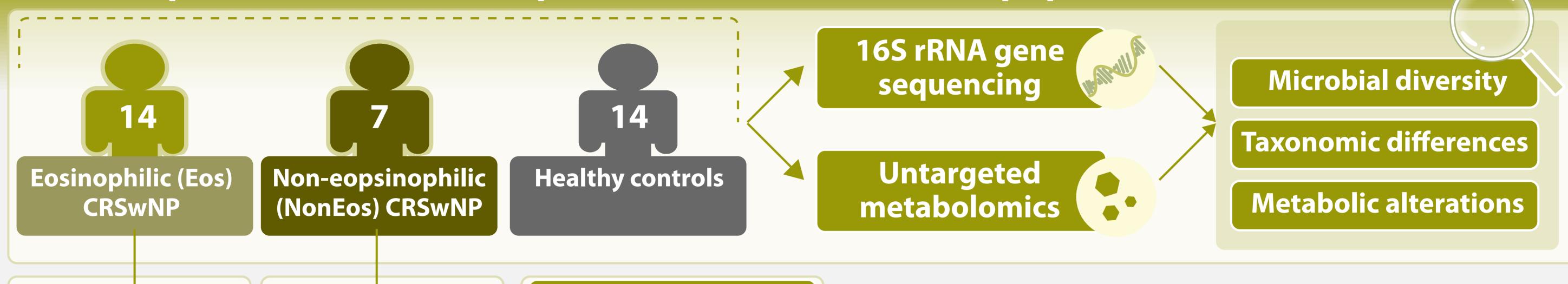
Integrated omics-based analysis reveals distinct microbial-metabolite interaction networks in eosinophilic and non-eosinophilic CRSwNP in a Chinese population

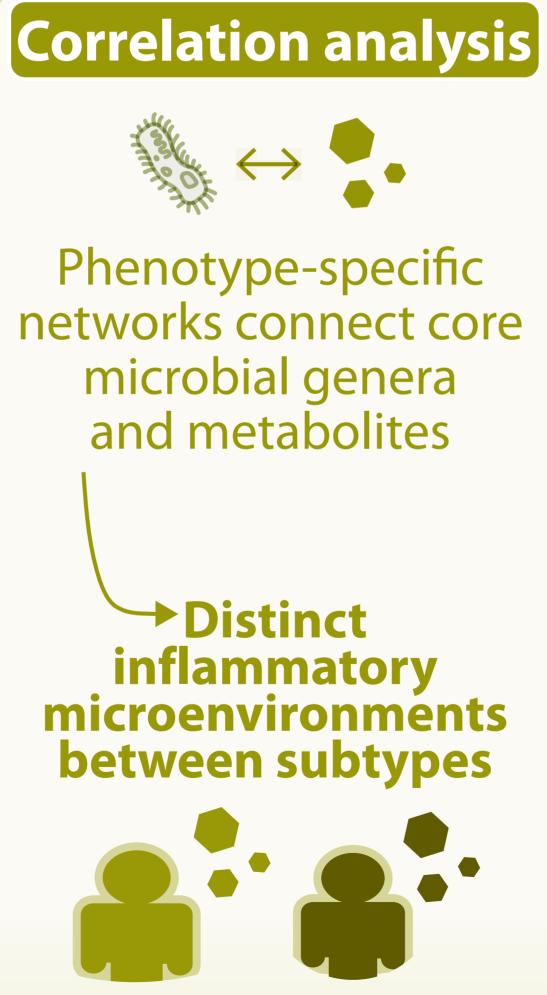


Microbial diversity Staphylococcus †† Corynebacterium Fumaric acid † Linoleic acid **↑↑ Arachidonic acid** Linked to oxidative stress lipid-mediated

inflammation

Zhang H, Zi X, Li X, et al.

Microbial diversity † Streptococcus † Anaerococcus Clostridium XIVa † Glutamine **††** Taurine **††** Ethanolamine phosphate Shifts in amino acid and nitrate metabolism



 Divergent microbial and metabolic signatures in Eos and nonEos CRSwNP Mechanistic insights into subtype-specific May guide disease processes and therapeutic



targeted diagnostic

development of

strategies