clear correlation between the presence of specific groups (such as species, orders, genera) and corrosion risk in industrial settings was rarely convincingly demonstrated. This was mainly because the same organisms were also found in scenarios without corrosion and different microorganisms were most often found in other corroded scenarios.

Based on the assumptions that a complex pool of microorganisms, rather than single components of it, can represent dangerous, uncontrollable, condition for MIC, the microbial pool sequenced on five different materials (pure copper, brass, pure iron, carbon steel and stainless steel) treated for fifteen days in the same inoculum (enriched idrogenothrofic archaea and bacteria) are here compared. Results shows a significant statistical difference correlated to the the microbial pool and the materials. This

difference reflected a different corrosion behaviour of each analyzed material detected by impedance spectroscopy analyses.

Keywords Microbial corrosion, Next generation sequencing, RNA 16S, impedance spectroscopy analyses, EIS

References

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