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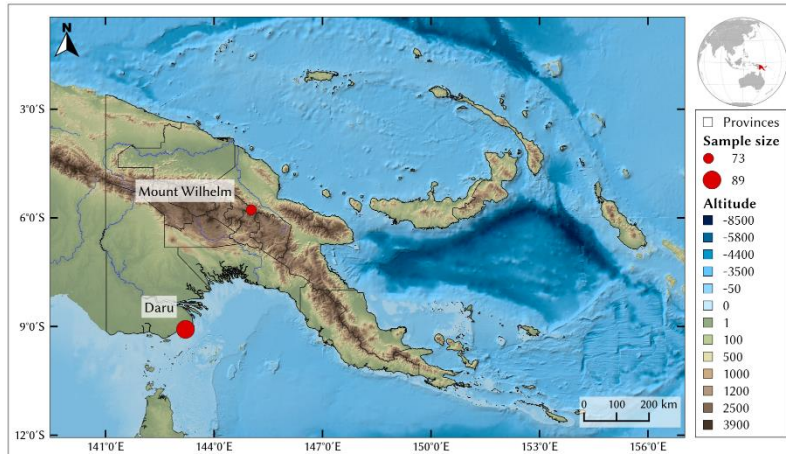
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Research background

The Papua New Guinean (PNG) highlands are inhabited by almost 3 million individuals ([Bourke & Allen, 2021](#)).

Despite population settlement of over 2,000m a.s.l. for at least 20 000 years ([Summerhayes et al., 2010](#)), PNG highlanders remain understudied regarding adaptation to altitude compared with other well documented high-altitude populations (e.g., Tibetans, Andeans, and Ethiopian Amharas).



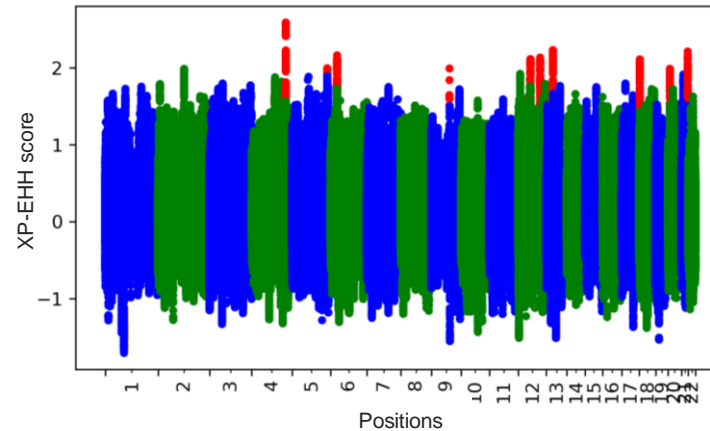
Map of the sampling places

Sébastien Plutniak/QGIS 3.14.16. Projection: EPSG 4326.

We have previously shown that PNG highlanders differ from PNG lowlanders for six phenotypes ([André et al., 2021](#)).

Aims: To explore the hypothesis that these differences might result from positive selection to altitude and looked for associations between signatures of positive selection in PNG highlanders and these phenotypes.

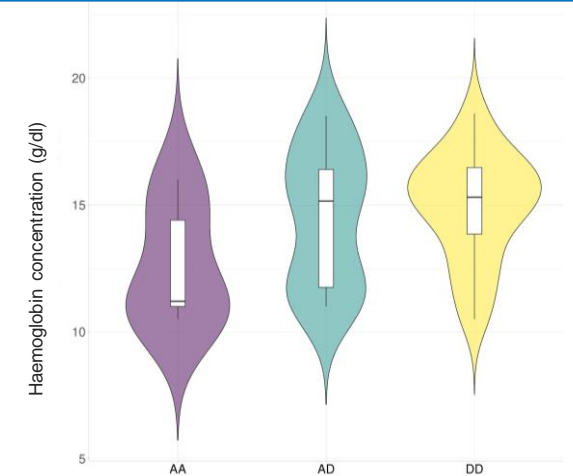
Are genomic regions under selective sweep ?



We looked for selective sweep to restrict the genome to regions most likely to host the selected variants. We computed the Cross Population Extended Haplotype Homozygosity score (XP-EHH) ([Sabeti et al. 2007](#)) of Papua New Guinean highlanders (n=49) in comparison with Papua New Guinean lowlanders (n=78).

Results: We selected the 10 top regions with the highest XPEHH score to continue the analyses.

Which SNPs drive selection ?



Haemoglobin concentration in PNG Highlanders
Comparison between genotypes

We used CLUES - an approximate full-likelihood method for inferring selection and allele frequency trajectories - ([Stern et al., 2019](#)) on each SNP in each region of interest. We then looked for associations between the SNPs the most likely to be selected and the phenotypes we have previously studied.

Results: We found several SNPs associated with haemoglobin concentration and ventilatory capacities.

Conclusion: SNPs under positive selection in PNG highlanders are associated with phenotypes that may benefit life at altitude.