

Precision medicine in CRSwNP

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CRS is one of most commonly diagnosed diseases of the upper airway. Ongoing research is focused on improving biomarkers for diagnosis, prognosis, and personalized optimal therapy. The determination of the inflammatory patterns of CRSwNP will not only define the characteristics of mucosal inflammation in subgroups of CRSwNP and improve understanding the pathophysiological mechanism, but also identify the treatment strategies. Understanding the pathogenesis of CRSwNP should identify novel predictive biomarkers of treatment responses. We have identified cellular phenotypes of CRSwNP using cluster analysis and defined an algorithm for different clusters associated with polyp recurrence. Five phenotypic clusters were identified. Clusters 1 and 2 were plasma cell-dominant and lymphocyte-dominant phenotypes, respectively. Cluster 3 revealed a mixed inflammatory pattern. Cluster 4 was characterized by infiltration of predominantly neutrophils. Cluster 5 was characterized by a marked tissue eosinophilia and highest recurrence rate of 98.5%. The clinical algorithm predicted clustering with 93.7% accuracy. Chinese CRSwNP patients may be classified into five phenotypes with different polyp recurrence rates, based on the presence of predominantly plasma cells, lymphocytes, neutrophils, eosinophils or mixed inflammatory cells in polyps.