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SRAP finger printings to highlight intra and interpopulation genetic diversity in *Sulla coronaria* and *Sulla spinosissima*

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The *Sulla* genus groups six wild species originated essentially in the western Mediterranean basin. As the forages leguminous, these species present many advantages principally their high nutritive value and their good soil protection and enrichment due to extensive rhizobium. These species are well adapted to large bioclimatic conditions varying from humid to arid areas. Among these species, we have been interested particularly to two ones. These are the allogamous and only cultivated species *S. coronaria* and the autogamous and spontaneous *S. spinosissima*.The use of molecular markers is an effective way to evaluate genetic variation because they are not affected by the environment. The chosen markers in this study are the Sequence-related amplified polymorphism (SRAP) markers. The usedSRAP primer combinations exhibited high polymorphism that was demonstrated by various indices of diversity calculated by both POPGENE version 3.2 and Genalex software version 6.5. The analysis of molecular variance (AMOVA) was used to partition the total SRAP variation into within population and between populations. Variance components and the sum of all the squared differences were calculated. Moreover, the systematics of the *Sulla* genus was elucidated using the standardized Jaccard's Distance Index. The matrix was subjected to a cluster analysis via the DARWIN Software. In conclusions, the use of these markers allowed us to estimate the genetic diversity and then to improve the adaptability of the crops in the Mediterranean soils. SRAP markers could also be anchored to virtual linkage groups and then used for gene mapping.

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Incidence of severe malaria syndromes and status of immune responses among Khat chewer malaria patients in Ethiopia

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Although more emphasis has been given to the genetic and environmental factors that determine host vulnerability to malaria, other factors that might have a crucial role in burdening the disease have not been evaluated yet. Therefore, this study was designed to assess the effect of Khat chewing on the incidence of severe malaria syndromes and immune responses during malaria infection in an area where the two problems co-exist. Clinical, physical, demographic, hematological, biochemical and immunological data were collected from *Plasmodium falciparum* mono-infected malaria patients (age ≥ 10 years) seeking medication in Halaba Kulito and Jimma Health Centers. In addition, incidences of severe malaria symptoms were assessed. The data were analyzed using SPSS (version 20) software. Prevalence of current Khat chewer malaria patients was 57.38% (95%CI =53-61.56%). Malaria symptoms such as hyperpyrexia, prostration and hyperparasitemia were significantly lower ($P<0.05$) among Khat chewer malaria patients. However, relative risk to jaundice and renal failure were significantly higher ($P<0.05$) in Khat chewers than in non-Khat chewer malaria patients. Longer duration of Khat use was positively associated with incidence of anemia. IgM and IgG antibody titers were significantly higher ($P<0.05$) among Khat chewer malaria patients than among malaria positive non-chewers. Although levels of IgG subclasses in malaria patients did not show significant differences ($P>0.05$), IgG3 antibody was significantly higher ($P<0.001$) among Khat chewer malaria patients. Moreover, IgM, IgG, IgG1and IgG3 antibodies had significant negative association ($P<0.001$) with parasite burden and clinical manifestations of severe malaria symptoms, but not with severe anemia and hypoglycemia. Additionally, a significant increment ($P<0.05$) in CD4+ T-lymphocyte population was observed among Khat users. Khat might be an important risk factor for incidence of some severe malaria complications. Nevertheless, it can enhance induction of humoral immune response and $CD4^+$ T-lymphocyte population during malaria infection. This calls for further investigation on the effect of Khat on parasite or antigen-specifc protective malaria immunity and analysis of cytokines released upon malaria infection among Khat chewers.

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