The potential for the application of genomic selection for small ruminants (SR) in developing countries

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The versatility of indigenous SR's to adapt to diverse agro-ecologies and production systems imply that they play a key role in sustaining livelihoods of (agro)-pastoralists and small holder farmers in many developing countries (DC). In most DC's, phenotypic and pedigree information remains problematic to collect, cohorts of contemporaries are often of inadequate size, breeding infrastructures are non-existent and advanced reproductive technologies are difficult to apply. These drawbacks can however be circumvented through community–based breeding programmes (CBBP) which can provide a framework to implement basic recording and design mating schemes. CBBP together with case-control protocols for use in genome-wide association analyses offer great opportunity for identifying genomic regions with major gene effects that could be used for genomic selection (GS) and/or introgression. The availability of genomic data can facilitate the implementation of GBLUP using genomic relationship matrices, determine breed composition and admixture in the absence of pedigree records, assessment of genetic diversity and structure, and the identification of genomic fingerprints of positive selection. Such data can provide a platform to design mating schemes that optimize productivity and adaptability in a diverse genepool of SR's and the development of suitable synthetic breeds. In the context of the CBBP, the propagation of alleles, underlying production and adaptation traits, via gene/genome/haplotype block editing could be combined with GS in the process of developing appropriate synthetic breeds that optimize productivity and adaptability.