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Impact of genomic selection on organisational structures in milk recording and breeding

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In the last decade genomic selection has become a standard tool in Holstein breeding in major dairy countries. Within this time period genomic breeding values (GEBV) based on bull reference populations have become the dominant base for selection within the breeding programs. Use of GEBV enables effective selection of young animals and thus generation interval in sire to son path has been significantly reduced from 6 to 2 years and the dam to son from 4 to 2 years, respectively.. Because of the genetic superiority of young AI bulls their market share in most countries is more than 50% some reaching 98%. In most European countries number of new AI bulls introduced to the market dropped by 50% or more compared to number of bulls in the former progeny-test program. These new opportunities have led to fewer Holstein breeding programs through mergers or acquisitions of organisations. So far milk performance testing organizations have been less affected by genomic selection. This may change with the current development of moving from the bull to cow or mixed reference populations mainly for the purpose of establishing genomic selection for new traits. On average, 3-8 reference cows (genotyped cow with phenotypic information) are as informative as one genotyped reference bull with phenotypic data of 100 (not genotyped) daughters included in traditional genetic evaluation. For an informative cow reference population, therefore, only a small proportion of all cows under milk recording would be needed. In parallel genotyping has become cheaper and a whole-herd genotyping as base for genomic herd management has become a new tool for commercial dairy herds. In future, the breeding programs may rely increasingly more on data from herds in the whole-herd genotyping program than the complete national milk recording program. Especially for new traits of economic importance these herds with genotyped cows will contribute the data on the new traits. Overall, these developments detangle the traditional strong link and synergy effects of breeding and nation wide milk recording. The very dynamic developments in on-farm data recording by sensors have the potential for further breaking down the traditional relationship between dairy farmers, DHI and breeding organizations. Data are collected on farm continuously by sensors and information for daily herd management is provided by apps from the sensor providers. For breeding or genomic herd management the dairy farmer is interested in GEBV of his animals. At the same time the breeding program and genomic evaluation system, could be interested in the sensor data for extending the reference population. Therefore, it is crucial for the future of DHI organizations to find its role in providing management services for farmers but at the same time be part of the collection of new phenotypes for selection. These developments may also change the traditional nation-wide genetic evaluation i.e. breeding structures. Relatively few well equipped (big) farms could provide sufficient reference cows for effective genomic evaluation. This could enable main players in the dairy breeding market establish an own genomic evaluation system apart from the national genomic evaluation