



Category: Clinical Genomics

# High-throughput genetic analysis in a cohort of patients with Ocular Developmental Anomalies

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## Abstract

Anophthalmia and microphthalmia (A/M) are developmental ocular malformations in which the eye fails to form or is smaller than normal with both genetic and environmental etiology. Microphthalmia is often associated with additional ocular anomalies, most commonly coloboma or cataract [1, 2]. A/M has a combined incidence between 1-3.2 cases per 10,000 live births in Caucasians [3, 4]. The spectrum of genetic abnormalities (chromosomal and molecular) associated with these ocular developmental defects are being investigated in the current study. A detailed pedigree analysis and ophthalmic examination have been documented for the enrolled patients followed by blood collection and DNA extraction. The strategies for genetic analysis included chromosomal analysis by conventional and array based (affymetrix cytoscan HD array) methods, targeted re-sequencing of the candidate genes and whole exome sequencing (WES) in Illumina HiSEQ 2500. WES was done in families excluded for mutations in candidate genes. Twenty four samples (Microphthalmia (M)-5, Anophthalmia (A)-7, Coloboma-2, M&A-1, microphthalmia and coloboma / other ocular features-9) were initially analyzed using conventional Geimsa Trypsin Geimsa banding of which 4 samples revealed gross chromosomal aberrations (deletions in 3q26.3-28, 11p13 (N=2) and 11q23 regions). Targeted re sequencing of candidate genes showed mutations in *CHX10*, *PAX6*, *FOXE3*, *ABCB6* and *SHH* genes in 6 samples. High throughput array based chromosomal analysis revealed aberrations in 4 samples (17q21dup (n=2), 8p11del (n=2)). Overall, genetic alterations in known candidate genes are seen in 50% of the study subjects. Whole exome sequencing was performed in samples that were excluded for mutations in candidate genes and the results are discussed.

## References

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