Spatial comparison of total vs. active bacterial populations by coupling genetic fingerprinting and clone library analysises in the NW Mediterranean Sea (2009).

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Spatial distributions of both total (i.e. 16S rDNA-based fingerprints) and active (i.e. 16S rRNA-based fingerprints) bacterial populations, together with total bacterial activity measured by ^{3}H-leucine incorporation, were studied along a 98 km transect in the NW Mediterranean Sea. Capillary electrophoresis-single strand conformation polymorphism (CE-SSCP) fingerprinting was coupled to a clone library, allowing CE-SSCP peaks identification and the monitoring of the spatial variation of bacterial phylotypes. Up to 80% of the community peaks matched those obtained from clone library sequences, accounting for 86.7% of the total fingerprinting area. A good agreement was found between the relative abundance of *Prochlorococcus* in the CE-SSCP fingerprints and flow cytometry counts (r^2=0.66, P<0.05). The largest differences between total and active bacterial populations distribution were found at depths with higher bacterial activity (i.e. surface and deep chlorophyll maximum, DCM). SAR11 at the surface and *Gammaproteobacteria* at the DCM were the most abundant groups on the 16S rDNA-based fingerprints. However, their ratio of relative importance between rRNA : rDNA was <1 in most cases. Conversely, ratios observed for *Prochlorococcus*, were consistently >1 both at the surface and at the DCM. These results emphasize the need for combining rDNA- and rRNA-based analyses to better understand the functional role of individual bacterial populations *in situ*.