Leptospirosis is a worldwide zoonosis caused by a spirochete that belongs to the genus Leptospira. In the last years, new methods, such as the PCR-based multiple-locus variable-number tandem repeat analysis (MLVA), have been developed for the genotyping of leptospires. In the present work, the MLVA patterns for all reference strains used in Argentina for bovine, ovine, porcine, equine, caprine and canine leptospirosis diagnosis, as well as in human and wild animal diagnosis, were obtained. MLVA results are presented in such a way that they can be readily used for the identification of these strains by the simple and direct comparison of agarose gels. Making the use and interpretation of the MLVA for leptospires typing easier will help increase the use of this method as a routine procedure for human and animal diagnosis, for epidemiological studies, vaccine control and other applications.

Keywords
Leptospira interrogans, Leptospira kirschneri, Leptospira borgpetersenii, Reference strains, MLVA, VNTR, Genotyping.