73%. Clinical and laboratory diagnosis: 100% splenomegaly, 91,6% hepatomegaly, 90% thrombocytopenia, 70% anemia, 37% leukopenia, 27% bone involvement. Enzyme replacement therapy with Imiglucerase in 5 patients and follow-up with ERT after 3.7 years. All patients achieved therapeutic targets (TTs). **Conclusion:** The achievement of TT at 3.7 years is high, demonstrating the efficiency of the ERT with Imiglucerase. The main difficulties are subdiagnoses as well as late diagnoses and a low percentage of patients receiving ERT.

051 - Gene Therapy for Morquio: Advances in the Development of Viral Vectors

C. J. Almeciga-Diaz[1], R. Cuaspa[1], J. Herrera[1], H. Barbosa[1], and L. A. Barrera[1]

[1]Instituto de Errores Innatos del Metabolismo, Facultad de Ciencias, Pontificia Universidad Javeriana, Bogotá DC, Colombia

Introduction: Morquio A disease is produced by the deficiency of the lysosomal enzyme N-acetylgalactosamine-6-sulfate sulfatase (GALNS). Previously, we reported the use of adeno-associated virus (AAV) vectors as tools to mediate GALNS gene delivery. In addition, the cotransduction with SUMF1, using separated vectors, significantly increased GALNS activity. **Objective:** In this study, we evaluated a new set of AAV vectors carrying both GALNS and SUMF1 complementary DNA (cDNA) into the same vector. **Methodology:** The AAV vectors expressing GALNS and SUMF1 were built using a viral (encephalomyocarditis virus) or human (nuclear respiratory factor) internal ribosome entry site (IRES) element. Furthermore, for the first time, lentiviral vectors carrying GALNS or SUMF1 cDNA were also evaluated. All vectors were assessed using HEK293 cells and Morquio A human skin fibroblasts. **Results:** The AAV vectors with SUMF1-IRES-GALNS configuration induced higher enzyme activity compared with cells cotransduced with AAV-GALNS and AAV-SUMF1 vectors. On the other hand, the use of lentiviral vectors increased up to 100 times the enzyme activity in comparison with the levels observed with AAV vectors. Possible therapeutic effect was evaluated in Morquio A fibroblast by measuring total Î²-hexosaminidase levels that were reduced after transduction with AAV-IRES and lentiviral vectors. **Conclusion:** These results show the potential use of this new set of vectors, especially lentiviral vectors, for the development of a gene therapy for Morquio A.

052 - Genetic Defects in the Liver Phosphorylase System in Argentine Patients: Nosological Definition Through a Strategy of Enzymatic and Molecular Analysis

C. J. Angaroni[1], A. N. Giner-Ayala[1], A. L. Castillo[1], V. Lanza[1], A. E. Paschini-Capra[1], and R. Dodelson de Kremer[1]

[1]Centro de Estudios de las Metabolopatías Congénitas (CEMECO), Hospital de Niños de la Santísima Trinidad, Facultad de Ciencias Médicas, UNC, Córdoba, Argentina

Phosphorylase and phosphorylase-b kinase (PHK) deficiencies in liver constitute the phosphorylase system defects (PSD), leading to glycogenosis Type VI (GSD-VI) and Type IX (GSD-IX), respectively. Hepatic phosphorylase is encoded by PYGL gene. The GSD-IX is caused by a genetic defect in one of the hepatic PHK subunits encoded by PHKA2, PHKG2, and PHKB genes, respectively. X-linked PHK deficiency (PHKA2 gene) presents 2 enzymatic variants, XLG1 (reduced in liver and erythrocytes) and XLG2 (only decreased in liver). The aim of this work is to nosologically define PSD taking into account patients' gender, PHK activity in erythrocytes, and molecular analysis of PYGL gene. In all, 2 women and 16 men (14 unrelated families) were studied. The PHK activity in erythrocytes was deficient in 14 male patients and was normal in 2 male probands (still without diagnostic definition) and in 2 women. In the latter, molecular analysis of PYGL gene identified 2 novel missense mutations: p.Gly233Ser and p.Gly686Arg and IVS15-2delA polymorphism. Allele frequency of P.Gly686Arg was 75%. In silico studies predict that both new mutations would affect enzyme functionality. This study allowed accurate diagnosis of GSD-VI (2/2) and GSD-IX (14/16). Molecular analysis of PHKA2 gene, responsible for X-linked EAG-IX, is currently in progress in our center. This research represents a continuation of the project for exact definition of PSD, a largely unknown area in our country.

053 - Geographic Distribution of Mucopolysaccharidosis Type VI in the Center of the Department of Cauca: Is It Possibly a Founder Effect?

H. Pachajoa[1], Y. Ariza[1], V. Villota[1], M. E. Miño[2], and M. A. Acosta-Aragon[3]

[1]Centro de Investigaciones Congénitas y Enfermedades Raras, Universidad Icesi, Cali, Colombia
[2]Hospital Universitario San José, Popayán, Facultad de Ciencias de la Salud, Universidad del Cauca, Cauca, Colombia
[3]Departamento de Pediatría, Facultad de Ciencias de la Salud, Universidad del Cauca, Popayán, Cauca, Colombia

Introduction: Mucopolysaccharidosis VI (MPS VI) is an autosomal recessive genetic disease caused by deficiency of the enzyme arylsulfatase. **Methodology:** Cross-sectional study, based on records review from patients attending Hospital Universitario San José de Popayan (Cauca, Colombia). Informed consent was obtained prior to medical history reviews, and interviews were performed in order to document the current geographical location and ancestors in 3 generations. Period prevalences were estimated for each municipality, and spatial aggregation of cases was analyzed according ancestor origin. Estimated prevalence was compared with hypothetical proposed by the literature, using the statistical program Stata12.